

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 14:31:32 ; Search time 0.001 Seconds
(without alignments)
6.042 Million cell updates/sec

Title: us-10-665-708-24
Perfect score: 19
Sequence: 1 gaacggaagccttcgg 19

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 0.5

Searched: 7 seqs, 159 residues

Total number of hits satisfying chosen parameters: 14

Minimum DB seq length: 18
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 7 summaries

Database : rni:db.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	1 US-09-738-274-24	Sequence 24, Appl
2	19	100.0	22	1 US-09-738-274-23	Sequence 23, Appl
3	18	94.7	24	1 US-09-738-274-22	Sequence 22, Appl
4	18	94.7	25	1 US-09-738-274-21	Sequence 21, Appl
5	16.4	86.3	23	1 US-08-485-602-56	Sequence 56, Appl
6	16.4	86.3	23	1 US-08-757-180-55	Sequence 55, Appl
7	16.4	86.3	23	1 US-08-745-638-56	Sequence 56, Appl

ALIGNMENTS

RESULT 1
US-09-738-274-24
; Sequence 24, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738, 274
; CURRENT FILING DATE: 2000-12-15
; PRIOR FILING DATE: 1999-12-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 24
; LENGTH: 19

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-24

Query Match 100.0%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCTTCGG 19
Db 1 GAACGGAAGCCTTCGG 19

RESULT 2

US-09-738-274-23
; Sequence 23, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738, 274
; CURRENT FILING DATE: 2000-12-15
; PRIOR FILING DATE: 1999-12-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 23
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-23

Query Match 100.0%; Score 19; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCTTCGG 19
Db 4 GAACGGAAGCCTTCGG 22

RESULT 3

US-09-738-274-22
; Sequence 22, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738, 274
; CURRENT FILING DATE: 2000-12-15
; PRIOR FILING DATE: 1999-12-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 22


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; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-738-274-22

Query Match          94.7%; Score 18; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCTTCG 18
Db 7 GAACGGAAGGCCTTCG 24

RESULT 4
US-09-738-274-21
; Sequence 21, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUGKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: ROBRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/112,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-738-274-21

Query Match          94.7%; Score 18; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCTTCG 18
Db 8 GAACGGAAGGCCTTCG 25

RESULT 5
US-08-485-602-56
; Sequence 56, Application US/08485602
; Patent No. 5712095
; GENERAL INFORMATION:
; APPLICANT: Britschgi, Theresa B.
; APPLICANT: Cangelosi, Gerard A.
; TITLE OF INVENTION: Rapid and Sensitive Detection of
; TITLE OF INVENTION: Antibiotic-Resistant Mycobacteria Using Oligonucleotide
; TITLE OF INVENTION: Probes Specific for Ribosomal RNA Precursors
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,602
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,068
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 11652-79-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: rRNA
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium intracellulare
; US-08-485-602-56

Query Match          86.3%; Score 16.4; DB 1; Length 23;
Best Local Similarity 78.9%; Pred. No. 3;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCTTCG 19
Db 1 GAACGGAAGGCCTTCG 19

RESULT 6
US-08-757-180-55
; Sequence 55, Application US/08757180
; Patent No. 5726021
; GENERAL INFORMATION:
; APPLICANT: Britschgi, Theresa B.
; APPLICANT: Cangelosi, Gerard A.
; TITLE OF INVENTION: RAPID LYSIS METHODS FOR RELEASING INTACT
; TITLE OF INVENTION: RIBOSOMAL RNA PRECURSORS FROM MYCOBACTERIUM
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,180
; FILING DATE: 27-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,068
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hsi, Petrina S.
; REGISTRATION NUMBER: 38,496
; REFERENCE/DOCKET NUMBER: BD3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
```

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Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GAACGGAAGGCCCTTTCGG 19
    |||||
Db 1 GAACGGAAGGCCCTTTCGG 19
    |||||

Search completed: May 26, 2006, 14:31:32
Job time : 0.001 secs

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 14:30:45 ; Search time 0.001 Seconds
(without alignments)
12.768 Million cell updates/sec

Title: us-10-665-708-24
Perfect score: 19
Sequence: 1 gaacggaaggccttcgg 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 15 seqs, 336 residues

Total number of hits satisfying chosen parameters: 30

Minimum DB seq length: 18
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 15 summaries

Database : rngdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	1 AAD11274	Mycobacterium 16S
2	19	100.0	19	1 ADG88355	Mycobacterium ampl
3	19	100.0	19	1 AEA08230	Mycobacterium xeno
4	19	100.0	22	1 AAD11273	Mycobacterium 16S
5	19	100.0	22	1 ADG88354	Mycobacterium ampl
6	19	100.0	22	1 AEA08229	Mycobacterium cela
7	18	94.7	24	1 AAD11272	Mycobacterium 16S
8	18	94.7	24	1 ADG88353	Mycobacterium ampl
9	18	94.7	24	1 AEA08228	Mycobacterium cela
10	18	94.7	25	1 AAD11271	Mycobacterium 16S
11	18	94.7	25	1 ADG88352	Mycobacterium ampl
12	18	94.7	25	1 AEA08227	Mycobacterium cela
13	16.4	86.3	23	1 AAV24413	Target sequence #2
14	16.4	86.3	23	1 AAV13021	Mycobacterium intr
15	14	73.7	20	1 AAT75816	Corynebacterium pr

ALIGNMENTS

RESULT 1
AAD11274
ID AAD11274 standard; DNA; 19 BP.
XX
AC AAD11274;
XX
DT 24-SEP-2001 (first entry)
XX
DE Mycobacterium 16S rRNA amplifying primer #18.
XX
KW Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
XX Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.

OS Mycobacterium sp.
XX WO200144510-A2.
PN
XX 21-JUN-2001.
PD
XX 17-DEC-1999; 99WO-US030346.
PF
XX 17-DEC-1999; 99WO-US030346.
PR
XX (GENP) GEN-PROBE INC.
PA (IMM) BIOMERIEUX SA.
XX
PI Brentano/ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2001-398170/42.
DR
XX
XX Detecting Mycobacterium species, involves in vitro amplification of 16S
PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using
PT specific primers, and detecting the amplified nucleic acid.
XX
XX Claim 1; Page 36; 44pp; English.
XX
XX The invention relates to a method of detecting Mycobacterium species,
CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture
CC comprising a polymerase, and at least two primers, and then detecting the
CC amplified nucleic acid. The method is relatively simple and useful for
CC detecting the presence of various Mycobacterium species in a biological
CC sample, and thus important for diagnosis of infections resulting from
CC them. The method is especially important for screening opportunistic
CC infections caused by M. tuberculosis or a Mycobacterium other than
CC tuberculosis (MOTT). The present sequence is a PCR primer used for
CC amplifying Mycobacterium 16S rRNA
XX
SQ Sequence 19 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTCGG 19
DB 1 GAACGGAAGGCTTCGG 19

RESULT 2
ADG88355
ID ADG88355 standard; DNA; 19 BP.
XX
AC ADG88355;
XX
XX 11-MAR-2004 (first entry)
DT
XX Mycobacterium amplifying PCR primer #24.
DE
XX In vitro amplification; PCR; primer; ss.
KW
XX Mycobacterium xenopi.
OS
XX US2003165824-A1.
PN
XX 04-SEP-2003.
PD
XX
XX 15-DEC-2000; 2000US-00738274.
PF
XX 17-DEC-1999; 99US-0172190P.
PR
XX (BREN) BRENTANO S T.
PA (JUCK) JUCKER M T.
XX
PA (DELG) DELGADO-F D.
XX (CLEU) CLEUZIAZ P.
PA (RODR) RODRIGUE M.

XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
DR WPI; 2003-898044/82.
XX
XX
PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample comprises performing in vitro nucleic acid
PT amplification and detection of amplified products.
XX
PS Claim 1; SEQ ID NO 24; 20pp; English.
XX
XX The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample comprises performing an in vitro
CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
CC detecting the amplified Mycobacterium nucleic acid. The present sequence
CC is Mycobacterium amplifying PCR primer.
XX
SQ Sequence 19 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 19; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 3.5;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GAACGGAAGGCTTTTCGG 19
Db 1 GAACGGAAGGCTTTTCGG 19
XX
RESULT 3
AEA08230
ID AEA08230 standard; DNA; 19 BP.
XX
AC AEA08230;
XX
DT 14-JUL-2005 (first entry)
XX
DE Mycobacterium xenopi 16S rRNA amplifying non-T7 primer, SEQ ID NO: 24.
XX
KW DNA amplification; microorganism detection; 16S ribosomal RNA; 16S rRNA;
KW PCR; primer; ss.
XX
OS Mycobacterium xenopi; ATCC 19250.
PN
PN US2005100915-A1.
XX
XX 12-MAY-2005.
XX
PF 18-SEP-2003; 2003US-00665708.
XX
PR 17-DEC-1999; 99US-0172190P.
PR 15-DEC-2000; 2000US-00738274.
XX
PA (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZAT P.
PA (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
XX WPI; 2005-345392/35.
XX
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample, comprises using in vitro nucleic acid
PT amplification and detection of amplified products.
XX
PS Claim 1; SEQ ID NO 24; 21pp; English.
XX
XX The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample. The method involves using in
CC vitro nucleic acid amplification and detection of amplified products. The
CC invention is useful for diagnostic detection of pathogenic bacteria such
CC as Mycobacterium species. The present sequence is the Mycobacterium

CC xenopi (ATCC 19250) 16S ribosomal RNA (16S-rRNA) amplifying non-T7 PCR
CC primer.
XX
SQ Sequence 19 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 19; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 3.5;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GAACGGAAGGCTTTTCGG 19
Db 1 GAACGGAAGGCTTTTCGG 19
XX
RESULT 4
AAD11273
ID AAD11273 standard; DNA; 22 BP.
XX
AC AAD11273;
XX
DT 24-SEP-2001 (first entry)
XX
DE Mycobacterium 16S rRNA amplifying primer #17.
XX
KW Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
KW Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
XX
OS Mycobacterium sp.
PN
PN WO200144510-A2.
XX
PD 21-JUN-2001.
XX
PF 17-DEC-1999; 99WO-US030346.
XX
PR 17-DEC-1999; 99WO-US030346.
XX
PA (GENP-) GEN-PROBE INC.
PA (INNR) BIOMERIEUX SA.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
XX WPI; 2001-398170/42.
XX
XX Detecting Mycobacterium species, involves in vitro amplification of 16S
PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using
PT specific primers, and detecting the amplified nucleic acid.
XX
PS Claim 1; Page 36; 44pp; English.
XX
XX The invention relates to a method of detecting Mycobacterium species,
CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture
CC comprising a polymerase, and at least two primers, and then detecting the
CC amplified nucleic acid. The method is relatively simple and useful for
CC detecting the presence of various Mycobacterium species in a biological
CC sample, and thus important for diagnosis of infections resulting from
CC them. The method is especially important for screening opportunistic
CC infections caused by M. tuberculosis or a Mycobacterium other than
CC tuberculosis (MOTT). The present sequence is a PCR primer used for
CC amplifying Mycobacterium 16S rRNA
XX
SQ Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 19; DB 1; Length 22;
XX Best Local Similarity 100.0%; Pred. No. 3;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GAACGGAAGGCTTTTCGG 19
Db 4 GAACGGAAGGCTTTTCGG 22

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RESULT 5
ADG88354
ID ADG88354 standard; DNA; 22 BP.
XX AC ADG88354;
XX DT 11-MAR-2004 (first entry)
XX DE Mycobacterium amplifying PCR primer #23.
XX KW In vitro amplification; PCR; primer; ss.
XX OS Mycobacterium celatum.
XX PN US2003165824-A1.
XX PD 04-SEP-2003.
XX PF 15-DEC-2000; 2000US-00738274.
XX PR 17-DEC-1999; 99US-0172190P.
XX PA (BREN/) BRENTANO S T.
XX PA (JUCK/) JUCKER M T.
XX PA (DELG/) DELGADO F D.
XX PA (CLEU/) CLEUZIAT P.
XX PA (RODR/) RODRIGUE M.
XX PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI-2003-898044/82.
XX
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX in a biological sample comprises performing in vitro nucleic acid
XX amplification and detection of amplified products.
XX
XX Claim 1; SEQ ID NO 23; 20pp; English.
XX
XX The present invention relates to a method of detecting Mycobacterium
XX species present in a biological sample. The method involves using in
XX vitro nucleic acid amplification and detection of amplified products.
XX CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
XX detecting the amplified Mycobacterium nucleic acid. The present sequence
XX is Mycobacterium amplifying PCR primer.
XX
XX Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 19; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTCGG 19
Db 4 GAACGGAAGGCGCTTCGG 22
|||||
RESULT 6
AEA08229
ID AEA08229 standard; DNA; 22 BP.
XX AC AEA08229;
XX DT 14-JUL-2005 (first entry)
XX DE Mycobacterium celatum 16S rRNA amplifying non-T7 primer, SEQ ID NO: 23.
XX KW Microorganism detection; DNA amplification; 16S ribosomal RNA; 16S rRNA;
XX KW PCR; primer; ss.
XX OS Mycobacterium celatum.
XX PN US2005100915-A1.
XX PD 12-MAY-2005.

Query Match 100.0%; Score 19; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTCGG 19
Db 4 GAACGGAAGGCGCTTCGG 22
|||||
RESULT 7
AAD11272
ID AAD11272 standard; DNA; 24 BP.
XX AC AAD11272;
XX DT 24-SEP-2001 (first entry)
XX DE Mycobacterium 16S rRNA amplifying primer #16.
XX KW Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
XX KW Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
XX OS Mycobacterium sp.
XX PN WO200144510-A2.
XX PD 21-JUN-2001.
XX PF 17-DEC-1999; 99WO-US030346.
XX PR 17-DEC-1999; 99WO-US030346.
XX PA (GENP-) GEN-PROBE INC.
XX PA (ENMR-) BIOMERIEUX SA.
XX PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI-2004-398170/42.
XX
XX Detecting Mycobacterium species, involves in vitro amplification of 16S
XX rRNA or DNA encoding RNA in nucleic acid amplification mixture using

```

PT specific primers, and detecting the amplified nucleic acid.

PS Claim 1; Page 36; 4pp; English.

XX The invention relates to a method of detecting Mycobacterium species, CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture CC comprising a polymerase, and at least two primers, and then detecting the CC amplified nucleic acid. The method is relatively simple and useful for CC detecting the presence of various Mycobacterium species in a biological CC sample, and thus important for diagnosis of infections resulting from CC them. The method is especially important for screening opportunistic CC infections caused by M. tuberculosis or a Mycobacterium other than CC tuberculosis (MOTT). The present sequence is a PCR primer used for CC amplifying Mycobacterium 16S rRNA

XX Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 94.7%; Score 18; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTTTCG 18
Db 7 GAACGGAAGGCTTTTCG 24

RESULT 8

ADG88353
ID ADG88353 standard; DNA; 24 BP.

AC ADG88353;

DT 11-MAR-2004 (first entry)

XX Mycobacterium amplifying PCR primer #22.

XX In vitro amplification; PCR; primer; ss.

XX Mycobacterium celatum.

XX US2003165824-A1.

PD 04-SEP-2003.

PF 15-DEC-2000; 2000US-00738274.

XX 17-DEC-1999; 99US-0172190P.

PA (BREN//) BRENTANO S T.

PA (JUCK//) JUCKER M T.

PA (DELG//) DELGADO F D.

PA (CLEU//) CLEUZIAT P.

PA (RODR//) RODRIGUE M.

XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;

XX WPI; 2003-898044/82.

XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
in a biological sample comprises performing in vitro nucleic acid
amplification and detection of amplified products.

PS Claim 1; SEQ ID NO 22; 20pp; English.

XX The present invention relates to a method of detecting Mycobacterium
species present in a biological sample comprises performing an in vitro
amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
detecting the amplified Mycobacterium nucleic acid. The present sequence
is Mycobacterium amplifying PCR primer.

XX Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 94.7%; Score 18; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTTTCG 18
Db 7 GAACGGAAGGCTTTTCG 24

RESULT 9

AEA08228

ID AEA08228 standard; DNA; 24 BP.

XX AEA08228;

DT 14-JUL-2005 (first entry)

XX Mycobacterium celatum 16S rRNA amplifying non-T7 primer, SEQ ID NO: 22.

XX Microorganism detection; DNA amplification; 16S ribosomal RNA; 16S rRNA;
PCR; primer; ss.

XX Mycobacterium celatum.

XX US2005100915-A1.

XX 12-MAY-2005.

XX 18-SEP-2003; 2003US-00665708.

XX 17-DEC-1999; 99US-0172190P.

XX 15-DEC-2000; 2000US-00738274.

XX (BREN//) BRENTANO S T.

XX (JUCK//) JUCKER M T.

XX (DELG//) DELGADO F D.

XX (CLEU//) CLEUZIAT P.

XX (RODR//) RODRIGUE M.

XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;

XX WPI; 2005-345392/35.

XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
in a biological sample, comprises using in vitro nucleic acid
amplification and detection of amplified products.

XX Claim 8; SEQ ID NO 22; 21pp; English.

XX The present invention relates to a method of detecting Mycobacterium
species present in a biological sample. The method involves using in
vitro nucleic acid amplification and detection of amplified products. The
invention is useful for diagnostic detection of pathogenic bacteria such
as Mycobacterium species. The present sequence is the Mycobacterium
celatum (ATCC 51130 and ATCC 51131) 16S ribosomal RNA (16SrRNA)
amplifying non-T7 PCR primer.

XX Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 94.7%; Score 18; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTTTCG 18
Db 7 GAACGGAAGGCTTTTCG 24

RESULT 10

AAD11271

ID AAD11271 standard; DNA; 25 BP.

XX AAD11271;

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XX 24-SEP-2001 (first entry)
XX Mycobacterium 16S rRNA amplifying primer #15.
XX Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
XX Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
XX Mycobacterium sp.
XX WO200144510-A2.
XX 21-JUN-2001.
XX 17-DEC-1999; 99WO-US030346.
XX 17-DEC-1999; 99WO-US030346.
XX (GENP-) GEN-PROBE INC.
XX (LINR-) BIOMERIEUX SA.
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2001-398170/42.
XX Detecting Mycobacterium species, involves in vitro amplification of 16S
XX rRNA or DNA encoding RNA in nucleic acid amplification mixture using
XX specific primers, and detecting the amplified nucleic acid.
XX Claim 1; Page 36; 44pp; English.
XX The invention relates to a method of detecting Mycobacterium species,
XX that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
XX encoding 16S rRNA in an in vitro nucleic acid amplification mixture
XX comprising a polymerase, and at least two primers, and then detecting the
XX amplified nucleic acid. The method is relatively simple and useful for
XX detecting the presence of various Mycobacterium species in a biological
XX sample, and thus important for diagnosis of infections resulting from
XX them. The method is especially important for screening opportunistic
XX infections caused by M. tuberculosis or a Mycobacterium other than
XX tuberculosis (MOTT). The present sequence is a PCR primer used for
XX amplifying Mycobacterium 16S rRNA
XX Sequence 25 BP; 7 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 94.7%; Score 18; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.9; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;
Qy 1 GAACGGAAGGCTTTTCG 18
Db 8 GAACGGAAGGCTTTTCG 25
RESULT 11
ADG88352
ID ADG88352 standard; DNA; 25 BP.
AC ADG88352;
XX 11-MAR-2004 (first entry)
XX Mycobacterium amplifying PCR primer #21.
XX In vitro amplification; PCR; primer; ss.
XX Mycobacterium celatum.
XX US2003165824-A1.
XX 04-SEP-2003.
XX 15-DEC-2000; 2000US-00738274.
```

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XX 17-DEC-1999; 99US-0172190P.
XX (BREN/) BRENTANO S T.
XX (JUCK/) JUCKER M T.
XX (DELG/) DELGADO F D.
XX (CLEU/) CLEUZIAZ P.
XX (RODR/) RODRIGUE M.
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2003-898044/82.
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX in a biological sample comprises performing in vitro nucleic acid
XX amplification and detection of amplified products.
XX Claim 1; SEQ ID NO 21; 20pp; English.
XX The present invention relates to a method of detecting Mycobacterium
XX species present in a biological sample comprises performing an in vitro
XX amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
XX detecting the amplified Mycobacterium nucleic acid. The present sequence
XX is Mycobacterium amplifying PCR primer.
XX Sequence 25 BP; 7 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 94.7%; Score 18; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.9; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;
Qy 1 GAACGGAAGGCTTTTCG 18
Db 8 GAACGGAAGGCTTTTCG 25
RESULT 12
AEA08227
ID AEA08227 standard; DNA; 25 BP.
XX AEA08227;
XX 14-JUL-2005 (first entry)
XX Mycobacterium celatum 16SrRNA amplifying non-T7 primer, SEQ ID NO: 21.
XX Microorganism detection; DNA amplification; 16S ribosomal RNA; 16S rRNA;
XX PCR; primer; ss.
XX Mycobacterium celatum.
XX US2005100915-A1.
XX 12-MAY-2005.
XX 18-SEP-2003; 2003US-00665708.
XX 17-DEC-1999; 99US-0172190P.
XX 15-DEC-2000; 2000US-00738274.
XX (BREN/) BRENTANO S T.
XX (JUCK/) JUCKER M T.
XX (DELG/) DELGADO F D.
XX (CLEU/) CLEUZIAZ P.
XX (RODR/) RODRIGUE M.
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2005-345392/35.
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX in a biological sample, comprises using in vitro nucleic acid
XX amplification and detection of amplified products.
```


XX Claim 8; SEQ ID NO 21; 21bp; English.

PS The present invention relates to a method of detecting Mycobacterium

CC species present in a biological sample. The method involves using in

CC vitro nucleic acid amplification and detection of amplified products. The

CC invention is useful for diagnostic detection of pathogenic bacteria such

CC as Mycobacterium species. The present sequence is the Mycobacterium

CC cellatum (ATCC 51130 and ATCC 51131) 16S ribosomal RNA (16SrRNA)

CC amplifying non-T7 PCR primer.

XX

SQ Sequence 25 BP; 7 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 94.7%; Score 18; DB 1; Length 25;

Best Local Similarity 100.0%; Pred.No. 3.9; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0;

QY 1 GAACGGAAGGCGCTTTCG 18

DB 8 GAACGGAAGGCGCTTTCG 25

RESULT 13

AAV24413

ID AAV24413 standard; preRNA; 23 BP.

XX

AC AAV24413;

XX

DT 24-AUG-1998 (first entry)

XX

DE Target sequence #2 for M. intracellulare specific probe.

XX

KW Probe; target sequence; hybridisation; mycobacterial cell sensitivity;

KW antimicrobial agent; pre-rRNA detection; ss.

XX

OS Synthetic.

OS Mycobacterium intracellulare.

PN US5770373-A.

XX

PD 23-JUN-1998.

XX

PF 08-NOV-1996; 96US-00745638.

XX

PR 16-JUN-1994; 94US-00261068.

PR 07-JUN-1995; 95US-00485602.

XX

PA (BECT) BECTON DICKINSON & CO.

XX

PI Cangelosi GA, Britschgi TB;

XX

DR WPI; 1998-376792/32.

XX

PT Mycobacterial sensitivity and drug screening assays - involving release

PT of pre-rRNA by lysis.

XX

PS Example 4; Col 17-18; 50pp; English.

XX

CC This sequence represents a target sequence for mycobacterial probes. This

CC sequence represents a precursor RNA fragment that is released during the

CC method of the invention. The method is for the determination of

CC mycobacterial cell sensitivity to an antimicrobial agent, and comprises:

CC (a) culturing the cells in the presence of the antimicrobial agent; (b)

CC treating the cells by enzymatic or mechanical means to expose the cell

CC membrane to lysis reagents, and contacting the cells with a lysis reagent

CC under conditions such that pre-rRNA is released from the cells but not

CC degraded; and (c) detecting the pre-rRNA with an oligonucleotide probe

CC capable of hybridizing to a region of the pre-rRNA that is not present in

CC mature mycobacterial RNA, where sensitivity to the antimicrobial agent

CC is indicated by an increase or decrease in pre-rRNA levels for cells

CC exposed to the antimicrobial agent compared with mycobacterial cells not

CC exposed to the antimicrobial agent. The lysis method, unlike known

CC methods, results in detectable levels of pre-rRNA

XX

SQ Sequence 23 BP; 6 A; 6 C; 7 G; 0 T; 3 U; 1 Other;

Query Match 86.3%; Score 16.4; DB 1; Length 23;

Best Local Similarity 78.9%; Pred.No. 7.9; Indels 0; Gaps 0;

Matches 15; Conservative 2; Mismatches 2;

QY 1 GAACGGAAGGCGCTTTCGG 19

DB 1 GAACGGAAGGCCUUCGG 19

RESULT 14

AAV13021

ID AAV13021 standard; rRNA; 23 BP.

XX

AC AAV13021;

XX

DT 18-MAY-1998 (first entry)

XX

DE Mycobacterium intracellulare mature rRNA target sequence SEQ ID NO:56.

XX

KW Mycobacterium; pre-rRNA; precursor ribosomal RNA; target sequence; probe;

KW hybridisation; antibiotic resistance; cell lysis; ss.

XX

OS Mycobacterium intracellulare.

XX

PN US5712095-A.

XX

PD 27-JAN-1998.

XX

PF 07-JUN-1995; 95US-00485602.

XX

PR 16-JUN-1994; 94US-00261068.

XX

PA (BECT) BECTON DICKINSON CO.

XX

PI Cangelosi GA, Britschgi TB;

XX

DR WPI; 1998-119975/11.

XX

PT Assay for pre-ribosomal RNA in mycobacterium cells - by hybridisation

PT with specific probes after cell lysis.

XX

PS Disclosure; Col 18; 54pp; English.

XX

CC The present sequence represents a mycobacterial mature ribosomal RNA

CC target sequence. The present invention describes a method for detecting

CC pre-rRNA in cells of a mycobacterial sample. The method comprises: (a)

CC treating the cells to release pre-rRNA by: (i) pretreating the cells by

CC enzymatic degradation using both lysozyme and protease until their cell

CC walls are rendered porous to expose their cell membranes, making the

CC cells susceptible to lysis; (ii) contacting the pretreated cells with a

CC combination of a magnesium chelator, a nonionic detergent and an anionic

CC detergent; and (iii) heating the cells to 75-99 degrees Celsius until the

CC mycobacterial cells are lysed; and (b) detecting the pre-rRNA using at

CC least one oligonucleotide probe which is capable of selectively

CC hybridizing to a region of the pre-rRNA that is not present in a mature

CC mycobacterial rRNA. The probes can be used to identify many Mycobacterium

CC spp. including M. tuberculosis, M. leprae, M. habana, M. avium, M. bovis,

CC M. lufu, M. paratuberculosis, M. marinum, M. simiae and/or M.

CC intracellulare. The probes may also be used to measure mycobacterial

CC response to inhibitors of RNA and protein synthesis and may therefore be

CC used to screen new antimycobacterial drugs. Mycobacteria have a slow

CC growth rate. By using the probes, drug developers can now identify

CC compounds that are more effective, but less stable than those previously

CC identified

XX

SQ Sequence 23 BP; 6 A; 6 C; 7 G; 0 T; 3 U; 1 Other;

Query Match 86.3%; Score 16.4; DB 1; Length 23;

Best Local Similarity 78.9%; Pred.No. 7.9; Indels 0; Gaps 0;

Matches 15; Conservative 2; Mismatches 2;

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QY      1 GAACGAAAGGCTTTCGG 19
Db      1 GAACGAAAGGCCCUUCGG 19

RESULT 15
AAT75816
ID AAT75816 standard; rRNA; 20 BP.
XX
AC AAT75816;
XX
DT 10-SEP-1997 (first entry)
XX
DE Corynebacterium propinquum 16S rRNA (from region 72-100).
XX
KW Ribosomal RNA; species specific; detection; reverse transcription;
KW primer; hybridisation probe; identification; ss.
XX
OS Corynebacterium propinquum.
XX
PN FR273755-A1.
XX
PD 08-NOV-1996.
XX
PF 03-MAY-1995; 95FR-00005494.
XX
PR 03-MAY-1995; 95FR-00005494.
XX
PA (INMR ) BIO MERIEUX.
XX
PI Mabilat C, Ruimy R;
XX
DR WPI; 1997-001738/01.
XX
PT Fragments of Corynebacterium 16S RNA - useful as probes and primers for
PT identifying Corynebacterium spp.
XX
PS Claim 2; Page 14; 60pp; French.
XX
CC Fragments covering 90 % of the sequence of 16S ribosomal RNA were
CC amplified from 28 strains of 25 different species of Corynebacterium by
CC PCR using primers specific for eubacteria. The amplification products
CC were sequenced and the sequences were aligned for comparison. It was
CC found that certain regions, i.e. those corresponding to nucleotides 72-
CC 100, 195-215, 466-494, 608-631, 838-853, 859-875 and 1013-1033 in the 16S
CC ribosomal RNA of C. diphtheriae, vary considerably between different
CC species. Probes and primers comprising at least 5 nucleotides from one of
CC these species-specific sequences, including the present sequence, or
CC their complements, are useful to distinguish between different
CC Corynebacterium species. DNA versions of the probes and primers are also
CC included
XX
SQ Sequence 20 BP; 5 A; 4 C; 7 G; 0 T; 4 U; 0 Other;

Query Match      73.7%; Score 14; DB 1; Length 20;
Best Local Similarity 78.6%; Pred. No. 20;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      3 ACGGAAAGGCTTT 16
Db      1 ACGGAAAGGCCUUU 14

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
8.588 Million cell updates/sec

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Sequence: 1 gaacggaagcctttcgg 19

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 10 seqs, 226 residues

Total number of hits satisfying chosen parameters: 20

Minimum DB seq length: 18
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 10 summaries

Database : rgedb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	19	100.0	22	1	AR438655
4	19	100.0	22	1	AX166857
5	18	94.7	24	1	AR438654
6	18	94.7	24	1	AX166856
7	18	94.7	25	1	AR438653
8	18	94.7	25	1	AX166855
9	16.4	86.3	23	1	I82017
10	16.4	86.3	23	1	I91705

ALIGNMENTS

RESULT 1
AR438656
LOCUS AR438656 19 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 24 from patent US 6664081.
ACCESSION AR438656
VERSION AR438656.1 GI:42663580
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and Rodriguez,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: US 6664081-A 24 16-DEC-2003;
Gen-Probe incorporated and Bio Merieux S.A.; San Diego, CA
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/organism="unknown"
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Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GAACGGAAGCCTTTTCGG 19
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Db 1 GAACGGAAGCCTTTTCGG 19
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RESULT 2
AX166858
LOCUS AX166858 19 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 24 from Patent WO0144510.
ACCESSION AX166858
VERSION AX166858.1 GI:14596461
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 19)
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and Rodriguez,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: WO 0144510-A 24 21-JUN-2001;
Gen-Probe Incorporated (US) ; Biomerieux S.A. (FR)
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Query Match 100.0%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GAACGGAAGCCTTTTCGG 19
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Db 1 GAACGGAAGCCTTTTCGG 19
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RESULT 3
AR438655
LOCUS AR438655 22 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 23 from patent US 6664081.
ACCESSION AR438655
VERSION AR438655.1 GI:42663579
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and Rodriguez,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: US 6664081-A 23 16-DEC-2003;
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA
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/mol_type="genomic DNA"

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Db 4 GAACGGAAGCCTTTTCGG 22
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RESULT 4
AXI166857
LOCUS AXI166857 22 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 23 from Patent WO0144510.
ACCESSION AXI166857
VERSION AXI166857.1 GI:14596460
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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Best Local Similarity 100.0%; Pred. No. 2.1; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 0;

Qy 1 GAACGGAAGGCGCTTTTCG 19
Db 4 GAACGGAAGGCGCTTTTCG 22

RESULT 5
AXI38654
LOCUS AR438654 24 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 22 from patent US 6664081.
ACCESSION AR438654
VERSION AR438654.1 GI:42663578
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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Matches 19; Conservative 0;

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Db 4 GAACGGAAGGCGCTTTTCG 22

RESULT 6
AXI166856
LOCUS AXI166856 24 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 22 from Patent WO0144510.
ACCESSION AXI166856
VERSION AXI166856.1 GI:14596459
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
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Query Match 94.7%; Score 18; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.9; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;

Qy 1 GAACGGAAGGCGCTTTTCG 18
Db 7 GAACGGAAGGCGCTTTTCG 24

RESULT 7
AXI166855
LOCUS AXI166855 25 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 21 from Patent WO0144510.
ACCESSION AXI166855
VERSION AXI166855.1 GI:14596458
KEYWORDS
SOURCE
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REFERENCE
AUTHORS
TITLE
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Db 8 GAACGGAAGGCGCTTTTCG 25

RESULT 8
AXI166855
LOCUS AXI166855 25 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 21 from Patent WO0144510.
ACCESSION AXI166855
VERSION AXI166855.1 GI:14596458
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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Matches 18; Conservative 0;

Qy 1 GAACGGAAGGCGCTTTTCG 18
Db 8 GAACGGAAGGCGCTTTTCG 25

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REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
Rodrigue,M.
Nucleic acid amplification and detection of mycobacterium species
Patent: WO 0144510-A 22 21-JUN-2001;
Gen-Probe Incorporated (US); Biomerieux S.A. (FR)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer oligonucleotide"

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Best Local Similarity 100.0%; Pred. No. 2.9; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;

Qy 1 GAACGGAAGGCGCTTTTCG 18
Db 7 GAACGGAAGGCGCTTTTCG 24

RESULT 7
AR438653
LOCUS AR438653 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 21 from patent US 6664081.
ACCESSION AR438653
VERSION AR438653.1 GI:42663577
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
Rodrigue,M.
Nucleic acid amplification and detection of mycobacterium species
Patent: US 6664081-A 21 16-DEC-2003;
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA
Location/Qualifiers
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Matches 18; Conservative 0;

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Db 8 GAACGGAAGGCGCTTTTCG 25

RESULT 8
AXI166855
LOCUS AXI166855 25 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 21 from Patent WO0144510.
ACCESSION AXI166855
VERSION AXI166855.1 GI:14596458
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
Rodrigue,M.
Nucleic acid amplification and detection of mycobacterium species
Patent: WO 0144510-A 21 21-JUN-2001;
Gen-Probe Incorporated (US); Biomerieux S.A. (FR)
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 8 GAACGGAAGGCTTTCG 25

RESULT 9
182017
LOCUS 23 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 56 from patent US 5712095.
ACCESSION 182017
VERSION 182017.1 GI:3210314
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Britschgi,T.B. and Cangelosi,G.A.
TITLE Rapid and sensitive detection of antibiotic-resistant mycobacteria
using oligonucleotide probes specific for ribosomal RNA precursors
JOURNAL Patent: US 5712095-A 56 27-JAN-1998;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"

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Best Local Similarity 89.5%; Pred. No. 5.4;
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|||||
DB 1 GAACGGAAGGCTTTCG 19

RESULT 10
191705
LOCUS 23 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 55 from patent US 5726021.
ACCESSION 191705
VERSION 191705.1 GI:3936175
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Britschgi,T.B. and Cangelosi,G.A.
TITLE Rapid and sensitive detection of antibiotic-resistant mycobacteria
using oligonucleotide probes specific for ribosomal RNA precursors
JOURNAL Patent: US 5726021-A 55 10-MAR-1998;
FEATURES Location/Qualifiers
source 1..23
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/mol_type="unassigned DNA"

Query Match 86.3%; Score 16.4; DB 1; Length 23;
Best Local Similarity 89.5%; Pred. No. 5.4;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTCG 19
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DB 1 GAACGGAAGGCTTTCG 19

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OM nucleic - nucleic search, using sw model

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(without alignments)
12.616 Million cell updates/sec

Title: us-10-665-708-24
Perfect score: 19
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 16 seqs, 332 residues

Total number of hits satisfying chosen parameters: 32

Minimum DB seq length: 18
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 16 summaries

Database : rnpbndb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	1 US-09-738-274-24	Sequence 24, Appl
2	19	100.0	19	1 US-10-665-708-24	Sequence 24, Appl
3	19	100.0	22	1 US-09-738-274-23	Sequence 23, Appl
4	19	100.0	22	1 US-10-665-708-23	Sequence 23, Appl
5	18	94.7	24	1 US-09-738-274-22	Sequence 22, Appl
6	18	94.7	24	1 US-10-665-708-22	Sequence 22, Appl
7	18	94.7	25	1 US-09-738-274-21	Sequence 21, Appl
8	18	94.7	25	1 US-10-665-708-21	Sequence 21, Appl
9	14.8	77.9	20	1 US-10-831-286A-38180	Sequence 38180, A
10	14.2	74.7	19	1 US-11-083-784-811277	Sequence 811277, A
11	14.2	74.7	19	1 US-11-083-784-811277	Sequence 811277, A
12	13.8	72.6	19	1 US-11-083-784-811307	Sequence 811307, A
13	13.8	72.6	19	1 US-11-083-784-811307	Sequence 811307, A
14	13.4	70.5	19	1 US-11-083-784-31921	Sequence 31921, A
15	13.4	70.5	19	1 US-11-083-784-31921	Sequence 31921, A
16	12.8	67.4	18	1 US-10-310-914A-193761	Sequence 193761, A

ALIGNMENTS

RESULT 1
US-09-738-274-24
; Sequence 24, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF MYCOBACTERIUM SPECIES

; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-24

Query Match 100.0%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCTTCGG 19
Db 1 GAACGGAAGCCTTCGG 19

RESULT 2
US-10-665-708-24
; Sequence 24, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-10-665-708-24

Query Match 100.0%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCTTCGG 19
Db 1 GAACGGAAGCCTTCGG 19

RESULT 3
US-09-738-274-23
; Sequence 23, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe


```

; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-23

```

```

Query Match          100.0%; Score 19; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 GAACGGAAGGCGCTTTTCG 19
    |||||
Db 4 GAACGGAAGGCGCTTTTCG 22

```

RESULT 4

```

US-10-665-708-23
; Sequence 23, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-10-665-708-23

```

```

Query Match          100.0%; Score 19; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 GAACGGAAGGCGCTTTTCG 19
    |||||
Db 4 GAACGGAAGGCGCTTTTCG 22

```

RESULT 5

```

US-09-738-274-22
; Sequence 22, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.

```

```

; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-22

```

```

Query Match          94.7%; Score 18; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 GAACGGAAGGCGCTTTTCG 18
    |||||
Db 7 GAACGGAAGGCGCTTTTCG 24

```

RESULT 6

```

US-10-665-708-22
; Sequence 22, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-10-665-708-22

```

```

Query Match          94.7%; Score 18; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 GAACGGAAGGCGCTTTTCG 18
    |||||
Db 7 GAACGGAAGGCGCTTTTCG 24

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RESULT 7

```

US-09-738-274-21
; Sequence 21, Application US/09738274

```

Publication No. US20030165824A1
 GENERAL INFORMATION:
 APPLICANT: BRENTANO, Steven T.
 APPLICANT: JUCKER, Markus T.
 APPLICANT: DELGADO, Francisco D.
 APPLICANT: CLEUZIAT, Philippe
 APPLICANT: RODRIGUE, Marc
 TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF MYCOBACTERIUM SPECIES
 FILE REFERENCE: GP107-02.UT
 CURRENT APPLICATION NUMBER: US/09/738,274
 CURRENT FILING DATE: 2000-12-15
 PRIOR APPLICATION NUMBER: 60/172,190
 PRIOR FILING DATE: 1999-12-17
 NUMBER OF SEQ ID NOS: 42
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 21
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: primer
 OTHER INFORMATION: oligonucleotide
 US-09-738-274-21

Query Match 94.7%; Score 18; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTTTCG 18
 |||||
 Db 8 GAACGGAAGGCTTTTCG 25

RESULT 8
 US-10-665-708-21
 Sequence 21, Application US/10665708
 Publication No. US20050100915A1
 GENERAL INFORMATION:
 APPLICANT: BRENTANO, Steven T.
 APPLICANT: JUCKER, Markus T.
 APPLICANT: DELGADO, Francisco D.
 APPLICANT: CLEUZIAT, Philippe
 APPLICANT: RODRIGUE, Marc
 TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF MYCOBACTERIUM SPECIES
 FILE REFERENCE: GP107-02.UT
 CURRENT APPLICATION NUMBER: US/10/665,708
 CURRENT FILING DATE: 2003-09-18
 PRIOR APPLICATION NUMBER: US/09/738,274
 PRIOR FILING DATE: 2000-12-15
 PRIOR APPLICATION NUMBER: 60/172,190
 PRIOR FILING DATE: 1999-12-17
 NUMBER OF SEQ ID NOS: 42
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 21
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: primer
 OTHER INFORMATION: oligonucleotide
 US-10-665-708-21

Query Match 94.7%; Score 18; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTTTCG 18
 |||||
 Db 8 GAACGGAAGGCTTTTCG 25

RESULT 9
 US-10-831-286A-38180
 Sequence 38180, Application US/10831286A
 Publication No. US20060046246A1
 GENERAL INFORMATION:
 APPLICANT: ZENG, QIANDONG
 APPLICANT: CHATELLIER, SONIA
 APPLICANT: MOIR, DONALD T.
 APPLICANT: LACROIX, BRUNA
 APPLICANT: CHILDRESS, DARRELL
 TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
 FILE REFERENCE: 032796-174.001
 CURRENT APPLICATION NUMBER: US/10/831,286A
 CURRENT FILING DATE: 2004-04-26
 PRIOR APPLICATION NUMBER: 60/464,955
 PRIOR FILING DATE: 2003-04-24
 NUMBER OF SEQ ID NOS: 48788
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 38180
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Corynebacterium jeikeium
 US-10-831-286A-38180

Query Match 77.9%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 9.4;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTTTCG 18
 |||||
 Db 1 GAACGGAAGGCTTTTCG 18

RESULT 10
 US-11-083-784-811277
 Sequence 811277, Application US/11083784
 Publication No. US20050245475A1
 GENERAL INFORMATION:
 APPLICANT: Dharmacon, Inc.
 APPLICANT: Khvorova, Anastasia
 APPLICANT: Reynolds, Angela
 APPLICANT: Leake, Devin
 APPLICANT: Marshall, William
 APPLICANT: Scaringe, Stephen
 TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 FILE REFERENCE: 13499US
 CURRENT APPLICATION NUMBER: US/11/083,784
 CURRENT FILING DATE: 2005-03-18
 PRIOR APPLICATION NUMBER: US/10/714,333
 PRIOR FILING DATE: 2003-11-14
 PRIOR APPLICATION NUMBER: 60/502,050
 PRIOR FILING DATE: 2003-09-10
 PRIOR APPLICATION NUMBER: 60/426,137
 PRIOR FILING DATE: 2002-11-14
 NUMBER OF SEQ ID NOS: 1591911
 SOFTWARE: Proprietary
 SEQ ID NO 811277
 LENGTH: 19
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-083-784-811277

Query Match 74.7%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 68.4%; Pred. No. 12;
 Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTTTCG 19
 |||||
 Db 1 GAACGGAAGGCTTTTCG 19

RESULT 11
 US-11-101-244-811277

; Sequence 811277, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 811277
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-811277

Query Match 74.7%; Score 14.2; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 12;
Matches 13; Conservative 3; Mismatches 0; Gaps 0;

Matches 13; Conservative 3; Mismatches 0; Gaps 0;
Indels 3; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCTTCGG 19
||||||| |:::|
Db 1 GAACGGAACGCCUUCAG 19

RESULT 12

US-11-083-784-811307
; Sequence 811307, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083.784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 811307
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-811307

Query Match 72.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 14;
Matches 12; Conservative 3; Mismatches 0; Gaps 0;

Matches 12; Conservative 3; Mismatches 0; Gaps 0;
Indels 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCTTCG 17
||||||| |:::|
Db 2 GAACGGAACGCCUUC 18

RESULT 13

US-11-101-244-811307
; Sequence 811307, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 811307
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-811307

Query Match 72.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 14;
Matches 12; Conservative 3; Mismatches 0; Gaps 0;

Matches 12; Conservative 3; Mismatches 0; Gaps 0;
Indels 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCTTC 17
||||||| |:::|
Db 2 GAACGGAACGCCUUC 18

RESULT 14

US-11-083-784-31921/c
; Sequence 31921, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083.784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 31921
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-31921

Query Match 70.5%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 15;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Indels 1; Indels 0; Gaps 0;

Qy 5 GGAAAGGCCTTCGG 19
||||||| |:::|
Db 15 GGGAAGGCCTTCGG 1

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RESULT 15
US-11-101-244-31921/c
; Sequence 31921, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 31921
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-31921
Query Match 70.5%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 15;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GGAAGGCGCTTCGG 19
Db 15 GGAAGGCGCTTCGG 1

RESULT 16
US-10-310-914A-193761
; Sequence 193761, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 193761
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-193761
Query Match 67.4%; Score 12.8; DB 1; Length 18;
Best Local Similarity 68.8%; Pred. No. 19;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTT 16
Db 2 GAACAGAAAGGCAUUU 17

Search completed: May 26, 2006, 14:32:50
Job time : 1 secs
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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 02:22:49 ; Search time 259.361 Seconds
(without alignments)
591.412 Million cell updates/sec

Title: US-10-665-708-25

Perfect score: 22
Sequence: 1 gaaagcccttcgggggtgctc 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

N_Geneseq_8:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001s:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

14: Geneseqn2005s:*

15: Geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	4	AD11275 Mycobacte
2	22	100.0	22	10	ADG88356 Mycobacte
3	22	100.0	22	14	AEA08231 Mycobacte
4	22	100.0	25	4	AD11276 Mycobacte
5	22	100.0	25	10	ADG88357 Mycobacte
6	22	100.0	25	14	AEA08232 Mycobacte
7	18.8	85.5	166	2	AX32480 Probe CNB
8	18.8	85.5	166	2	AX32481 Preferred
9	18.8	85.5	110000	11	ADM27081 Hyperther
10	17.8	80.9	487	11	ADP65654 Human per
11	17.8	80.9	40491	11	ACN44798 Human gen
12	17.4	79.1	74849	11	ACN44932_3 Continuation (4 of
13	17.2	78.2	569	4	ABA59963 Human foe
14	17.2	78.2	569	4	AAI39835 Probe #85
15	17.2	78.2	569	4	ABA28379 Probe #68
16	17.2	78.2	569	4	AAK34112 Human bon
17	17.2	78.2	569	4	AAK08233 Human bra
18	17.2	78.2	569	4	ABS33911 Human liv

19	17.2	78.2	569	6	ABS08880 Human gen
20	17.2	78.2	1440	8	ACA36105 Prokaryot
21	17.2	78.2	58822	9	ADA02540 Human TCO
22	17.2	78.2	58822	10	ADB72278 Human TCO
23	17.2	78.2	58822	10	ADP95788 Human TCO
24	17.2	78.2	63686	11	ACN44158 Human gen
25	16.8	76.4	276	11	ABD17022 Pseudomon
26	16.8	76.4	601	13	ACN53618 Cotton an
27	16.8	76.4	21007	8	ACA31638 Prokaryot
28	16.8	76.4	110000	14	AD213575_1 Continuation (2 of
29	16.8	76.4	289190	13	ABD33143 Murine ca
30	16.4	74.5	309	4	AAH36786 Human col
31	16.4	74.5	521	13	ACN47886 Cotton pr
32	16.4	74.5	47804	10	ADC86176 Human imm
33	16.2	73.6	420	4	AAK76977 Human
34	16.2	73.6	420	4	AAK76978 Human imm
35	16.2	73.6	426	11	ADL96630 M. paratu
36	16.2	73.6	511	12	ACH76350 Human gen
37	16.2	73.6	590	4	AAH31560 Human olf
38	16.2	73.6	607	12	ADO36603 Isoquinol
39	16.2	73.6	771	11	ABD02872 Pseudomon
40	16.2	73.6	828	11	ABD03097 Pseudomon
41	16.2	73.6	909	7	ADS31309 Human gen
42	16.2	73.6	909	7	ADY36697 HIRA geno
43	16.2	73.6	1218	4	AAI23344 Probe #13
44	16.2	73.6	1218	4	ABA68451 Human foe
45	16.2	73.6	1218	4	AAI48666 Probe #17
46	16.2	73.6	1218	4	ABA50502 Human bre
47	16.2	73.6	1218	4	ABA35441 Probe #13
48	16.2	73.6	1218	4	AAK42594 Human bon
49	16.2	73.6	1218	4	AAK16823 Human bra
50	16.2	73.6	1218	4	ABS42209 Human liv
51	16.2	73.6	1218	5	AAI08981 Probe #89
52	16.2	73.6	1218	6	ABS16646 Human gen
53	16.2	73.6	1239	11	ABD02999 Pseudomon
54	16.2	73.6	1377	8	ACA38376 Prokaryot
55	16.2	73.6	1380	8	ACA40722 Prokaryot
56	16.2	73.6	1704	6	AAS94778 Human DNA
57	16.2	73.6	1740	4	AAC85094 Atheroscl
58	16.2	73.6	1740	11	ADM29578 Human ath
59	16.2	73.6	1954	4	AAI14134 Probe #40
60	16.2	73.6	1954	4	ABA55860 Human foe
61	16.2	73.6	1954	4	AAI35517 Probe #42
62	16.2	73.6	1954	4	ABA45372 Human bre
63	16.2	73.6	1954	4	ABA25535 Probe #40
64	16.2	73.6	1954	4	AAK29561 Human bon
65	16.2	73.6	1954	4	AAK04079 Human bra
66	16.2	73.6	1954	4	ABS29189 Human liv
67	16.2	73.6	1954	5	AAI03983 Probe #39
68	16.2	73.6	2772	6	ABS04116 Human gen
69	16.2	73.6	3135	13	ADV35075 Human ova
70	16.2	73.6	4258	11	ADP65658 Human mit
71	16.2	73.6	4395	3	AAK77830 Human can
72	16.2	73.6	4415	11	ADL96632 M. paratu
73	16.2	73.6	4670	14	AEA20710 Novel hum
74	16.2	73.6	4738	14	ADY91665 Human pro
75	16.2	73.6	4758	10	ABX93240 Full-leng
76	16.2	73.6	4831	10	ADK41009 Novel hum
77	16.2	73.6	4831	13	ADR15723 Kinase 69
78	16.2	73.6	5970	2	AAK26546 Nucleic a
79	16.2	73.6	5994	10	ADP65658 Human ova
80	16.2	73.6	5994	10	ADP65658 Human ova
81	16.2	73.6	5994	12	ADQ19074 Human sof
82	16.2	73.6	5994	12	ADQ19074 Human sof
83	16.2	73.6	6332	14	AEA19724 Novel hum
84	16.2	73.6	6332	14	ABA09565 Human car
85	16.2	73.6	8411	12	ADL12831 Human ste
86	16.2	73.6	8412	12	ADE77058 Human cdn
87	16.2	73.6	14063	4	AAK82933 Human imm
88	16.2	73.6	14063	4	AAK82934 Human imm
89	16.2	73.6	25759	11	ADM22177 Rat hepat
90	16.2	73.6	104932	13	ABE96542 Human STA
91	16.2	73.6	106664	13	ADV35021 Murine cd

C 92	16.2	73.6	110000	4	AAI99682_30	Continuation (31 o	C 165	15.6	70.9	487	6	ABS02690	Abso2690 Human gen
C 93	16.2	73.6	110000	4	AAI99682_31	Continuation (32 o	C 166	15.6	70.9	502	4	ABA08675	ABA08675 Human R31
C 94	16.2	73.6	110000	4	AAI99683_30	Continuation (31 o	C 167	15.6	70.9	502	10	ADF60129	ADF60129 Human con
C 95	16	72.7	287	9	ADB82110	Human CDN	C 168	15.6	70.9	516	12	ACH77191	ACH77191 Human gen
C 96	16	72.7	331	6	ABQ89167	Human gen	C 169	15.6	70.9	597	12	ACH68923	ACH68923 Human gen
C 97	15.8	71.8	132	8	ABX64840	Human gen	C 170	15.6	70.9	641	4	AAH31571	AAH31571 Human oif
C 98	15.8	71.8	362	13	ADQ50381	Novel can	C 171	15.6	70.9	651	4	AAH31541	AAH31541 Human oif
C 99	15.8	71.8	579	9	ADA28874	DNA encod	C 172	15.6	70.9	701	4	AAK92121	AAK92121 Human CDN
C 100	15.8	71.8	665	8	ABZ54797	Aspergill	C 173	15.6	70.9	701	4	AAK93385	AAK93385 Human CDN
C 101	15.8	71.8	859	5	ABV03387	Human pro	C 174	15.6	70.9	701	12	ADL28548	ADL28548 5' end of
C 102	15.8	71.8	900	14	ADY26912	Vimentin	C 175	15.6	70.9	701	12	ADL29812	ADL29812 5' end of
C 103	15.8	71.8	2000	12	ADJ40830	Plant CDN	C 176	15.6	70.9	729	12	ACH70806	ACH70806 Human gen
C 104	15.8	71.8	2001	14	ADY26869	Vimentin	C 177	15.6	70.9	777	3	AACT78029	AACT78029 Human can
C 105	15.8	71.8	3789	12	ADQ64482	Novel hum	C 178	15.6	70.9	783	6	ABQ45189	ABQ45189 Oligonuc1
C 106	15.8	71.8	5328	4	AAK76010	Human imm	C 179	15.6	70.9	783	6	ABQ45188	ABQ45188 Oligonuc1
C 107	15.8	71.8	5328	4	AAK76011	Human imm	C 180	15.6	70.9	820	5	ABV11138	ABV11138 Human pro
C 108	15.8	71.8	6279	4	ABL09392	Drosophil	C 181	15.6	70.9	875	4	AAK94431	AAK94431 Human ful
C 109	15.8	71.8	9661	4	ABL09504	Drosophil	C 182	15.6	70.9	875	12	ADL31179	ADL31179 Full leng
C 110	15.8	71.8	48300	5	AAF61281	N. magada	C 183	15.6	70.9	893	2	AAZ40786	AAZ40786 Secreted
C 111	15.8	71.8	118544	12	ADQ97100	Human can	C 184	15.6	70.9	893	11	ADM77763	ADM77763 Human CDN
C 112	15.8	71.8	159400	6	ABQ88126	Human ost	C 185	15.6	70.9	893	12	ADP19084	ADP19084 Human sec
C 113	15.8	71.8	172984	8	ACF62733	Cancer ba	C 186	15.6	70.9	933	14	ADH89223	ADH89223 Secreted
C 114	15.8	71.8	172984	8	ADB20848	MRP1 base	C 187	15.6	70.9	933	4	AAH00857	AAH00857 Leishmani
C 115	15.8	71.8	172984	10	ADB87937	Human UGT	C 188	15.6	70.9	948	4	AAH31841	AAH31841 Human oif
C 116	15.8	71.8	172984	10	ADB96920	Human MDR	C 189	15.6	70.9	948	4	AAH32188	AAH32188 Human oif
C 117	15.8	71.8	172984	10	ADB92111	Human MDR	C 190	15.6	70.9	948	4	AAH32375	AAH32375 Human oif
C 118	15.6	70.9	114	4	ABA70662	Human foe	C 191	15.6	70.9	951	6	ABZ43029	ABZ43029 Human GPC
C 119	15.6	70.9	114	4	AAI50828	Probe #19	C 192	15.6	70.9	960	6	ABL99835	ABL99835 Human sec
C 120	15.6	70.9	114	4	AAK44852	Human bon	C 193	15.6	70.9	967	6	ABT04182	ABT04182 Human G-p
C 121	15.6	70.9	114	4	AAK18908	Human bra	C 194	15.6	70.9	967	6	ABT04183	ABT04183 Human G-p
C 122	15.6	70.9	114	4	ABS44514	Human liv	C 195	15.6	70.9	967	12	ADH30905	ADH30905 Human G-p
C 123	15.6	70.9	114	6	ABS19093	Human gen	C 196	15.6	70.9	967	12	ADH30903	ADH30903 Human G-p
C 124	15.6	70.9	208	8	ABX35037	Bovine ES	C 197	15.6	70.9	1015	3	AAZ87206	AAZ87206 Human NTA
C 125	15.6	70.9	221	12	ACH82623	Human gen	C 198	15.6	70.9	1057	10	ADL21845	ADL21845 Novel hum
C 126	15.6	70.9	329	2	AAH40619	Human sec	C 199	15.6	70.9	1098	6	ABL40538	ABL40538 Basidiomy
C 127	15.6	70.9	367	6	ABK15957	Human lun	C 200	15.6	70.9	1247	2	AAQ90650	AAQ90650 Rat galec
C 128	15.6	70.9	367	10	ADB95220	Human lun	C 201	15.6	70.9	1247	10	ADD90597	ADD90597 Rat galec
C 129	15.6	70.9	367	9	ACH18348	Human adu	C 202	15.6	70.9	1247	12	ADL13480	ADL13480 Rat galec
C 130	15.6	70.9	386	4	ABA58058	Human foe	C 203	15.6	70.9	1263	6	ABQ50083	ABQ50083 Oligonuc1
C 131	15.6	70.9	386	4	AAI37658	Probe #63	C 204	15.6	70.9	1263	6	ABQ50082	ABQ50082 Oligonuc1
C 132	15.6	70.9	396	4	AAK31783	Human bon	C 205	15.6	70.9	1265	6	ABQ28517	ABQ28517 Oligonuc1
C 133	15.6	70.9	396	4	AAK06130	Human bra	C 206	15.6	70.9	1265	6	ABQ28516	ABQ28516 Oligonuc1
C 134	15.6	70.9	396	4	ABS31469	Human liv	C 207	15.6	70.9	1325	12	ADK14124	ADK14124 Human aut
C 135	15.6	70.9	396	6	ABS06541	Human gen	C 208	15.6	70.9	1325	12	ADN14333	ADN14333 Human hom
C 136	15.6	70.9	405	4	AAI02356	Human rep	C 209	15.6	70.9	1325	13	ADR25738	ADR25738 Breast ca
C 137	15.6	70.9	407	4	AAI14836	Probe #47	C 210	15.6	70.9	1325	14	ADW80340	ADW80340 Human typ
C 138	15.6	70.9	407	4	ABA56566	Human foe	C 211	15.6	70.9	1343	12	ACH90897	ACH90897 Human gen
C 139	15.6	70.9	407	4	AAI36194	Probe #48	C 212	15.6	70.9	1388	3	AAAC59295	AAAC59295 Human sec
C 140	15.6	70.9	407	4	ABA46028	Human bra	C 213	15.6	70.9	1400	14	AED73400	AED73400 Human pla
C 141	15.6	70.9	407	4	ABA26185	Probe #46	C 214	15.6	70.9	1410	6	ABK73375	ABK73375 Bacillus
C 142	15.6	70.9	407	4	AAK30233	Human bon	C 215	15.6	70.9	1429	11	ADL31363	ADL31363 Human CDN
C 143	15.6	70.9	407	4	AAK04717	Human bra	C 216	15.6	70.9	1429	13	ADH83430	ADH83430 Human lym
C 144	15.6	70.9	407	5	AAI04622	Probe #46	C 217	15.6	70.9	1449	11	ACH96943	ACH96943 Klebsiell
C 145	15.6	70.9	407	6	ABS04821	Human gen	C 218	15.6	70.9	1596	12	ADN98896	ADN98896 Novel hum
C 146	15.6	70.9	422	10	ADC31993	Human nov	C 219	15.6	70.9	1596	12	ADO00465	ADO00465 Novel hum
C 147	15.6	70.9	436	9	ACH47589	Human inf	C 220	15.6	70.9	1746	2	AAK58059	AAK58059 Canine GA
C 148	15.6	70.9	459	9	ACH28774	Human adu	C 221	15.6	70.9	1761	8	ACA26579	ACA26579 Prokaryot
C 149	15.6	70.9	477	10	ADA19380	Human ins	C 222	15.6	70.9	1862	10	ADB62746	ADB62746 Human CDN
C 150	15.6	70.9	477	13	ACF85952	Human SIR	C 223	15.6	70.9	1917	10	ADL21386	ADL21386 Novel hum
C 151	15.6	70.9	479	3	AAZ43020	Human 5'	C 224	15.6	70.9	1918	4	AAH98371	AAH98371 Human EST
C 152	15.6	70.9	479	13	ADU72182	Signal pe	C 225	15.6	70.9	1934	10	ADC29972	ADC29972 Human nov
C 153	15.6	70.9	479	14	ADZ73173	Human 5'	C 226	15.6	70.9	1990	10	ACA56458	ACA56458 Human sig
C 154	15.6	70.9	485	13	ACF89723	Human SIR	C 227	15.6	70.9	1990	12	ADL56254	ADL56254 Human pol
C 155	15.6	70.9	486	2	AAZ33493	Human pro	C 228	15.6	70.9	2120	13	ADH61102	ADH61102 Bacterial
C 156	15.6	70.9	487	4	AAI12753	Probe #26	C 229	15.6	70.9	2129	10	ABZ79877	ABZ79877 Human nuc
C 157	15.6	70.9	487	4	ABA54448	Human foe	C 230	15.6	70.9	2130	13	ADR07764	ADR07764 Full leng
C 158	15.6	70.9	487	4	AAI34102	Probe #27	C 231	15.6	70.9	2287	10	ADC30627	ADC30627 Human nov
C 159	15.6	70.9	487	4	ABA43994	Human bre	C 232	15.6	70.9	2297	10	ADA52853	ADA52853 Human cod
C 160	15.6	70.9	487	4	ABA24230	Probe #26	C 233	15.6	70.9	2304	14	AED30768	AED30768 Human pos
C 161	15.6	70.9	487	4	AAK28180	Human bon	C 234	15.6	70.9	2708	4	ABU12610	ABU12610 Drosophil
C 162	15.6	70.9	487	4	AAK02739	Human bra	C 235	15.6	70.9	2895	2	AAK58058	AAK58058 Canine GA
C 163	15.6	70.9	487	4	ABS27785	Human liv	C 236	15.6	70.9	3205	13	ADV41710	ADV41710 Rat cardl
C 164	15.6	70.9	487	5	AAI02663	Probe #26	C 237	15.6	70.9	3568	3	AACT76411	AACT76411 Human ORF

c 238	15.6	70.9	3995	6	ABK35489	Abk35489 Human end	XX
c 239	15.6	70.9	3995	6	ABK35548	Abk35548 Gene DLG4	DT
c 240	15.6	70.9	3995	6	ABV78023	ABV78023 Hypoxia-r	XX
c 241	15.6	70.9	3995	9	ACC85074	Acc85074 Human MBC	DE
c 242	15.6	70.9	4857	10	ACC42643	Acc42643 Maize dek	XX
c 243	15.6	70.9	4928	4	ABL12611	Ab112611 Drosophil	KW
c 244	15.6	70.9	5514	4	ABL12193	Ab112193 Drosophil	KW
c 245	15.6	70.9	5862	4	AAL04675	Aal04675 Human rep	XX
c 246	15.6	70.9	5862	4	ABL97582	Ab197582 Human tes	XX
c 247	15.6	70.9	6065	4	AAL06964	Aal06964 Human rep	OS
c 248	15.6	70.9	6831	10	ADC24898	Adc24898 Human bre	PN
c 249	15.6	70.9	7110	10	ACC42659	Acc42659 Maize dek	XX
c 250	15.6	70.9	7110	13	ADT16606	Adt16606 Plant cDN	XX
c 251	15.6	70.9	15762	4	ABL06916	Ab106916 Drosophil	PD
c 252	15.6	70.9	22970	10	ADK70082	Adk70082 Mutant hu	XX
c 253	15.6	70.9	22970	10	ADK70081	Adk70081 Wild type	XX
c 254	15.6	70.9	25411	10	ACC42660	Acc42660 Maize dek	XX
c 255	15.6	70.9	32249	4	AAL04676	Aal04676 Human rep	XX
c 256	15.6	70.9	32249	4	ABL97583	Ab197583 Human tes	PA
c 257	15.6	70.9	32548	4	ABL29482	Ab129482 Drosophil	PA
c 258	15.6	70.9	33634	11	ACN45028	Acn45028 Mouse gen	XX
c 259	15.6	70.9	34115	8	AAL56708	Aal56708 Rhesus mo	PI
c 260	15.6	70.9	34115	14	ADM42639	Adm42639 Chimpanze	XX
c 261	15.6	70.9	34471	13	ADR66979	Adr66979 Mouse can	DR
c 262	15.6	70.9	34471	14	ADZ12758	Adz12758 Murine ca	XX
c 263	15.6	70.9	38726	4	AAS59513	Aas59513 Propionib	PT
c 264	15.6	70.9	38726	8	ACF64442	Acf64442 Propionib	PT
c 265	15.6	70.9	41400	10	ABX77189	Abx77189 Mouse BAC	XX
c 266	15.6	70.9	47988	10	ADR86070	Adr86070 Streptomy	XX
c 267	15.6	70.9	52659	9	AAL60188	Aal60188 Paederus	PS
c 268	15.6	70.9	82615	9	ACA60905	Ac60905 Human tra	XX
c 269	15.6	70.9	82615	14	AEA04986	Aea04986 Human tra	CC
c 270	15.6	70.9	94001	13	ADJ33491	Adj33491 Human LAR	CC
c 271	15.6	70.9	94941	15	AEF80170	Aef80170 Cancer-as	CC
c 272	15.6	70.9	110000	13	ABD32629_2	Abd32629_2	CC
c 273	15.6	70.9	110000	14	ADQ12821_3	Adq12821_3	CC
c 274	15.6	70.9	114771	12	ADQ17641	Adq17641 Human sof	CC
c 275	15.6	70.9	12722	12	ADQ97301	Adq97301 Human can	CC
c 276	15.6	70.9	142299	10	ADP50651	Adp50651 BAC seque	CC
c 277	15.6	70.9	142299	14	ADV77909	Adv77909 Human BAC	CC
c 278	15.6	70.9	227246	13	ABD33272	Abd33272 Human can	CC
c 279	15.4	70.0	23	12	ADH09470	Adh09470 Propionib	CC
c 280	15.4	70.0	383	12	ADF13121	Adf13121 Hypermeth	XX
c 281	15.4	70.0	383	12	ADJ37267	Adj37267 Hypermeth	XX
c 282	15.4	70.0	668	13	AAF12059	Aaf12059 Aspergill	XX
c 283	15.4	70.0	668	13	ADU56100	Adu56100 Aspergill	XX
c 284	15.4	70.0	668	14	ADZ94103	Adz94103 Aspergill	XX
c 285	15.4	70.0	911	6	ABN73985	Abn73985 Bovine em	XX
c 286	15.4	70.0	1463	15	AEF24215	Aef24215 16S rRNA	XX
c 287	15.4	70.0	3198	5	AAH81777	Aah81777 Human dif	XX
c 288	15.4	70.0	3198	6	AAI67787	Aai67787 Human lys	XX
c 289	15.4	70.0	3198	6	ABQ88184	Abq88184 Human ost	XX
c 290	15.4	70.0	3198	6	ABX04181	Abx04181 Human mRN	XX
c 291	15.4	70.0	3432	12	ADQ85032	Adq85032 Human tum	XX
c 292	15.4	70.0	3573	13	ACN43163	Acn43163 Human dia	XX
c 293	15.4	70.0	3594	13	ACN43162	Acn43162 Human dia	XX
c 294	15.4	70.0	3609	13	ACN43161	Acn43161 Human dia	XX
c 295	15.4	70.0	3630	13	ACN43160	Acn43160 Human dia	XX
c 296	15.4	70.0	3723	13	ACN43159	Acn43159 Human dia	XX
c 297	15.4	70.0	3804	13	ACN43158	Acn43158 Human dia	XX
c 298	15.4	70.0	8653	5	ABAI5780	Abai5780 Human ner	XX
c 299	15.4	70.0	61710	4	AAK83782	Aak83782 Human imm	XX
c 300	15.4	70.0	61710	4	AAK83782	Aak83782 Human imm	XX

ALIGNMENTS

RESULT 1
 AAD11275
 ID AAD11275 standard; DNA; 22 BP.
 XX
 AC AAD11275;

24-SEP-2001 (first entry)
 Mycobacterium 16S rRNA amplifying primer #19.
 Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
 Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
 Mycobacterium sp.
 WO200144510-A2.
 21-JUN-2001.
 17-DEC-1999; 99WO-US030346.
 17-DEC-1999; 99WO-US030346.
 (GENP-GEN-PROBE INC.
 (INMR) BIOMERIEUX SA.
 Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
 WFI; 2001-398170/42.
 Detecting Mycobacterium species, involves in vitro amplification of 16S
 rRNA or DNA encoding RNA in nucleic acid amplification mixture using
 specific primers, and detecting the amplified nucleic acid.
 Claim 1; Page 37; 44pp; English.
 The invention relates to a method of detecting Mycobacterium species,
 that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
 encoding 16S rRNA in an in vitro nucleic acid amplification mixture
 comprising a polymerase, and at least two primers, and then detecting the
 amplified nucleic acid. The method is relatively simple and useful for
 detecting the presence of various Mycobacterium species in a biological
 sample, and thus important for diagnosis of infections resulting from
 them. The method is especially important for screening opportunistic
 infections caused by M. tuberculosis or a Mycobacterium other than
 tuberculosis (MOTT). The present sequence is a PCR primer used for
 amplifying Mycobacterium 16S rRNA
 Query Match 100.0%; Score 22; DB 4; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.7;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GAAAGGCGCTTCGGGGTGCTC 22
 Db 1 GAAAGGCGCTTCGGGGTGCTC 22
 RESULT 2
 ADG88356
 ID ADG88356 standard; DNA; 22 BP.
 XX
 AC ADG88356;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Mycobacterium amplifying PCR primer #25.
 XX
 KW In vitro amplification; PCR; primer; ss.
 XX
 OS Mycobacterium celatum.
 XX
 PN US2003165824-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 15-DEC-2000; 2000US-00738274.


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XX 17-DEC-1999; 99US-0172190P.
XX (BREN/) BRENTANO S T.
XX (JUCK/) JUCKER M T.
XX (DELG/) DELGADO F D.
XX (CLEU/) CLEUZIAT P.
XX (RODR/) RODRIGUE M.
XX
XX PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2003-898044/82.
XX
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX in a biological sample comprises performing in vitro nucleic acid
XX amplification and detection of amplified products.
XX
XX Claim 1; SEQ ID NO 25; 20pp; English.
XX
XX The present invention relates to a method of detecting Mycobacterium
XX species present in a biological sample comprises performing an in vitro
XX amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
XX detecting the amplified Mycobacterium nucleic acid. The present sequence
XX is Mycobacterium amplifying PCR primer.
XX
XX Sequence 22 BP; 3 A; 5 C; 9 G; 5 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 22; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GAAAGGCCTTTCGGGGTGCTC 22
Db 1 GAAAGGCCTTTCGGGGTGCTC 22
XX
RESULT 4
ID AAD11276 standard; DNA; 25 BP.
XX
XX AAD11276;
XX
XX 24-SEP-2001 (first entry)
XX
XX Mycobacterium 16S rRNA amplifying primer #20.
XX
XX Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
XX Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
XX
XX Mycobacterium sp.
XX
XX WO200144510-A2.
XX
XX 21-JUN-2001.
XX
XX 17-DEC-1999; 99WO-US030346.
XX
XX 17-DEC-1999; 99WO-US030346.
XX
XX (GENP-) GEN-PROBE INC.
XX (INMR ) BIOMERIEUX SA.
XX
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2001-398170/42.
XX
XX Detecting Mycobacterium species, involves in vitro amplification of 16S
XX rRNA or DNA encoding RNA in nucleic acid amplification mixture using
XX specific primers, and detecting the amplified nucleic acid.
XX
XX Claim 1; Page 37; 44pp; English.
XX
XX The invention relates to a method of detecting Mycobacterium species,
XX that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
XX encoding 16S rRNA in an in vitro nucleic acid amplification mixture
XX comprising a polymerase, and at least two primers, and then detecting the
XX amplified nucleic acid. The method is relatively simple and useful for
XX detecting the presence of various Mycobacterium species in a biological
XX sample, and thus important for diagnosis of infections resulting from
XX the method is especially important for screening opportunistic
XX infections caused by M. tuberculosis or a Mycobacterium other than
XX tuberculosis (MOTT). The present sequence is a PCR primer used for
XX amplifying Mycobacterium 16S rRNA
XX
XX Sequence 25 BP; 4 A; 5 C; 11 G; 5 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 22; DB 4; Length 25;

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Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTTCGGGGGTGCTC 22
Db 1 GAAAGGCCTTTCGGGGGTGCTC 22

RESULT 5
ADG88357
ID ADG88357 standard; DNA; 25 BP.
AC ADG88357;
XX
DT 11-MAR-2004 (first entry)
DE Mycobacterium amplifying PCR primer #26.
XX
XX In vitro amplification; PCR; primer; ss.
KW
XX
OS Mycobacterium celatum.
XX
XX US2003165824-A1.
XX
PD 04-SEP-2003.
XX
PF 15-DEC-2000; 2000US-00738274.
XX
PR 17-DEC-1999; 99US-0172190P.
XX
XX (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAT P.
PA (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodriguez M;
XX
XX WPI; 2003-898044/82.
XX
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX in a biological sample comprises performing in vitro nucleic acid
XX amplification and detection of amplified products.
XX
XX Claim 1; SEQ ID NO 26; 20pp; English.
XX
XX The present invention relates to a method of detecting Mycobacterium
XX species present in a biological sample comprises performing an in vitro
XX amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
XX detecting the amplified Mycobacterium nucleic acid. The present sequence
XX is Mycobacterium amplifying PCR primer.
XX
XX Sequence 25 BP; 4 A; 5 C; 11 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTTCGGGGGTGCTC 22
Db 1 GAAAGGCCTTTCGGGGGTGCTC 22

RESULT 6
AEA08232
ID AEA08232 standard; DNA; 25 BP.
XX
AC AEA08232;
XX
DT 14-JUL-2005 (first entry)
XX
XX Mycobacterium celatum 16S rRNA amplifying non-T7 primer, SEQ ID NO: 26.
DE
XX

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KW Microorganism detection; DNA amplification; 16s ribosomal RNA; 16s rRNA;
KW PCR; primer; ss.
XX
XX Mycobacterium celatum.
XX
XX US2005100915-A1.
XX
XX 12-MAY-2005.
XX
XX 18-SEP-2003; 2003US-00665708.
XX
XX 17-DEC-1999; 99US-0172190P.
XX
XX 15-DEC-2000; 2000US-00738274.
XX
XX (BREN/) BRENTANO S T.
XX (JUCK/) JUCKER M T.
XX (DELG/) DELGADO F D.
XX (CLEU/) CLEUZIAT P.
XX (RODR/) RODRIGUE M.
XX
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodriguez M;
XX
XX WPI; 2005-345392/35.
XX
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX in a biological sample, comprises using in vitro nucleic acid
XX amplification and detection of amplified products.
XX
XX Example 3; SEQ ID NO 26; 21pp; English.
XX
XX The present invention relates to a method of detecting Mycobacterium
XX species present in a biological sample. The method involves using in
XX vitro nucleic acid amplification and detection of amplified products. The
XX invention is useful for diagnostic detection of pathogenic bacteria such
XX as Mycobacterium species. The present sequence is the Mycobacterium
XX celatum (ATCC 51130 and AFCC 51131) 16S ribosomal RNA (16SrRNA)
XX amplifying non-T7 PCR primer.
XX
XX Sequence 25 BP; 4 A; 5 C; 11 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTTCGGGGGTGCTC 22
Db 1 GAAAGGCCTTTCGGGGGTGCTC 22

RESULT 7
AAX32480
ID AAX32480 standard; DNA; 23 BP.
XX
AC AAX32480;
XX
XX 22-JUN-1999 (first entry)
XX
XX Probe CNB-ESP derived from a variable region of 16S rRNA.
XX
XX 16S rRNA; maduromycetes; hybridisation; streptomycetes; probe; ss.
XX
XX Synthetic.
XX
XX Streptomyces ambofaciens.
XX
XX WO9914361-A1.
XX
XX 25-MAR-1999.
XX
XX 16-SEP-1998; 98WO-EP006038.
XX
XX 18-SEP-1997; 97US-0059295P.
XX
XX 16-DEC-1997; 97US-0069748P.
XX
XX

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PA (MERI ) MERCK SHARP & DOHME ESPANA SAE.
XX
XX Genilloud O, Mellado RP, Parro V, Rodriguez V;
XX WPI; 1999-229548/19.
DR
XX
XX New probes used for detection of maduromycetes bacteria and to
PT differentiate between maduromycetes and streptomycetes.
PT
XX
XX Claim 5; Page 13; 22pp; English.
PS
XX
XX The invention relates to a novel nucleic acid probe hybridises to a
CC nucleic acid encoding a portion of 16S rRNA of maduromycetes bacteria
CC under hybridisation conditions, and does not hybridise to nucleic acids
CC encoding a portion of 16S rRNA of streptomycetes under identical
CC hybridisation conditions. The probes can be used for detecting the
CC presence of maduromycetes bacteria in a sample and for differentiating
CC between maduromycetes and streptomycetes bacteria in a sample. The
CC present sequence represents a probe derived from a highly variable region
CC of 16S rRNA molecule
XX
XX Sequence 23 BP; 4 A; 6 C; 9 G; 4 T; 0 U; 0 Other;
SQ
Query Match 85.5%; Score 18.8; DB 2; Length 23;
Best Local Similarity 90.9%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GAAAGCCCTTCGGGGTGCTC 22
DB 1 GAAAGCCCTTCGGGGTGACTC 22
RESULT 8
ID AAX32481 standard; DNA; 166 BP.
AC
XX
XX 22-JUN-1999 (first entry)
DT
DE Preferred probe of the invention.
XX
XX 16S rRNA; maduromycetes; hybridisation; streptomycetes; probe; ss.
XX
XX Synthetic.
OS Streptomycetes ambofaciens.
XX
XX WO9914361-A1.
PN
XX
XX 25-MAR-1999.
PD
XX
XX 16-SEP-1998; 98WO-EP006038.
PF
XX
XX 18-SEP-1997; 97US-0059295P.
PR
XX 16-DEC-1997; 97US-0069748P.
XX
XX (MERI ) MERCK SHARP & DOHME ESPANA SAE.
PA
XX Genilloud O, Mellado RP, Parro V, Rodriguez V;
PI
XX WPI; 1999-229548/19.
DR
XX
XX New probes used for detection of maduromycetes bacteria and to
PT differentiate between maduromycetes and streptomycetes.
PT
XX
XX Disclosure; Fig 1; 22pp; English.
PS
XX
XX The invention relates to a novel nucleic acid probe hybridises to a
CC nucleic acid encoding a portion of 16S rRNA of maduromycetes bacteria
CC under hybridisation conditions, and does not hybridise to nucleic acids
CC encoding a portion of 16S rRNA of streptomycetes under identical
CC hybridisation conditions. The probes can be used for detecting the
CC presence of maduromycetes bacteria in a sample and for differentiating
CC

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```

CC between maduromycetes and streptomycetes bacteria in a sample. The
CC present sequence represents a preferred probe of the invention
XX
XX Sequence 166 BP; 39 A; 43 C; 55 G; 29 T; 0 U; 0 Other;
SQ
Query Match 85.5%; Score 18.8; DB 2; Length 166;
Best Local Similarity 90.9%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GAAAGCCCTTCGGGGTGCTC 22
DB 68 GAAAGCCCTTCGGGGTGACTC 89
RESULT 9
ADM27081_00/c
WP Sequence split into 17 fragments LOCUS ADM27081 Accession Adm27081
WP Fragment Name Begin End
WP ADM27081_00 1 110000
WP ADM27081_01 100001 210000
WP ADM27081_02 200001 310000
WP ADM27081_03 300001 410000
WP ADM27081_04 400001 510000
WP ADM27081_05 500001 610000
WP ADM27081_06 600001 710000
WP ADM27081_07 700001 810000
WP ADM27081_08 800001 910000
WP ADM27081_09 900001 1010000
WP ADM27081_10 1000001 1110000
WP ADM27081_11 1100001 1210000
WP ADM27081_12 1200001 1310000
WP ADM27081_13 1300001 1410000
WP ADM27081_14 1400001 1510000
WP ADM27081_15 1500001 1610000
WP ADM27081_16 1600001 1694968
ID ADM27081 standard; DNA; 1694968 BP.
XX
XX ADM27081;
AC
XX
XX 20-MAY-2004 (first entry)
DT
XX
DE Hyperthermophile Methanopyrus kandleri complete genome.
XX
XX hyperthermophile; protein stability enhancement;
KW protein activity enhancement; ds.
XX
XX Methanopyrus kandleri.
OS
XX WO2003076575-A2.
XX
XX 18-SEP-2003.
PD
XX
XX 04-MAR-2003; 2003WO-US006664.
PF
XX
XX 04-MAY-2002; 2002US-0361742P.
PR
XX 14-MAY-2002; 2002US-0380423P.
PR
XX 16-SEP-2002; 2002US-0410974P.
XX
XX (FIDE-) FIDELITY SYSTEMS INC.
PA (MALY/) MALYKH A.
XX
XX Slesarev AI, Pavlov A, Pavlova N, Kozyavkin S;
PI
XX WPI; 2003-748383/70.
DR
XX
XX New isolated nucleic acids encoding any of about 1700 Methanopyrus
PT kandleri proteins, and the encoded proteins, useful as a medicaments or
PT as diagnostic agents.
XX
XX Claim 17; SEQ ID NO 1693; 1023pp; English.
PS
XX The invention comprises the amino acid sequence of proteins from the
XX hyperthermophile Methanopyrus kandleri, the invention also comprises the
CC

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complete genome from Methanopyrus kandleri. The Methanopyrus kandleri proteins of the invention are useful for enhancing the stability and/or activity of other proteins. The Methanopyrus kandleri genome is useful in a variety of diagnostic and analytical methods. The present DNA sequence CC represents the Methanopyrus kandleri complete genome.

Sequence 1694968 BP; 329927A; 520759C; 515869G; 328413T; 0U; 0Other;
Query Match 85.5%; Score 18.8; DB 11; Length 110000;
Best Local Similarity 90.9%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 1 GAAAGGCCCTTCGGGGGTGC TC 22
||||| ||||| ||||| ||
Db 54678 GAAAGGCCCTTCGGGGGTGATC 54657

RESULT 10
ADP65654
ID ADP65654 standard; DNA; 487 BP.
XX AC
AC ADP65654;
DT 12-AUG-2004 (first entry)
XX
DE Human peripheral benzodiazepine receptor gene, exon 2 DNA.
XX
KW autoimmune disease; arthritis; gene expression analysis;
KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
KW antiarthritis; osteopathic; antigout; antiinflammatory; dermatological;
KW immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;
KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
KW immune; ds; human.
XX
OS Homo sapiens.
XX
XX WO2003072827-A1.
XX
XX PD 04-SEP-2003.
XX
XX PF 31-OCT-2002; 2002WO-US035433.
XX
XX PR 31-OCT-2001; 2001US-03362220P.
XX
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX
PI Hirsch R, Thorton SL;
DR WPI; 2003-712740/67.
XX GENBANK; L21952.
XX
PT Diagnosing and analyzing autoimmune disease using gene expression
PT profiles and microarray technology, useful for diagnosing and treating
PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
PT gout.
PS Disclosure; Page; 56pp; English.
XX
XX The invention relates to a novel method for diagnosing and analysing
CC autoimmune disease or arthritides. The method comprises obtaining a
CC patient sample containing mRNA, analysing gene expression using the mRNA
CC that results in a gene expression signature of the mRNA, and using that
CC gene expression signature to diagnose or analyse the autoimmune disease
CC or arthritides in the patient, where gene expression of at least 60% of
CC the genes correlates with that of the gene signature. The invention
CC further comprises: a treatment of rheumatoid arthritis; identification of
CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
CC analyses of autoimmune disease or rheumatoid arthritis; screening the
CC efficacy of a candidate drug in vitro for the treatment of collagen-
CC induced arthritis; and reducing the symptoms associated with collagen-
CC induced arthritis. The compositions of the invention have the following

CC activities: immunosuppressive, antiarthritic, antirheumatic, antiinflammatory, dermatological, and immunomodulatory. The
CC antigenout, antiinflammatory, dermatological, and immunomodulatory. The
CC methods and compositions of the present invention are useful for
CC diagnosing and treating autoimmune disease or arthritides, such as
CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
CC immune disease caused by an infectious agent. This polynucleotide
CC represents a DNA sequence relating to the genes used in the analysis and
CC treatment of autoimmune diseases or arthritides. Note: This sequence is
CC not shown in the specification. It has been supplied in an electronic
CC format from WIPO.

XX

SQ Sequence 487 BP; 67 A; 168 C; 156 G; 96 T; 0 U; 0 Other;

Query Match 80.9%; Score 17.8; DB 11; Length 487;
Best Local Similarity 90.5%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAGGCGCTTCGGGGTGCT 21
||| |||||||||
DB 79 GACAGGCGCTTCGGGGATGCT 99

RESULT 11
ACN44798/c
ID ACN44798 standard; DNA; 40491 BP.
XX
AC ACN44798;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human genomic sequence hCG41911.
XX
KW Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
XX
OS Homo sapiens.
XX
PN W02003073826-A2.
XX
PD 12-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-US006235.
XX
PR 01-MAR-2002; 2002US-00087192.
XX
(SAGR-) SAGRES DISCOVERY.
XX
PA Morris DW;
XX
PI
XX
DR WFI; 2003-328604/31.
XX
PT Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
comprises a nucleotide sequence.
XX
PS Claim 1; SEQ ID NO 1426; Opp; English.
XX
CC The present invention relates to novel DNA and protein sequences which
are associated with carcinomas. The sequences are useful for: (i) for
screening drug candidates; (ii) for screening of bioactive agent capable
of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
a bioactive agent capable of modulating the activity of CAP; (iv) for
evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
(x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
determining Carcinoma Associated (CA) gene copy number. In addition, the
CA genes are useful as DNA vaccines and the CAP are useful as markers of
carcinoma including lymphoma. The present sequence is one such CA coding
sequence. Note: This patent is an equivalent to basic patent
US2002182586A1, for which no sequence data was published

XX
SQ Sequence 40491 BP; 9332 A; 11009 C; 11280 G; 8870 T; 0 U; 0 Other;

Query Match 80.9%; Score 17.8; DB 11; Length 40491;
Best Local Similarity 90.5%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGCCCTTCGGGGTGCT 21
DB 37999 GACAGGCCTTCGGGGTGCT 37979

RESULT 12
ACN44932_3
Continuation (4 of 4) of ACN44932 from base 300001 (Mouse genomic sequence mCG5728.)
WP Sequence split into 4 fragments LOCUS ACN44932 Accession ACN44932
Fragment Name Begin End
WP ACN44932_0 1 110000
WP ACN44932_1 100001 210000
WP ACN44932_2 200001 310000
WP ACN44932_3 300001 374849

Query Match 79.1%; Score 17.4; DB 11; Length 74849;
Best Local Similarity 94.7%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AAGGCCTTCGGGGTGCT 21
DB 53594 AAGGCCTTCAGGGTGCT 53612

RESULT 13
ABA59963
ID ABA59963 standard; DNA; 569 BP.
XX AC ABA59963;
XX AC ABA59963;
DT 01-FEB-2002 (first entry)
XX XX
DE Human foetal liver single exon nucleic acid probe #8268.
XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX Homo sapiens.
XX WO200157277-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US000669.
XX 04-FEB-2000; 2000US-0180312P.
XX 25-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234587P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human foetal liver.
XX Claim 1; SEQ ID NO 8268; 639pp + Sequence Listing; English.
XX The invention relates to a single exon nucleic acid probe for measuring
XX human gene expression in a sample derived from human foetal liver. The
XX single exon nucleic acid probes may be used for predicting, measuring and
XX displaying gene expression in samples derived from human foetal liver. The
XX present sequence is a single exon nucleic acid probe of the invention.
XX Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 569 BP; 144 A; 123 C; 151 G; 151 T; 0 U; 0 Other;
Query Match 78.2%; Score 17.2; DB 4; Length 569;
Best Local Similarity 86.4%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCCCTTCGGGGTGCTC 22
DB 290 GAAAGCCCTTCAGGGTGCTC 311

RESULT 14
AAI39835
ID AAI39835 standard; DNA; 569 BP.
XX AC AAI39835;
XX AC AAI39835;
DT 17-OCT-2001 (first entry)
XX XX
DE Probe #8521 used to measure gene expression in human placenta sample.
XX Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder; ss.
XX Homo sapiens.
XX WO200157272-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US000663.
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234587P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human placenta.
XX Claim 25; SEQ ID NO 8521; 654pp; English.
XX The present invention relates to single exon nucleic acid probes (SENP).
XX The present sequence is one such probe. The probes are useful for
XX producing a microarray for predicting, measuring and displaying gene
XX expression in samples derived from human placenta. The probes are useful
XX for antenatal diagnosis of human genetic disorders
XX
SQ Sequence 569 BP; 144 A; 123 C; 151 G; 151 T; 0 U; 0 Other;
Query Match 78.2%; Score 17.2; DB 4; Length 569;
Best Local Similarity 86.4%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCCCTTCGGGGTGCTC 22
DB 290 GAAAGCCCTTCAGGGTGCTC 311

RESULT 15
ABA28379

```
ID  ABA28379 standard; DNA; 569 BP.
XX
AC  ABA28379;
XX
DT  23-JAN-2002 (first entry)
XX
XX  Probe #6845 for gene expression analysis in human heart cell sample.
DE
XX  Human; gene expression; heart; microarray; vascular system; probe;
KW  cardiovascular disease; hypertension; cardiac arrhythmia;
KW  congenital heart disease; ss.
XX
OS  Homo sapiens.
XX
XX  WO200157274-A2.
PN
XX  09-AUG-2001.
PD
XX
XX  30-JAN-2001; 2001WO-US000666.
PF
XX  04-FEB-2000; 2000US-0180312P.
PR  26-MAY-2000; 2000US-0207456P.
PR  30-JUN-2000; 2000US-00608408.
PR  03-AUG-2000; 2000US-00632366.
PR  21-SEP-2000; 2000US-0234687P.
PR  27-SEP-2000; 2000US-0236359P.
PR  04-OCT-2000; 2000GB-00024263.
XX
XX  (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX  Penn SG, Hanzel DK, Chen W, Rank DR;
PI  WPI; 2001-488899/53.
XX
XX  Single exon nucleic acid probes for analyzing gene expression in human
PT  hearts.
XX
XX  Claim 1; SEQ ID NO 6845; 530pp; English.
PS
XX  The present invention relates to single exon nucleic acid probes for
XX  measuring human gene expression in a sample derived from human heart. The
CC  present sequence is one such probe. The probes may be used for
CC  predicting, measuring and displaying gene expression in samples derived
CC  from the human heart via microarrays. By measuring gene expression, the
CC  probes are useful for predicting, diagnosing, grading, staging,
CC  monitoring and prognosing diseases of the human heart and vascular system
CC  e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC  congenital heart disease. Note: The sequence data for this patent did not
CC  form part of the printed specification, but was obtained in electronic
CC  format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX  Sequence 569 BP; 144 A; 123 C; 151 G; 151 T; 0 U; 0 Other;
SQ
Query Match      78.2%; Score 17.2; DB 4; Length 569;
Best Local Similarity 86.4%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  1 GAAAGGCTTTCGGGGTGCTC 22
    ||||| ||||| ||||| |||||
Db   290 GAAAGGCTCTCAGGGTGCTC 311

RESULT 16
AAK34112
ID  AAK34112 standard; DNA; 569 BP.
XX
XX  AAK34112;
AC
XX  06-NOV-2001 (first entry)
DT
XX  Human bone marrow expressed single exon probe SEQ ID NO: 8669.
DE
XX  Human; bone marrow expressed exon; gene expression analysis; probe;
KW  Human; bone marrow expressed exon; gene expression analysis; probe;
```

```
KW  microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS  Homo sapiens.
XX
XX  WO200157276-A2.
PN
XX  09-AUG-2001.
PD
XX
XX  30-JAN-2001; 2001WO-US000668.
PF
XX  04-FEB-2000; 2000US-0180312P.
PR  26-MAY-2000; 2000US-0207456P.
PR  30-JUN-2000; 2000US-00608408.
PR  03-AUG-2000; 2000US-00632366.
PR  21-SEP-2000; 2000US-0234687P.
PR  27-SEP-2000; 2000US-0236359P.
PR  04-OCT-2000; 2000GB-00024263.
XX
XX  (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX  Penn SG, Hanzel DK, Chen W, Rank DR;
PI  WPI; 2001-488900/53.
XX
XX  Human genome-derived single exon nucleic acid probes useful for analyzing
PT  gene expression in human bone marrow.
XX
XX  Example 4; SEQ ID NO 8669; 658pp + Sequence Listing; English.
PS
XX  The present invention provides a number of single exon nucleic acid
XX  probes which are derived from genomic sequences expressed in the human
CC  bone marrow. They can be used to measure gene expression in bone marrow
CC  samples, which may enable the improved diagnosis and treatment of cancers
CC  such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC  the probes of the invention
XX
XX  Sequence 569 BP; 144 A; 123 C; 151 G; 151 T; 0 U; 0 Other;
SQ
Query Match      78.2%; Score 17.2; DB 4; Length 569;
Best Local Similarity 86.4%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  1 GAAAGGCTTTCGGGGTGCTC 22
    ||||| ||||| ||||| |||||
Db   290 GAAAGGCTCTCAGGGTGCTC 311

RESULT 17
AAK08233
ID  AAK08233 standard; DNA; 569 BP.
XX
XX  AAK08233;
AC
XX  05-NOV-2001 (first entry)
DT
XX  Human brain expressed single exon probe SEQ ID NO: 8224.
DE
XX  Human; brain expressed exon; gene expression analysis; probe; microarray;
KW  Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
XX  ss.
XX
XX  Homo sapiens.
OS
XX  WO200157275-A2.
PN
XX  09-AUG-2001.
PD
XX
XX  30-JAN-2001; 2001WO-US000667.
PF
XX  04-FEB-2000; 2000US-0180312P.
PR  26-MAY-2000; 2000US-0207456P.
PR  30-JUN-2000; 2000US-00608408.
PR  03-AUG-2000; 2000US-00632366.
```

PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-483446/52.
 XX
 XX Single exon nucleic acid probes for analyzing gene expression in human
 PT brains.
 PT
 XX Example 4; SEQ ID NO 8224; 650pp + Sequence Listing; English.
 PS
 XX The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is one of the probes of the
 CC invention
 XX
 SQ Sequence 569 BP; 144 A; 123 C; 151 G; 151 T; 0 U; 0 Other;
 Query Match 78.2%; Score 17.2; DB 4; Length 569;
 Best Local Similarity 86.4%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
 Matches 19; Conservative 0; Indels 3; Indels 0; Gaps 0;
 QY 1 GAAAGGCTTTCGGGGTGCTC 22
 Db 290 GAAAGGCTTTCAGGGTGCTC 311
 RESULT 18
 ABS33911
 ID ABS33911 standard; DNA; 569 BP.
 XX
 AC ABS33911;
 XX
 DT 25-FEB-2003 (first entry)
 XX
 DE Human liver single exon probe, SEQ ID No 8901.
 XX
 XX Human; single exon nucleic acid probe; liver; cirrhosis;
 KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
 KW coronary heart disease; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200157273-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 30-JAN-2001; 2001WO-US0000664.
 XX
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488898/53.
 XX
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human adult liver.
 PT
 XX

PS Claim 1; SEQ ID NO 8901; 658pp; English.
 XX
 CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
 CC measuring human gene expression in a sample derived from human adult
 CC liver, comprising one of 13109 defined nucleotide sequences given in the
 CC specification (or complements/ fragments). The probe hybridizes at high
 CC stringency to a nucleic acid molecule expressed in the human adult liver.
 CC (I) may be used for predicting, measuring and displaying gene expression
 CC in samples derived from human adult liver. The genes identified may be
 CC involved in genetic liver diseases such as cirrhosis,
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
 CC associated with coronary heart disease. ABS25011-ABS51005 represent human
 CC liver single exon nucleic acid probes of the invention. Note: The
 CC sequence information for this patent does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 569 BP; 144 A; 123 C; 151 G; 151 T; 0 U; 0 Other;
 Query Match 78.2%; Score 17.2; DB 4; Length 569;
 Best Local Similarity 86.4%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
 Matches 19; Conservative 0; Indels 3; Indels 0; Gaps 0;
 QY 1 GAAAGGCTTTCGGGGTGCTC 22
 Db 290 GAAAGGCTTTCAGGGTGCTC 311
 RESULT 19
 ABS08880
 ID ABS08880 standard; DNA; 569 BP.
 XX
 AC ABS08880;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human genome-derived single exon probe from lung SEQ ID No 8871.
 XX
 XX Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.
 XX
 OS Homo sapiens.
 XX
 XX WO200186003-A2.
 XX
 XX 15-NOV-2001.
 XX
 XX 30-JAN-2001; 2001WO-US0000665.
 XX
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2002-114183/15.
 XX
 XX Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples.
 PT
 XX

PS Claim 1; SEQ ID NO 8871; 634pp; English.

XX The invention relates to a spatially-addressable set of single exon

CC nucleic acid probes for measuring gene expression in a sample derived

CC from human lung comprising single exon nucleic acid probes having one of

CC 12614 nucleic acid sequences mentioned in the specification, or their

CC complements or the 12387 open reading frames derived from the 12614

CC probes. Also included are a microarray comprising the novel set of probes

CC; the novel set of probes which hybridise at high stringency to a nucleic

CC acid expressed in the human lung; measuring gene expression in a sample

CC derived from human lung, comprising (a) contacting the array with a

CC collection of detectably labeled nucleic acids derived from human lung

CC mRNA, and (b) measuring the label detectably bound to each probe of the

CC array; identifying exons in a eukaryotic genome, comprising (a)

CC algorithmically predicting at least one exon from genomic sequences of

CC the eukaryote; and (b) detecting specific hybridisation of detectably

CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,

CC having a fragment identical to the predicted exon, the probe is included

CC in the above mentioned microarray; assigning exons to a single gene,

CC comprising (a) identifying exons from genomic sequence by the method

CC above and (b) measuring the expression of each of the exons in several

CC tissues and/or cell types using hybridisation to a single exon

CC microarrays having a probe with the exon, where a common pattern of

CC expression of the exons in the tissues and/or cell types indicates that

CC the exons should be assigned to a single gene; a peptide comprising one

CC of 12011 sequences, mentioned in the specification, or encoded by the

CC probes/open reading frames (ORF). The probes are used for gene expression

CC analysis, and for identifying exons in a gene, particularly using human

CC lung derived mRNA and for the study of lung diseases such as asthma, lung

CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung

CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,

CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-

CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary

CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,

CC Karagenes syndrome, fibrocystic pulmonary dysplasia, primary ciliary

CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The

CC present sequence is a single exon probe of the invention. Note: The

CC sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences

XX

XX Sequence 569 BP; 144 A; 123 C; 151 G; 151 T; 0 U; 0 Other;

Query Match 78.2%; Score 17.2; DB 6; Length 569;

Best Local Similarity 86.4%; Pred. No. 2e+02;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTCGGGGTGCTC 22

Db 290 GAAAGGCTTCAGGGTGCTC 311

RESULT 20

ACA36105

ID ACA36105 standard; DNA; 1440 BP.

XX

XX ACA36105;

XX

XX 19-JUN-2003 (first entry)

XX

XX Prokaryotic essential gene #17762.

XX

XX Antisense; ds; prokaryotic essential gene; cell proliferation;

XX drug design; gene.

XX

XX Klebsiella pneumoniae.

XX

XX WO200277183-A2.

XX

XX 03-OCT-2002.

XX

XX 21-MAR-2002; 2002WO-US009107.

XX

PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362899P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wali D, Trawick JB, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR P-PSDB; ABU32235.

DR

XX New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.

XX

XX Claim 14; SEQ ID NO 23975; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression

CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense

CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

CC proliferation or the activity of a gene in an operon required for

CC proliferation; (7) identifying a compound that influences the activity of

CC the gene product or that has an activity against a biological pathway

CC required for proliferation, or that inhibits cellular proliferation; (8)

CC identifying a gene required for cellular proliferation or the biological

CC pathway in which a proliferation-required gene or its gene product lies

CC or a gene on which the test compound that inhibits proliferation of an

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

CC compound's activity; (11) a culture comprising strains in which the gene

CC product is overexpressed or underexpressed; (12) determining the extent

CC to which each of the strains is present in a culture or collection of

CC strains; or (13) identifying the target of a compound that inhibits the

CC proliferation of an organism. The antisense nucleic acids are useful for

CC identifying proteins or screening for homologous nucleic acids required

CC for cellular proliferation to isolate candidate molecules for rational

CC drug discovery programs, or for screening homologous nucleic acids

CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,

CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target

CC prokaryotic essential genes. Note: The sequence data for this patent did

CC not form part of the printed specification, but was obtained in

CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX

XX Sequence 1440 BP; 242 A; 437 C; 464 G; 297 T; 0 U; 0 Other;

Query Match 78.2%; Score 17.2; DB 8; Length 1440;

Best Local Similarity 86.4%; Pred. No. 2.2e+02;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTCGGGGTGCTC 22

Db 141 GAAAGGCTTCGGGGTGCTC 162

RESULT 21

ADA02540

ID ADA02540 standard; DNA; 58822 BP.

XX

XX ADA02540;

XX

XX 06-NOV-2003 (first entry)

XX

XX Human TCOF1 carcinoma associated gene, SEQ ID NO:1058.

XX

KW Human; carcinoma associated; oncogene; carcinoma; cancer; breast;
KW prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
KW gene; ds.
XX Homo sapiens.
OS
XX WO2003057146-A2.
PN
XX 17-JUL-2003.
XX
XX 26-DEC-2002; 2002WO-US041414.
PF
XX 26-DEC-2001; 2001US-00035832.
PR
XX (SAGR-) SAGRES DISCOVERY.
PA
XX Morris DW;
PI
XX WPI; 2003-587068/55.
DR
XX New recombinant nucleic acid encoding carcinoma associated protein,
PT useful for preparing compositions for treating carcinomas.
PT
XX Claim 1; SEQ ID NO 1058; 245pp; English.
PS
XX The invention relates to recombinant carcinoma associated (CA) nucleic
CC acid sequences from mouse and human (ADA01482-ADA03094), and to
CC recombinant carcinoma associated proteins (CAP) encoded by them. The
CC invention also encompasses expression vectors and host cells comprising a
CC CA nucleic acid, a polypeptide (especially an antibody) that specifically
CC binds to the protein, and a biochip comprising CA nucleic acid or
CC fragments thereof. The sequences of the invention were identified using
CC oncogenic retroviruses, which insert into the genome of the host organism
CC at random. Many of these do not carry transduced host oncogenes or
CC pathogenic trans-acting viral genes, meaning that cancer incidence is a
CC direct consequence of the effects of proviral integration into host
CC protooncogenes. The CA nucleic acid sequences can be used to diagnose
CC carcinoma (especially breast cancer, prostate cancer, lymphoma or
CC leukaemia) or a propensity to carcinoma by determination of the sequence
CC of a CA gene, or by determination of CA gene expression in particular
CC tissues. CA nucleic acids, proteins and antibodies are also useful as
CC therapeutic agents and in screening and evaluating drug candidates. The
CC present sequence represents a specifically claimed human CA nucleic acid
CC sequence of the invention. Note: The complete sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 58822 BP; 14199 A; 14875 C; 15625 G; 13656 T; 0 U; 467 Other;
Query Match 78.2%; Score 17.2; DB 9; Length 58822;
Best Local Similarity 86.4%; Pred. No. 2.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GAAAGGCCCTTTCGGGGTGCTC 22
Db 26859 GACAGGCCCTTTCGGGGTTCTC 26880
RESULT 22
ADB72278
ID ADB72278 standard; DNA; 58822 BP.
XX
XX ADB72278;
AC
XX 04-DEC-2003 (first entry)
DT
XX Human TCOF1 gene.
DE
XX human; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;
KW cancer; neoplasm; adenocarcinoma; sarcoma; gene.
KW
XX Homo sapiens.
XX
PT New carcinoma associated nucleic acids and proteins, useful for screening

XX WO2003008583-A2.
PN
XX 30-JAN-2003.
PD
XX
XX 26-DEC-2001; 2001WO-US051291.
PF
XX
XX 02-MAR-2001; 2001US-00798586.
PR
XX 23-OCT-2001; 2001US-00004113.
PR
XX 08-NOV-2001; 2001US-00052482.
PR
XX 30-NOV-2001; 2001US-00997722.
PR
XX 20-DEC-2001; 2001US-00034650.
XX
XX (SAGR-) SAGRES DISCOVERY.
PA
XX Morris DW, Engelhard EK;
XX WPI; 2003-239337/23.
XX
XX New recombinant nucleic acid, useful for treating carcinomas, lymphomas,
PT cancers, neoplasm, adenocarcinoma, or sarcomas.
PT
XX Claim 1; SEQ ID NO 106; 2304pp; English.
PS
XX The invention relates to a novel recombinant nucleic acid comprising a
CC nucleotide sequence selected from any of the 660 sequences fully defined
CC in the specification. A polynucleotide of the invention has cytostatic
CC activity, and may have a use in gene therapy, or in a vaccine. The
CC recombinant nucleic acids and polypeptides are useful for treating
CC carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and
CC sarcomas. The present sequence represents a human gene of the invention.
XX
SQ Sequence 58822 BP; 14199 A; 14875 C; 15625 G; 13656 T; 0 U; 467 Other;
Query Match 78.2%; Score 17.2; DB 10; Length 58822;
Best Local Similarity 86.4%; Pred. No. 2.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GAAAGGCCCTTTCGGGGTGCTC 22
Db 26859 GACAGGCCCTTTCGGGGTTCTC 26880
RESULT 23
ADE95788
ID ADE95788 standard; DNA; 58822 BP.
XX
XX ADE95788;
AC
XX 12-FEB-2004 (first entry)
DT
XX Human TCOF1 gene genomic DNA sequence.
DE
XX cancer diagnosis; cancer treatment; carcinoma; cytostatic; gene therapy;
KW lymphoma; breast cancer; prostate cancer; leukaemia; ds; human; TCOF1.
KW
XX Homo sapiens.
OS
XX WO2003039484-A2.
PN
XX 15-MAY-2003.
PD
XX 08-NOV-2002; 2002WO-US036071.
PF
XX 08-NOV-2001; 2001US-00052482.
PR
XX (SAGR-) SAGRES DISCOVERY.
PA
XX Morris DW, Engelhard EK;
XX WPI; 2003-441462/41.
XX
XX New carcinoma associated nucleic acids and proteins, useful for screening

PT drug candidates, or for diagnosing and treating carcinomas, e.g.
XX lymphoma, breast cancer, prostate cancer or leukemia.
PS Claim 1; SEQ ID NO 46; 793pp; English.
XX
CC This invention relates to novel recombinant nucleic acids for use in
CC diagnosis and treatment of cancer, especially carcinomas, as well as the
CC use of compositions in screening methods. The compositions of the
CC invention may have cytostatic activity whilst the disclosed sequences may
CC be useful for gene therapy. The carcinoma associated nucleic acids and
CC proteins are useful for diagnosing and treating carcinomas, for example
CC lymphoma, breast cancer, prostate cancer or leukemia, or for screening
CC drug candidates or bioactive agents capable of binding to, or modulating
CC the activity of, a carcinoma associated protein. The present sequence is
CC the genomic DNA sequence of the human TCOF1 gene which is a carcinoma
CC associated gene of the invention.
XX
SQ Sequence 58822 BP; 14199 A; 14881 C; 15619 G; 13656 T; 0 U; 467 Other;

Query Match 78.2%; Score 17.2; DB 10; Length 58822;
Best Local Similarity 86.4%; Pred. No. 2.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTCGGGGTGTCTC 22
Db 26859 GACAGGCCTTTCGGGGTGTCTC 26880

RESULT 24
ACN44158
ID ACN44158 standard; DNA; 63686 BP.
XX
AC ACN44158;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human genomic sequence hCG1783275.
XX
KW Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
XX
OS Homo sapiens.
XX
PN W02003073826-A2.
XX
PD 12-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-US006235.
XX
PR 01-MAR-2002; 2002US-00087192.
XX
PA (SAGR-) SAGRES DISCOVERY.
XX
PI Morris DW;
XX
DR WPI; 2003-328604/31.
XX
PT Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
PT comprises a nucleotide sequence.
XX
PS Claim 1; SEQ ID NO 466; opp; English.
XX
CC The present invention relates to novel DNA and protein sequences which
CC are associated with carcinomas. The sequences are useful for: (i) for
CC screening drug candidates; (ii) for screening of bioactive agent capable
CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
CC a bioactive agent capable of modulating the activity of CAP; (iv) for
CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC determining Carcinoma Associated (CA) gene copy number. In addition, the
CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC carcinoma including lymphoma. The present sequence is one such CA coding

CC sequence. Note: This patent is an equivalent to basic patent
CC US2002182586A1, for which no sequence data was published
XX
SQ Sequence 63686 BP; 15766 A; 14989 C; 15180 G; 17751 T; 0 U; 0 Other;

Query Match 78.2%; Score 17.2; DB 11; Length 63686;
Best Local Similarity 86.4%; Pred. No. 2.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTCGGGGTGTCTC 22
Db 45915 GAAAGGCCTTTCAGGGCTGCTC 45936

RESULT 25
ABD17022/c
ID ABD17022 standard; DNA; 276 BP.
XX
AC ABD17022;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polynucleotide #15626.
XX
KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
DR P-PSDB; AB083451.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 15626; 455pp; English.
XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABD01397-
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 276 BP; 72 A; 82 C; 66 G; 56 T; 0 U; 0 Other;

Query Match 76.4%; Score 16.8; DB 11; Length 276;
Best Local Similarity 90.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAAGGCTTTTCGGGGTGCT 21
 DB 87 AAAGGCTTTTCGAGGTGCT 68

RESULT 26
 ACN53618/c
 ID ACN53618 standard; cDNA; 601 BP.
 AC ACN53618;
 DT 02-DEC-2004 (first entry)
 DE Cotton androecium tissue EST Clone ID: LIB3828-009-Q1-K6-G5, SEQ:8399.
 DE Cotton; plant; EST; expressed sequence tag; transgenic plant; androecium;
 KW variety Nucotton33B; library LIB3828; molecular tag; molecular marker;
 KW genetic mapping; molecular mapping; seed germination; plant growth;
 KW plant quality; plant yield; plant breeding; tissue printing; ss.
 XX Gossypium hirsutum.
 OS
 XX
 PN US2004123340-A1.
 XX 24-JUN-2004.
 XX 12-DEC-2001; 2001US-00021323.
 XX 14-DEC-2000; 2000US-0255619P.
 XX (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FING/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 XX
 PI Deikman J, Feng PCC, Fincher KL, Ziegler TE;
 DR WPI; 2004-479808/45.
 XX
 PT New isolated nucleic acid molecule that encodes a plant protein or its
 PT fragment, useful for isolating a variety of agronomically significant
 PT genes associated with plant growth, quality or yield, and as molecular
 PT tags to map genes.
 XX
 PS Claim 1; SEQ ID NO 8399; 34pp; English.
 XX
 CC The invention relates to 17880 cotton expressed sequence tags (ESTs;
 CC ACN45220-ACN63099). The ESTs were isolated from cDNA libraries generated
 CC from primed or non-primed seeds from variety DP50B, mature seeds from
 CC variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium
 CC tissue, developing fibres, carpel walls and septa from variety
 CC Nucotton33B. The invention also relates to substantially purified
 CC proteins or their fragments encoded by nucleic acid molecules of the
 CC invention, and to transformed plants having a nucleic acid construct
 CC comprising a nucleic acid of the invention. The cotton ESTs are useful as
 CC molecular tags to isolate genetic regions, to isolate genes, to map
 CC genes, to determine gene function and to determine whether genes are
 CC members of a particular gene family. The nucleic acid molecules may be
 CC used for isolating a variety of agronomically significant genes
 CC associated with plant growth, quality, yield, and could also serve as
 CC links in metabolic and catabolic pathways. The nucleic acid molecules are
 CC also useful for identifying genes important in initiating and maintaining
 CC seed germination or that may be used to mitigate stresses encountered
 CC during seed germination. The ESTs additionally enable the acquisition of
 CC promoters and cis-regulatory elements which will be useful to express
 CC agronomically significant genes in these tissues and/or other tissues,
 CC and also permits the acquisition of molecular markers useful in breeding
 CC schemes, genetic and molecular mapping, and in cloning of agronomically
 CC significant genes. The nucleic acid molecules are further useful for
 CC detecting the expression level or pattern of a protein or mRNA and for
 CC detecting the presence or quantity of a protein by tissue printing. The
 CC present sequence represents a specifically claimed EST isolated from a

CC cotton variety Nucotton33B androecium tissue cDNA library (LIB3828). The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the US
 CC patent office at seqdata.uspto.gov/sequence.html?DocID=US20040123340
 XX
 SQ Sequence 601 BP; 273 A; 89 C; 106 G; 133 T; 0 U; 0 Other;
 Query Match 76.4%; Score 16.8; DB 13; Length 601;
 Best Local Similarity 90.0%; Pred. No. 3.2e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GAAAGGCTTTTCGGGGTGCT 20
 DB 525 GAAAGGCTTTTCGGGGGGGC 506

RESULT 27
 ACN31638
 ID ACN31638 standard; DNA; 2107 BP.
 XX ACN31638;
 AC ACN31638;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Prokaryotic essential gene #13295.
 KW Antisense; ds; prokaryotic essential gene; cell proliferation;
 KW drug design; gene.
 XX
 OS Enterobacter cloacae.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 DR P-PSDB; ABU27768.
 XX
 WPI; 2003-029926/02.
 DR P-PSDB; ABU27768.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 14; SEQ ID NO 19508; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2107 BP; 498 A; 511 C; 618 G; 480 T; 0 U; 0 Other;

Query Match 76.4%; Score 16.8; DB 8; Length 2107;
Best Local Similarity 90.0%; Pred. No. 3.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AAGGCCCTTCGGGGTGCTC 22
|||||
Db 113 AAGCGTTCGGGGTGCTC 132

RESULT 28
AD213575_1
Continuation (2 of 6) of AD213575 from base 100001 (Murine cancer-associated genomic DNA
WP Sequence split into 6 fragments LOCUS AD213575 Accession AD213575
WP Fragment Name Begin End
WP AD213575_0 1 110000
WP AD213575_1 100001 210000
WP AD213575_2 200001 310000
WP AD213575_3 300001 410000
WP AD213575_4 400001 510000
WP AD213575_5 500001 582589

Query Match 76.4%; Score 16.8; DB 14; Length 110000;
Best Local Similarity 90.0%; Pred. No. 4.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAGGCCCTTCGGGGTGCTC 21
|||||
Db 16886 AAGGCCCTTCGTGTGCTC 16905

RESULT 29
ABD33143
ID ABD33143 standard; DNA; 289190 BP.
XX
AC ABD33143;
XX
DT 18-NOV-2004 (first entry)
XX
DE Murine cancer-associated (CA) gene MD07-018.
XX
KW Mouse; cancer-associated protein; CAP; cancer-associated gene; CA; gene;
KW ds; cancer; cytostatic.
XX
OS Mus musculus.
XX
PN WO2004058146-A2.
XX
PD 15-JUL-2004.
XX
PF 15-DEC-2003; 2003WO-US040081.
XX
PR 17-DEC-2002; 2002US-00322281.
XX
PA (SAGR-) SAGRES DISCOVERY INC.
XX

PI Morris DW, Malandro MS;
XX WPI; 2004-499109/47.
DR
XX Novel human cancer associated protein encoded within open reading frame
PT of cancer associated gene, useful as targets for diagnosing cancer.
XX
PS Disclosure; SEQ ID NO 115; 182pp; English.
XX
CC The invention relates to cancer-associated proteins (CAP) and the cancer-
CC associated (CA) nucleic acids encoding them. The invention also relates
CC to a method for treating cancers involving administering to a patient an
CC inhibitor of CAP, and a method of screening for anticancer activity in a
CC potential drug involving providing a cell that expresses a CA gene,
CC contacting a tissue sample derived from a cancer cell with an anticancer
CC drug candidate and monitoring the effect of the anticancer drug candidate
CC on expression of the CA gene. The CAP proteins are useful for detecting
CC cancer associated with expression of a CAP protein in a test cell sample
CC and for screening for a bioactive agent capable of modulating the
CC activity of a CAP protein. The CA nucleic acids are useful for diagnosing
CC cancer, involving determining the expression of a CA nucleic acid in a
CC tissue. This sequence represents a murine CA gene of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 289190 BP; 79193 A; 58337 C; 57759 G; 83755 T; 0 U; 10146 Other;

Query Match 76.4%; Score 16.8; DB 13; Length 289190;
Best Local Similarity 90.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAGGCCCTTCGGGGTGCTC 21
|||||
Db 116861 AAGGCCCTTCGTGTGCTC 116880

RESULT 30
AAH36786
ID AAH36786 standard; cDNA; 309 BP.
XX
AC AAH36786;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen encoding cDNA SEQ ID NO:3868.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; ss.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US026524.
XX
PR 29-SEP-1999; 99US-0157137P.
PR 03-NOV-1999; 99US-0163280P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX WPI; 2001-235357/24.
DR P-PSDB; AAG77379.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX useful for preventing, diagnosing and/or treating colorectal cancers.
PS Claim 1; Page 5728-5732; 9803pp; English.
XX

AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAG77789 represent sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922

XX
SQ Sequence 309 BP; 70 A; 94 C; 73 G; 59 T; 0 U; 13 Other;

Query Match 74.5%; Score 16.4; DB 4; Length 309;
Best Local Similarity 94.4%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 AAAGGCCTTTCGGGGTGTG 19
|||||
Db 74 AAAGGCCTTTCGGGGTGTG 91

RESULT 31
ACN47886
ID ACN47886 standard; cDNA; 521 BP.
XX
AC ACN47886;
XX
DT 02-DEC-2004 (first entry)
XX
DE Cotton primed seed EST Clone ID: L1B3825-016-Q1-N6-D3, SEQ:2667.
XX
KW Cotton; plant; EST; expressed sequence tag; transgenic plant; seed;
KW variety DP50B; library L1B3825; molecular tag; molecular marker;
KW genetic mapping; molecular mapping; seed germination; plant growth;
KW plant quality; plant yield; plant breeding; tissue printing; ss.
XX
OS Gossypium hirsutum.
XX
PN US2004123340-A1.
XX
PD 24-JUN-2004.
XX
PF 12-DEC-2001; 2001US-00021323.
XX
PR 14-DEC-2000; 2000US-0255619P.
XX
PA (DEIK/) DEIKWAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
XX
PI Deikman J, Feng PCC, Fincher KL, Ziegler TE;
PI WPI; 2004-479808/45.
XX
DR
XX
PT New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular tags to map genes.
XX
PS Claim 1; SEQ ID NO 2667; 34pp; English.
XX
CC The invention relates to 17880 cotton expressed sequence tags (ESTs; ACN45220-ACN63099). The ESTs were isolated from cDNA libraries generated

from primed or non-primed seeds from variety DP50B, mature seeds from variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium tissue, developing fibres, carpel wallis and septa from variety Nuctoton38B. The invention also relates to substantially purified proteins or their fragments encoded by nucleic acid molecules of the invention, and to transformed plants having a nucleic acid construct comprising a nucleic acid of the invention. The cotton ESTs are useful as molecular tags to isolate genetic regions, to isolate genes, to map genes, to determine gene function and to determining whether genes are members of a particular gene family. The nucleic acid molecules may be used for isolating a variety of agronomically significant genes associated with plant growth, quality, yield, and could also serve as links in metabolic and catabolic pathways. The nucleic acid molecules are also useful for identifying genes important in initiating and maintaining seed germination or that may be used to mitigate stresses encountered during seed germination. The ESTs additionally enable the acquisition of promoters and cis-regulatory elements which will be useful to express agronomically significant genes in these tissues and/or other tissues, and also permits the acquisition of molecular markers useful in breeding schemes, genetic and molecular mapping, and in cloning of agronomically significant genes. The nucleic acid molecules are further useful for detecting the expression level or pattern of a protein or mRNA and for detecting the presence or quantity of a protein by tissue printing. The present sequence represents a specifically claimed EST isolated from a cotton variety DP50B primed seed cDNA library (L1B3825). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at seqdata.uspto.gov/sequence.html?DocID=US20040123340

XX
SQ Sequence 521 BP; 277 A; 32 C; 136 G; 76 T; 0 U; 0 Other;

Query Match 74.5%; Score 16.4; DB 13; Length 521;
Best Local Similarity 94.4%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 AAAGGCCTTTCGGGGTGTG 19
|||||
Db 232 AAAGGCCTTTCGGGGGAG 249

RESULT 32
ADC86176/c
ID ADC86176 standard; DNA; 47804 BP.
XX
AC ADC86176;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human GPCR gene SEQ ID NO:629.
XX
KW ds; gene; human; GPCR;
KW guanosine triphosphate-binding protein coupled receptor; gene therapy.
XX
OS Homo sapiens.
XX
PN EP1270724-A2.
XX
PD 02-JAN-2003.
XX
PF 18-JUN-2002; 2002EP-00013517.
XX
PR 18-JUN-2001; 2001JP-00246789.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX
PI Suwa M, Asai K, Akiyama Y, Aburatani H;
PI WPI; 2003-315783/31.
DR
DR P-PSDB; ADC86177.
XX
PT New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the

PT guanosine triphosphate-binding protein coupled receptor.
 XX Claim 1; SEQ ID NO 629; 28pp; English.
 XX
 CC The invention relates to a novel polynucleotide encoding a guanosine
 CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
 CC the invention may have a use in gene therapy. The polynucleotide and
 CC polypeptide are useful for preparing a composition for treating a patient
 CC in need of increased or suppressed activity or expression of the
 CC guanosine triphosphate-binding protein coupled receptor. The
 CC polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
 CC invention.
 XX
 XX Sequence 47804 BP; 13080 A; 10916 C; 11116 G; 12192 T; 0 U; 500 Other;
 SQ
 Query Match 74.5%; Score 16.4; DB 10; Length 47804;
 Best Local Similarity 94.4%; Pred. No. 7.le+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 5 GGCCTTTTCGGGGTTC 22
 Db 47345 GGCCTTTTCGGGGTTC 47328
 RESULT 33
 ID AAK76977/c
 AA AAK76977 standard; DNA; 420 BP.
 XX
 AC AAK76977;
 XX
 DT 07-NOV-2001 (first entry)
 XX
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:31789.
 XX
 XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cytosstatic; gene therapy; vaccine; metastasis; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO200157182-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 17-JAN-2001; 2001WO-US001354.
 XX
 XX 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225266P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225759P.
 PR 18-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226681P.
 PR 22-AUG-2000; 2000US-0226868P.
 PR 22-AUG-2000; 2000US-0227182P.
 PR 30-AUG-2000; 2000US-0227009P.
 PR 01-SEP-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 06-SEP-2000; 2000US-0229513P.
 PR 06-SEP-2000; 2000US-0230437P.
 PR 08-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231124P.
 PR 08-SEP-2000; 2000US-0231143P.
 PR 08-SEP-2000; 2000US-0231144P.
 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0232080P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231968P.
 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0232398P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 14-SEP-2000; 2000US-0233065P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 25-SEP-2000; 2000US-0234998P.
 PR 26-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 27-SEP-2000; 2000US-0235836P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 13-OCT-2000; 2000US-0239335P.
 PR 13-OCT-2000; 2000US-0239337P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 20-OCT-2000; 2000US-0241826P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246474P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.

PR 08-SEP-2000; 2000US-0232080P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231968P.
 PR 14-SEP-2000; 2000US-0232337P.
 PR 14-SEP-2000; 2000US-0232338P.
 PR 14-SEP-2000; 2000US-0232339P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0232402P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 14-SEP-2000; 2000US-0233065P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 23-SEP-2000; 2000US-0234937P.
 PR 25-SEP-2000; 2000US-0234938P.
 PR 26-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 27-SEP-2000; 2000US-0235836P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 13-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241212P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 20-OCT-2000; 2000US-0241826P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246474P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.

PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Barash SC, Ruben SM;
 PI
 XX WPI; 2001-483426/52.
 XX
 DR Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and metastasis.
 PT
 XX Disclosure; SEQ ID NO 31790; 3071pp + Sequence Listing; English.
 PS
 XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting the
 CC nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention
 XX
 SQ Sequence 420 BP; 132 A; 93 C; 110 G; 85 T; 0 U; 0 Other;
 Query Match 73.6%; Score 16.2; DB 4; Length 420;
 Best Local Similarity 85.7%; Pred. No. 6.1e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 AAAGGCGCTTTCGGGGTGCTC 22
 Db 104 ACAGGGCGCTTTCGGGGTGCTC 84
 RESULT 35
 ADL96630
 ID ADL96630 standard; DNA; 426 BP.
 XX
 AC ADL96630;
 XX
 XX 20-MAY-2004 (first entry)
 DT
 XX M. paratuberculosis DNA #21.
 DE
 XX M. paratuberculosis; gene; ds; milk; faeces; blood;
 KW M. paratuberculosis infection; Johne's disease; polypeptide purification.
 XX
 OS Mycobacterium avium subsp. paratuberculosis.
 XX
 PN US2003175725-A1.
 XX
 PD 18-SEP-2003.


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XX PD 19-APR-2001.
XX XX
XX PF 06-OCT-2000; 2000WO-US027582.
XX XX
XX PR 08-OCT-1999; 99US-0158615P.
XX PR 24-FEB-2000; 2000US-0184809P.
XX XX
XX PA (DIGI-) DIGISCENTS.
XX PA (YEDA ) YEDA RES & DEV CO LTD.
XX XX
XX PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX XX
XX DR WPI; 2001-290713/30.
XX XX
XX PT New polynucleotides which encode polypeptides involved in olfactory
XX PT sensation for identifying olfactory agonists and antagonists.
XX XX
XX PS Claim 1; Fig 2; 1857pp; English.
XX XX
XX CC The present sequence is one of a number of isolated polynucleotides which
XX CC encode polypeptides involved in olfactory sensation. The polynucleotides
XX CC can be used in screening for olfactory agonists and antagonists. The
XX CC methods allow for the determination of primary scents and the
XX CC identification of the odour receptors used to detect these primary
XX CC scents. The methods also enable determination of secondary scents and the
XX CC identification of combinations of odour receptors that are involved in
XX CC detecting such secondary scents. This enables the construction of a scent
XX CC representation (also called a scent fingerprint or scent profile), which
XX CC may be used to re-create and edit scents. Libraries of olfactory
XX CC receptors are useful for determining the interaction pattern of a
XX CC composition with the receptors, and can be used for determining
XX CC differences in the olfactory faculties of different individuals
XX XX
XX SQ Sequence 590 BP; 133 A; 124 C; 137 G; 128 T; 0 U; 68 Other;

Query Match 73.6%; Score 16.2; DB 4; Length 590;
Best Local Similarity 81.8%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTCGGGGTGCTC 22
Db 172 GAAAGGCCTTTCGGGGTGCTC 151

RESULT 38
ADO36603/c
ID ADO36603 standard; DNA; 607 BP.
XX AC
XX AD ADO36603;
XX DT
XX DT 15-JUL-2004 (first entry)
XX DE Isoquinoline alkaloid biosynthesis protein related EST DNA, SEQ ID No 52.
XX XX
XX KW biosynthesis; isoquinoline alkaloid; columbamine 7-O-methyltransferase;
XX KW nor coclaurine synthetase; expressed sequence tag; ds.
XX XX
XX OS Unidentified.
XX XX
XX PN JP2004121233-A.
XX XX
XX PD 22-APR-2004.
XX XX
XX PF 02-SEP-2003; 2003JP-00310660.
XX XX
XX PR 05-SEP-2002; 2002JP-00260642.
XX XX
XX PA (KYOU ) UNIV KYOTO.
XX XX
XX DR WPI; 2004-322858/30.
XX XX
XX PT New protein concerned in biosynthesis of isoquinoline alkaloid, and

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PT having columbamine 7-O-methyltransferase and nor coclaurine synthetase
PT activity, useful for producing isoquinoline alkaloid.
XX PS Claim 1; SEQ ID NO 52; 35pp; Japanese.
XX XX
XX CC The invention relates to a novel protein concerned in biosynthesis of an
XX CC isoquinoline alkaloid. The protein has a fully defined sequence of 351 or
XX CC 352 amino acids as given in the specification, or a sequence in which one
XX CC or more amino acids are deleted, added, or substituted in the protein,
XX CC and having columbamine 7-O-methyltransferase, and nor coclaurine
XX CC synthetase activity. The protein and a transformed host are useful for
XX CC producing isoquinoline alkaloid. The isoquinoline alkaloid biosynthesis
XX CC protein encoding polynucleotide and cDNA library are useful for isolating
XX CC a full length gene concerned in biosynthesis of an isoquinoline alkaloid.
XX CC The alkaloid biosynthesis protein encoding polynucleotide is useful as a
XX CC probe for isolating a full length gene concerned in biosynthesis of an
XX CC isoquinoline alkaloid which is useful as a pharmaceutical raw material.
XX CC This polynucleotide sequence represents the DNA of an expressed sequence
XX CC tag relating to the isoquinoline alkaloid biosynthesis protein of the
XX CC invention.
XX SQ Sequence 607 BP; 169 A; 122 C; 140 G; 173 T; 0 U; 3 Other;

Query Match 73.6%; Score 16.2; DB 12; Length 607;
Best Local Similarity 85.7%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTCGGGGTGCTC 22
Db 76 AAAGGCCTTTCGGGGTGCTC 56

RESULT 39
ABD02872/c
ID ABD02872 standard; DNA; 771 BP.
XX AC
XX AD ABD02872;
XX DT
XX DT 29-JUL-2004 (first entry)
XX DE Pseudomonas aeruginosa polynucleotide #1476.
XX XX
XX KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
XX KW antibacterial.
XX XX
XX OS Pseudomonas aeruginosa.
XX XX
XX PN US6551795-B1.
XX XX
XX PD 22-APR-2003.
XX XX
XX PF 18-FEB-1999; 99US-00252991.
XX XX
XX PR 18-FEB-1998; 98US-0074788P.
XX PR 27-JUL-1998; 98US-0094190P.
XX XX
XX PA (GENO-) GENOME THERAPEUTICS CORP.
XX XX
XX PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX XX
XX DR WPI; 2003-615309/58.
XX DR P-PSDB; ABO69301.
XX XX
XX PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
XX PT useful as molecular targets for diagnostics, prophylaxis and treatment of
XX PT pathological conditions resulting from bacterial infection.
XX XX
XX PS Disclosure; SEQ ID NO 1476; 455pp; English.
XX XX
XX CC The invention relates to Pseudomonas aeruginosa polypeptides and the
XX CC polynucleotides encoding them. The sequences are useful in diagnosis and
XX CC therapy of pathological conditions, as molecular targets for diagnostics,
XX CC prophylaxis and treatment of pathological conditions resulting from a

```

CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences ABD01397-
 CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 CC
 XX
 SQ Sequence 771 BP; 120 A; 270 C; 259 G; 122 T; 0 U; 0 Other;
 Query Match 73.6%; Score 16.2; DB 11; Length 771;
 Best Local Similarity 85.7%; Pred. No. 6.4e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GAAAGGCGCTTTCGGGGTGCT 21
 ||| ||||| ||| |||||
 Db 615 GAAGGCGCTTTCGGCGTGCT 595
 RESULT 40
 ABD03097
 ID ABD03097 standard; DNA; 828 BP.
 XX
 AC ABD03097;
 XX
 XX 29-JUL-2004 (first entry)
 DT
 DE Pseudomonas aeruginosa polynucleotide #1701.
 XX
 KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
 KW antibacterial.
 XX
 OS Pseudomonas aeruginosa.
 XX
 PN US6551795-B1.
 XX
 PD 22-APR-2003.
 XX
 PF 18-FEB-1999; 99US-00252991.
 XX
 PR 18-FEB-1998; 98US-0074788P.
 PR 27-JUL-1998; 98US-0094190P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 PI
 XX WPI; 2003-615309/58.
 DR
 DR P-PSDB; ABO69526.
 XX
 XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.
 XX
 PS Disclosure; SEQ ID NO 1701; 455pp; English.
 XX
 CC The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences ABD01397-

CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 CC
 XX
 SQ Sequence 828 BP; 127 A; 282 C; 284 G; 135 T; 0 U; 0 Other;
 Query Match 73.6%; Score 16.2; DB 11; Length 828;
 Best Local Similarity 85.7%; Pred. No. 6.4e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GAAAGGCGCTTTCGGGGTGCT 21
 ||| ||||| ||| |||||
 Db 226 GAAGGCGCTTTCGGCGTGCT 246
 RESULT 41
 ADS31309
 ID ADS31309 standard; DNA; 909 BP.
 XX
 AC ADS31309;
 XX
 DT 18-NOV-2004 (first entry)
 DE
 DE Human genome high complexity repeat found in the HIRA gene #342.
 XX
 XX Human; ds;
 KW histone cell cycle regulation defective, S. cerevisiae homologue A; HIRA;
 KW high complexity repeat; in situ hybridisation; Southern blot;
 KW chromosome breakpoint; inherited genetic disease; neoplastic disorder;
 KW chromosome 22; DiGeorge syndrome; Velo-Cardio-facial syndrome.
 XX
 OS Homo sapiens.
 XX
 PN US2003224356-A1.
 XX
 PD 04-DEC-2003.
 XX
 PF 14-MAY-2001; 2001US-00854867.
 XX
 PR 16-MAY-2000; 2000US-00573080.
 XX
 PA (KNOLL/) KNOLL J H M.
 PA (ROGA/) ROGAN P K.
 XX
 PI Knoll JHM, Rogan PK;
 XX
 DR WPI; 2002-062378/08.
 XX
 XX Single copy genomic hybridization probes for detecting specific nucleic
 PT acid sequences in sample by in situ hybridization useful for detection of
 PT acquired or inherited genetic diseases.
 XX
 PS Example 1; SEQ ID NO 342; 30pp; English.
 XX
 CC The invention relates to a nucleic acid hybridisation probe comprising a
 CC labelled, single copy nucleic acids of at least 50 nucleotides, which
 CC will hybridise to a deduced single copy sequence interval in target
 CC nucleic acid (TNA) of known sequence. The single copy sequence is deduced
 CC by comparing the target nucleic acid (e.g. a disease causing gene) with a
 CC collection of high and low complexity repeat sequences as found in the
 CC genome of the organism from containing the target nucleic acid. The probe
 CC is generated by PCR on the target sequence. The probe is essentially free
 CC of blocking nucleic acid sequences which will hybridise to repeat
 CC sequences within the genome of which the TNA is a part, and is labelled
 CC with a label selected from fluorochrome-responsive labels, fluorochromes,
 CC calorimetric chemical, conjugated proteins, antibodies, antigens and
 CC their mixtures. The probe is useful in a hybridisation method, where the
 CC hybridisation method is from in situ hybridisation, Southern blot, and
 CC other methods in which nucleic acid is immobilised, where the method
 CC further comprises selecting a single copy nucleic acid which will
 CC hybridise to a duplicon or triplicon sequence domain. The probe is useful
 CC for determining the existence of previously unknown repeat sequence

will hybridize to a deduced single copy sequence interval in target nucleic acid (TNA) of known sequence. (I) is useful in a hybridization method which comprises preparing a reaction mixture comprising TNA and (I) which hybridizes to TNA, and causing (I) to hybridize to TNA, where the hybridization method is from in situ hybridization, Southern blot, and other methods in which nucleic acid is immobilized, where the method further comprises selecting a single copy nucleic acid which will hybridize to a duplcon or triplicon sequence domain. (I) is useful for determining the existence of previously unknown repeat sequence families in a genome; determining a chromosome breakpoint and in the fields of cytogenetics and molecular genetics for determining the presence of specific nucleic acid sequences in a sample of eukaryotic origin, e.g. the probes may be used to analyze specific chromosomal locations by in situ hybridization as a detection of acquired or inherited genetic diseases especially for detection of genetic or neoplastic disorders. Unlike prior art techniques, (I) permits more precise chromosomal breakpoint determinations by in situ hybridization. Hybridization techniques utilizing (I), have made it possible to obtain reliable, easily detectable signals with relatively small probes. A readily detectable signal was obtained with a probe on the order of 2 kb in length, using fluorescent in situ hybridization (FISH) technology. This sensitivity of (I) is improved compared to the prior art, because the probes of (I) are homogeneous single copy sequences. However, smaller amplified segments, each comprising non-repetitive sequences, may also be used in combination as probes to achieve adequate signals for in situ hybridization. Complex single copy probes that hybridize to duplicated or triplicated targets can also increase hybridization signals. This sequence represents a human HIRA genomic sequence that shows homology to a known high-complexity repeat sequence family of the human genome and is used in the creation of an HIRA gene probe.

CC used in combination as probes to achieve adequate signals for
CC hybridization. Complex single copy probes that hybridize to
CC triplicated targets can also increase hybridization signals.
CC sequence represents a human HIRA genomic sequence that show
CC a known high-complexity repeat sequence family of the human
CC used in the creation of an HIRA gene probe.
XX
SQ Sequence 909 BP; 353 A; 160 C; 162 G; 215 T; 0 U; 19 Other;

CC triplicated targets can also increase hybridization signals. This
CC sequence represents a human HIRA genomic sequence that shows homology to
CC a known high-complexity repeat sequence family of the human genome and is
CC used in the creation of an HIRA gene probe.
XX
SQ Sequence 909 BP; 353 A; 160 C; 162 G; 215 T; 0 U; 19 Other;

SQ	Sequence	909 BP;	353 A;	160 C;	162 G;	215 T;	0 U;	19 Other;
Query Match								73.6%
Best Local Similarity								85.7%
Matches	18:	Conservative						0
Indels								0
Gaps								0

XX	Sequence 909 BP; 353 A; 160 C; 152 G	Scored 73.6%;	Scored
XX	Best Local Similarity 85.7%;	Pred	
SQ	Matches 18; Conservative	0; Mi	
Qy	1	GAAGGCGCTTCGGGGTGCT	21
Db	762	GAGAGGGCTTTCGGGGTGCT	782

Seq	Sequence	909 bp	333 bp	160 C ₁	160 C ₂	Score
Qy	1	GAAGAGCCCTTTCGGGGTGCT	21			73.6%; 85.7%; 0; 0
Db	762	GAGAGGGCTTTCGGGGTGCT	762			

Qy
Db
RESULT 43

Qy 1 GAAAGGCCTTTCGGGGTGCT 21
 ||| ||| ||| ||| |||
Dd 762 GAGAGGCTTTCGGGGTGCT 782

RESULT 43
AAI23344/C
TD AAI23344 standard: DNA: 1218 BP.

Db	762	GAGAGGCTTTCTGGGGTCT	7
RESULT	43		
AAI23344/C			
ID	AAI23344	standard; DNA; 1218 BP.	
XX			
AC	AAI23344;		

RESULT 43	
AAI23344/C	
ID AAI23344	standard; DNA; 1218 BP.
XX	
XX	
AC	AAI23344;
XX	
XX	
DT	12-OCT-2001 (first entry)

AAI23344/c
ID AAI23344 standard: DNA: 1218 BP.

XX
XX
XX
AC
XX
XX
DT
XX
XX

AAI23344;
12-OCT-2001 (first entry)
Probe #13277 for gene expression analysis in human cervical cell sample.

12-OCT-2001 (first entry)

DE probe #13277 for gene expression analysis in human cervical cell sample.

Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer; ss.

OS Homo sapiens.
XX
PN WO200157278-A2.
XX
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US0000670.

PN WO200157278-A2.

PD 09-AUG-2001.

30-JAN-2001: 2001WO-US0000670.

XX
PR 04-FEB-2000; 2000US-0180312P.

PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.

PR 04-OCT-2000: 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

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PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488901/53.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human cervical epithelial cells.
XX Claim 25; SEQ ID NO 13277; 487pp; English.
XX The present invention relates to human single exon nucleic acid probes
CC (SENP). The present sequence is one such probe. The SENPs are derived
CC from human HeLa cells. The SENPs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging of
CC diseases of the cervix, notably cervical cancer. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1218 BP; 256 A; 339 C; 273 G; 350 T; 0 U; 0 Other;

Query Match 73.6%; Score 16.2; DB 4; Length 1218;
Best Local Similarity 85.7%; Pred. No. 6.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCTTTCGGGGTGCTC 22
Db 139 AAATGCTTTGGGGAGTGCTC 119

RESULT 44
ABA68451/c
ID ABA68451 standard; DNA; 1218 BP.
XX
AC ABA68451;
XX
DT 01-FEB-2002 (first entry)
XX
DE Human foetal liver single exon nucleic acid probe #16756.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000669.
XX
PR 04-FEB-2000; 2000US-0180312P.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PR 30-JUN-2000; 2000US-00608408.
XX
PR 03-AUG-2000; 2000US-00632366.
XX
PR 21-SEP-2000; 2000US-0234567P.
XX
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488901/53.
XX
DR Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
XX Claim 4; SEQ ID NO 16756; 639pp + Sequence Listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
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CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1218 BP; 256 A; 339 C; 273 G; 350 T; 0 U; 0 Other;

Query Match 73.6%; Score 16.2; DB 4; Length 1218;
Best Local Similarity 85.7%; Pred. No. 6.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCTTTCGGGGTGCTC 22
Db 139 AAATGCTTTGGGGAGTGCTC 119

RESULT 45
AAI48666/c
ID AAI48666 standard; DNA; 1218 BP.
XX
AC AAI48666;
XX
DT 17-OCT-2001 (first entry)
XX
DE Probe #17352 used to measure gene expression in human placenta sample.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000663.
XX
PR 04-FEB-2000; 2000US-0180312P.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PR 30-JUN-2000; 2000US-00608408.
XX
PR 03-AUG-2000; 2000US-00632366.
XX
PR 21-SEP-2000; 2000US-0234687P.
XX
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488901/53.
XX
DR Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
XX Claim 25; SEQ ID NO 17352; 654pp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENP).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders
XX
XX Sequence 1218 BP; 256 A; 339 C; 273 G; 350 T; 0 U; 0 Other;

Query Match 73.6%; Score 16.2; DB 4; Length 1218;
Best Local Similarity 85.7%; Pred. No. 6.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCTTTCGGGGTGCTC 22
Db 139 AAATGCTTTGGGGAGTGCTC 119
```

```
RESULT 46
ABA50502/c
ID ABA50502 standard; DNA; 1218 BP.
XX AC ABA50502;
XX AC ABA50502;
XX DT 01-FEB-2002 (first entry)
XX DE Human breast cell single exon nucleic acid probe #9197.
XX KW Human; microarray; single exon probe; gene expression; breast; disease;
XX KW cancer; ss.
XX OS Homo sapiens.
XX PN WO200157271-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000662.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-496933/54.
XX PT New spatially-addressable set of single exon nucleic acid probes, useful
XX PT for measuring gene expression in sample derived from human breast,
XX PT comprises number of single exon nucleic acid probes.
XX PS Claim 4; SEQ ID NO 9197; 327pp + Sequence Listing; English.
XX CC The invention relates to a spatially-addressable set of single exon
XX CC nucleic acid probes for measuring gene expression in a sample derived
XX CC from human breast and BT 474 cells. The method involves contacting the
XX CC probes with a collection of detectably labelled nucleic acids derived
XX CC from mRNA of human breast, and then measuring the label bound to each
XX CC probe of the microarray. The probes are useful for verifying the
XX CC expression of regions of genomic DNA predicted to encode proteins. They
XX CC are useful for gene discovery, and for determining predisposition and/or
XX CC prognosing breast disease. Gene expression analysis is useful for
XX CC assessing the toxicity of chemical agents on cells. The microarray of
XX CC this invention presents a far greater diversity of probes for measuring
XX CC gene expression, with far less bias than expressed sequence tag
XX CC microarrays. The method is suitable for rapid production of functional
XX CC information from genomic sequence. The present sequence is a single exon
XX CC nucleic acid probe of the invention. Note: The sequence data for this
XX CC patent did not form part of the printed specification, but was obtained
XX CC in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 1218 BP; 256 A; 339 C; 273 G; 350 T; 0 U; 0 Other;
Query Match 73.6%; Score 16.2; DB 4; Length 1218;
Best Local Similarity 85.7%; Pred. No. 6.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 AAAGCCTTCGGGGTGCTC 22
Db 139 AAATGCCTTTGGGAGTGCTC 119
RESULT 47
ABA50502/c
ID ABA50502 standard; DNA; 1218 BP.
XX AC ABA50502;
XX AC ABA50502;
XX DT 01-FEB-2002 (first entry)
XX DE Human breast cell single exon nucleic acid probe #9197.
XX KW Human; microarray; single exon probe; gene expression; breast; disease;
XX KW cancer; ss.
XX OS Homo sapiens.
XX PN WO200157271-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000662.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-496933/54.
XX PT New spatially-addressable set of single exon nucleic acid probes, useful
XX PT for measuring gene expression in sample derived from human breast,
XX PT comprises number of single exon nucleic acid probes.
XX PS Claim 4; SEQ ID NO 9197; 327pp + Sequence Listing; English.
XX CC The invention relates to a spatially-addressable set of single exon
XX CC nucleic acid probes for measuring gene expression in a sample derived
XX CC from human breast and BT 474 cells. The method involves contacting the
XX CC probes with a collection of detectably labelled nucleic acids derived
XX CC from mRNA of human breast, and then measuring the label bound to each
XX CC probe of the microarray. The probes are useful for verifying the
XX CC expression of regions of genomic DNA predicted to encode proteins. They
XX CC are useful for gene discovery, and for determining predisposition and/or
XX CC prognosing breast disease. Gene expression analysis is useful for
XX CC assessing the toxicity of chemical agents on cells. The microarray of
XX CC this invention presents a far greater diversity of probes for measuring
XX CC gene expression, with far less bias than expressed sequence tag
XX CC microarrays. The method is suitable for rapid production of functional
XX CC information from genomic sequence. The present sequence is a single exon
XX CC nucleic acid probe of the invention. Note: The sequence data for this
XX CC patent did not form part of the printed specification, but was obtained
XX CC in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 1218 BP; 256 A; 339 C; 273 G; 350 T; 0 U; 0 Other;
Query Match 73.6%; Score 16.2; DB 4; Length 1218;
Best Local Similarity 85.7%; Pred. No. 6.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 AAAGCCTTCGGGGTGCTC 22
Db 139 AAATGCCTTTGGGAGTGCTC 119
RESULT 48
ABA42594/c
ID ABA42594 standard; DNA; 1218 BP.
XX AC ABA42594;
XX AC ABA42594;
XX DT 06-NOV-2001 (first entry)
XX DE Human bone marrow expressed single exon probe SEQ ID NO: 17151.
XX
```

KW Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200157276-A2.
 XX
 PD 09-AUG-2001.
 XX
 XX 30-JAN-2001; 2001WO-US0000668.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488900/53.
 XX
 DR Human genome-derived single exon nucleic acid probes useful for analyzing
 XX gene expression in human bone marrow.
 PT
 XX Example 4; SEQ ID NO 17151; 659pp + Sequence Listing; English.
 XX
 CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
 CC the probes of the invention
 XX
 SQ Sequence 1218 BP; 256 A; 339 C; 273 G; 350 T; 0 U; 0 Other;
 Query Match 73.6%; Score 16.2; DB 4; Length 1218;
 Best Local Similarity 85.7%; Pred. No. 6.6e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 QY 2 AAAGGCTTTCGGGGTGCTC 22
 ||| ||||| ||||| |||||
 Db 139 AAATGCTTTGGGAGTGCTC 119
 RESULT 49
 AAK16823/c
 ID AAK16823 standard; DNA; 1218 BP.
 XX
 AC AAK16823;
 XX
 DT 05-NOV-2001 (first entry)
 XX
 DE Human brain expressed single exon probe SEQ ID NO: 16814.
 XX
 DE Human; brain expressed exon; gene expression analysis; probe; microarray;
 KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
 KW ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200157275-A2.
 PN
 XX
 PD 09-AUG-2001.
 XX
 XX 30-JAN-2001; 2001WO-US0000667.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488900/53.
 XX
 DR Human genome-derived single exon nucleic acid probes useful for analyzing
 XX gene expression in human adult liver.

PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-483446/52.
 XX
 DR Single exon nucleic acid probes for analyzing gene expression in human
 XX brains.
 PT
 XX Example 4; SEQ ID NO 16814; 650pp + Sequence Listing; English.
 PS
 XX The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system,
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is one of the probes of the
 CC invention
 XX
 SQ Sequence 1218 BP; 256 A; 339 C; 273 G; 350 T; 0 U; 0 Other;
 Query Match 73.6%; Score 16.2; DB 4; Length 1218;
 Best Local Similarity 85.7%; Pred. No. 6.6e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 QY 2 AAAGGCTTTCGGGGTGCTC 22
 ||| ||||| ||||| |||||
 Db 139 AAATGCTTTGGGAGTGCTC 119
 RESULT 50
 ABS42209/c
 ID ABS42209 standard; DNA; 1218 BP.
 XX
 AC ABS42209;
 XX
 DT 25-FEB-2003 (first entry)
 XX
 DE Human liver single exon probe, SEQ ID NO 17199.
 XX
 XX Human; single exon nucleic acid probe; liver; cirrhosis;
 KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
 KW coronary heart disease; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200157273-A2.
 PN
 XX
 PD 09-AUG-2001.
 XX
 XX 30-JAN-2001; 2001WO-US0000664.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-488998/53.
 XX
 DR Human genome-derived single exon nucleic acid probes useful for analyzing
 XX gene expression in human adult liver.

```
XX Claim 4; SEQ ID NO 17199; 658pp; English.
XX
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABS25011-ABS51005 represent human
CC liver single exon nucleic acid probes of the invention. Note: The
CC sequence information for this patent does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1218 BP; 256 A; 339 C; 273 G; 350 T; 0 U; 0 Other;
SQ
Query Match 73.6%; Score 16.2; DB 4; Length 1218;
Best Local Similarity 85.7%; Pred. No. 6.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 AAAGCGCTTCGGGGGTGCTC 22
DB 139 AAATGCGCTTTGGGGAGTGCTC 119
RESULT 51
AA108981/c
ID AA108981 standard; DNA; 1218 BP.
XX
XX AA108981;
XX
XX 09-OCT-2001 (first entry)
XX
XX Probe #8972 used to measure gene expression in human breast sample.
XX
XX Probe; human; breast disease; breast cancer; development disorder; ss;
XX inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
XX Homo sapiens.
XX
XX WO200157270-A2.
XX
XX 09-AUG-2001.
XX
XX 29-JAN-2001; 2001WO-US0000661.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-476286/51.
XX
XX Novel single exon nucleic acid probe used to measuring gene expression in
XX a human breast.
XX
XX Claim 25; SEQ ID NO 8972; 322pp; English.
XX
XX The present invention relates to novel single exon nucleic acid probes.
XX The present sequence is one such probe. The probes are useful for
XX measuring human gene expression in a human breast sample, where the probe
XX hybridises at high stringency to a nucleic acid expressed in the human
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CC breast. The probes are useful for predicting, diagnosing, grading,
CC staging, monitoring and prognosing diseases of the human breast,
CC particularly those diseases with polygenic aetiology. The diseases
CC include: breast cancer, disorders of development, inflammatory diseases
CC of the breast, fibrocystic changes, proliferative breast disease and non-
CC carcinoma tumours. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1218 BP; 256 A; 339 C; 273 G; 350 T; 0 U; 0 Other;
SQ
Query Match 73.6%; Score 16.2; DB 5; Length 1218;
Best Local Similarity 85.7%; Pred. No. 6.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 AAAGCGCTTCGGGGGTGCTC 22
DB 139 AAATGCGCTTTGGGGAGTGCTC 119
RESULT 52
ABS16646/c
ID ABS16646 standard; DNA; 1218 BP.
XX
XX ABS16646;
XX
XX 19-AUG-2002 (first entry)
XX
XX Human genome-derived single exon probe ORF from lung SEQ ID NO 16637.
XX
XX Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
XX chronic obstructive pulmonary disease; interstitial lung disease;
XX familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
XX Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
XX pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
XX pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
XX primary ciliary dyskinesia; pulmonary hypertension;
XX hyaline membrane disease; open reading frame; ORF.
XX
XX Homo sapiens.
XX
XX WO200186003-A2.
XX
XX 15-NOV-2001.
XX
XX 30-JAN-2001; 2001WO-US0000665.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2002-114183/15.
XX
XX Spatially-addressable set of single exon nucleic acid probes, used to
XX measure gene expression in human lung samples.
XX
XX Claim 4; SEQ ID NO 16637; 634pp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human lung comprising single exon nucleic acid probes having one of
XX 12614 nucleic acid sequences mentioned in the specification, or their
XX complements or the 12387 open reading frames derived from the 12614
XX probes. Also included are a microarray comprising the novel set of probes
```


PT isolate candidate molecules for rational drug discovery programs.

PS Claim 14; SEQ ID NO 26246; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 1377 BP; 257 A; 452 C; 465 G; 203 T; 0 U; 0 Other;

Query Match 73.6%; Score 16.2; DB 8; Length 1377;
 Best Local Similarity 85.7%; Pred. No. 6.7e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGGCTTTCGGGGTGCTC 22
 ||||| ||| |||||
 Db 538 AAAGCGCGTTCGGGGTGCTC 558

RESULT 55
 ACA40722
 ID ACA40722 standard; DNA; 1380 BP.

XX ACA40722;
 AC ACA40722;
 XX 19-JUN-2003 (first entry)
 XX Prokaryotic essential gene #2379.
 DE Antisense; da; prokaryotic essential gene; cell proliferation;
 XX drug design; gene.
 KW Mycobacterium tuberculosis.
 XX WO200277183-A2.
 XX 03-OCT-2002.
 XX 21-MAR-2002; 2002WO-US009107.
 XX 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.

(ELIT-) ELITRA PHARM INC.

Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 DR WPI; 2003-0299926/02.
 P-PSDB; ABU36852.

XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

XX Claim 14; SEQ ID NO 28592; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 1380 BP; 258 A; 452 C; 466 G; 204 T; 0 U; 0 Other;
 Query Match 73.6%; Score 16.2; DB 8; Length 1380;
 Best Local Similarity 85.7%; Pred. No. 6.7e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGGCTTTCGGGGTGCTC 22
 ||||| ||| |||||
 Db 538 AAAGCGCGTTCGGGGTGCTC 558

RESULT 56
 AAS94778/c
 ID AAS94778 standard; DNA; 1704 BP.

XX AAS94778;
 AC AAS94778;
 XX 14-FEB-2002 (first entry)
 XX Human DNA sequence #33 expressed during foam cell differentiation.
 DE Human; foam cell differentiation; atherosclerosis; cerebral stroke;
 XX cardiovascular disorder; coronary artery disease; gene therapy; da.
 XX Homo sapiens.
 XX

PN WO200177389-A2.
XX 18-OCT-2001.
XX 04-APR-2001; 2001WO-US011128.
XX 05-APR-2000; 2000US-0195106P.
XX (INCY-) INCYTE GENOMICS INC.
XX Shiffman D, Somogyi R, Lawn R, Seilhamer JU, Porter GJ, Mikita T;
PI Tai J;
XX WPI; 2002-010925/01.
XX Composition useful for diagnosis of conditions, disorders or diseases
PT associated with atherosclerosis, comprises several polynucleotides that
PT are differentially expressed in foam cell development.
XX PS Claim 1; Page 90; 315pp; English.
XX The present invention relates to the isolation of human polynucleotide
CC sequences that are differentially expressed during foam cell
CC differentiation. The polynucleotide sequences of the invention or a
CC composition comprising these polynucleotides are useful as a high
CC throughput method for detecting altered expression of one or more
CC polynucleotides in a sample. The polynucleotides can be used in the
CC diagnosis of disorders associated with foam cell development such as
CC atherosclerosis, cerebral stroke, and cardiovascular disorders such as
CC coronary artery disease. The polynucleotide sequences can also be used as
CC PCR primers and probes. The polynucleotides of the invention are also
CC useful in gene therapy. AAS94746-AAS95021 represent the human
CC polynucleotide sequences of the invention which are differentially
CC expressed during foam cell differentiation
XX SQ Sequence 1704 BP; 382 A; 354 C; 326 G; 422 T; 0 U; 220 Other;
Query Match 73.6%; Score 16.2; DB 6; Length 1704;
Best Local Similarity 85.7%; Pred. No. 6.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GAAAGGCGCTTCGGGGTGCT 21
Db |||||
41 GAAAGGCGCTTCGAGATGCT 21
RESULT 57
AAC85094/c
ID AAC85094 standard; DNA; 1740 BP.
XX AAC85094;
XX 08-MAY-2001 (first entry)
XX Homo sapiens.
XX Atherosclerosis-associated gene seq ID No. 30.
XX Atherosclerosis-associated gene; stroke; myocardial infarction; human;
KW ischemia; coronary artery disease; angina pectoris; hypertension;
KW peripheral vascular disease; renal artery stenosis; atherosclerotic;
KW cerebroprotective; cardiac; gene therapy; hypotensive; vasotropic;
KW antianginal; ds.
XX OS
XX Homo sapiens.
XX WO200104264-A2.
XX 18-JAN-2001.
XX 28-JUN-2000; 2000WO-US017887.
XX 07-JUL-1999; 99US-00349015.
XX (INCY-) INCYTE GENOMICS INC.
PI Jones KA, Volkmut W, Walker MG, Murry LE;
XX WPI; 2003-617118/58.
XX New combination of atherosclerosis-associated genes, useful for the
PT differential diagnosis of e.g. myocardial infarction, hypertension,
PT ischemia or stroke, or for staging or treating atherosclerosis-associated
PT disorders.

XX Jones KA, Volkmut W, Walker MG;
XX WPI; 2001-138330/14.
XX Composition comprising atherosclerosis-associated polynucleotide useful
PT in diagnosis, prognosis, treatment, and prevention of atherosclerosis and
PT stroke, myocardial infarction, or hypertension.
XX PS Claim 1; Page 54; 58pp; English.
XX The invention provides novel atherosclerosis-associated polynucleotides
CC and polypeptides encoded by the genes. Expression vectors and host cells
CC for producing the polypeptides are disclosed and methods for screening or
CC purifying ligands which specifically bind to the polypeptides are also
CC provided. The polynucleotides are useful for treating diseases associated
CC with the altered expression of a gene that is coexpressed with one or
CC more known atherosclerosis-associated genes in a subject. They are useful
CC in diagnosis, prognosis, treatment, prevention, selection and evaluation
CC of therapies for atherosclerosis including stroke, myocardial infarction,
CC transient cerebral ischemia, mesenteric ischemia, coronary artery
CC disease, angina pectoris, peripheral vascular disease, renal artery
CC stenosis, and hypertension. Sequences AAC85065-85098 represent
CC atherosclerosis-associated genes of the invention
XX SQ Sequence 1740 BP; 394 A; 362 C; 333 G; 432 T; 0 U; 219 Other;
Query Match 73.6%; Score 16.2; DB 4; Length 1740;
Best Local Similarity 85.7%; Pred. No. 6.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GAAAGGCGCTTCGGGGTGCT 21
Db |||||
41 GAAAGGCGCTTCGAGATGCT 21
RESULT 58
ADM29578/c
ID ADM29578 standard; cDNA; 1740 BP.
XX ADM29578;
XX 20-MAY-2004 (first entry)
XX Human atherosclerosis associated cDNA #22.
XX Human; ss; gene; atherosclerosis; angina pectoris;
KW coronary artery disease; myocardial infarction; hypertension;
KW transient cerebral ischemia; mesenteric ischemia;
KW peripheral vascular disease; renal artery stenosis; diabetes mellitus;
KW obesity; polycystic ovarian syndrome; stroke; diabetes mellitus; obesity;
KW polycystic ovarian syndrome; cancer.
XX OS
XX Homo sapiens.
XX US2003129176-A1.
XX 10-JUL-2003.
XX 14-AUG-2002; 2002US-00219664.
XX 07-JUL-1999; 99US-00349015.
XX (INCY-) INCYTE GENOMICS INC.
XX Jones KA, Volkmut W, Walker MG, Murry LE;
XX WPI; 2003-617118/58.
XX New combination of atherosclerosis-associated genes, useful for the
PT differential diagnosis of e.g. myocardial infarction, hypertension,
PT ischemia or stroke, or for staging or treating atherosclerosis-associated
PT disorders.

XX Claim 1; SEQ ID NO 22; 60pp; English.

XX The invention relates to a combination of several cDNAs, which are co-

CC expressed with one or more known human atherosclerosis-associated genes,

CC is new. The cDNAs comprise any of 25 sequences appearing as ADM29557-

CC ADM29581or the complements of any of these sequences. Also included are

CC detecting differential expression of one or more cDNAs in a sample

CC containing nucleic acids, using cDNAs to screen a sample and identify a

CC ligand that specifically binds a cDNA, a vector containing the cDNA, a

CC host cell containing the vector, producing a protein, an atherosclerosis-

CC associated protein appearing as ADM29582, using a protein to screen

CC several molecules or compounds (and identify at least one ligand that

CC specifically binds the protein), using a protein to produce an antibody,

CC an antibody produced by the method, and using an antibody to detect gene

CC expression in a sample. The cDNAs are useful for detecting differential

CC expression of one or more cDNAs in a sample containing nucleic acids.

CC This differential expression is diagnostic of angina pectoris, coronary

CC artery disease, myocardial infarction, hypertension, transient cerebral

CC ischaemia, mesenteric ischaemia, peripheral vascular disease, renal

CC artery stenosis, diabetes mellitus, obesity, polycystic ovarian syndrome,

CC or stroke. The cDNAs or proteins are useful for screening a sample and

CC identifying a ligand, which specifically binds a cDNA or protein,

CC respectively. The protein is also useful for producing an antibody for

CC detecting gene expression in a sample. The combination of cDNAs is also

CC useful for staging, treating, or monitoring the progression of, disorders

CC associated with atherosclerosis, such as diabetes mellitus, obesity,

CC polycystic ovarian syndrome, and cancers. The present sequence is a human

CC atherosclerosis-associated cDNA of the invention.

XX

XX Sequence 1740 BP; 394 A; 362 C; 333 G; 432 T; 0 U; 219 Other;

Query Match 73.6%; Score 16.2; DB 11; Length 1740;

Best Local Similarity 85.7%; Pred. No. 6.8e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCGCTTCGGGGTGCT 21

Db 41 GAAAGGCGCTTCGGGGTGCT 21

RESULT 59

AAI14134/c

AAI14134 standard; DNA; 1954 BP.

AAI14134;

12-OCT-2001 (first entry)

Probe #4067 for gene expression analysis in human cervical cell sample.

Probe; human; microarray; gene expression; cervical epithelial cell;

cervical cancer; ss.

Homo sapiens.

WO200157278-A2.

09-AUG-2001.

30-JAN-2001; 2001WO-US000670.

04-FEB-2000; 2000US-0180312P.

26-MAY-2000; 2000US-0207456P.

30-JUN-2000; 2000US-00608408.

03-AUG-2000; 2000US-00632366.

21-SEP-2000; 2000US-0234687P.

27-SEP-2000; 2000US-0236359P.

04-OCT-2000; 2000GB-00024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;

WPI; 2001-483447/52.

Human genome-derived single exon nucleic acid probes useful for analyzing

gene expression in human fetal liver.

Claim 1; SEQ ID NO 4165; 639pp + Sequence Listing; English.

The invention relates to a single exon nucleic acid probe for measuring

human gene expression in a sample derived from human foetal liver. The

single exon nucleic acid probes may be used for predicting, measuring and

displaying gene expression in samples derived from human fetal liver. The

XX WPI; 2001-488901/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human cervical epithelial cells.

XX Claim 25; SEQ ID NO 4067; 487pp; English.

XX The present invention relates to human single exon nucleic acid probes

CC (SENPs). The present sequence is one such probe. The SENPs are derived

CC from human HeLa cells. The SENPs can be used to produce a single exon

CC microarray, which can be used for measuring human gene expression in a

CC sample derived from human cervical epithelial cells. By measuring gene

CC expression, the probes are therefore useful in grading and/or staging of

CC diseases of the cervix, notably cervical cancer. Note: The sequence data

CC for this patent did not form part of the printed specification, but was

CC obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX

XX Sequence 1954 BP; 410 A; 510 C; 444 G; 590 T; 0 U; 0 Other;

Query Match 73.6%; Score 16.2; DB 4; Length 1954;

Best Local Similarity 85.7%; Pred. No. 6.9e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGGCGCTTCGGGGTGCTC 22

Db 394 AAATGCGCTTCGGGGTGCTC 374

RESULT 60

ABA55860/c

ABA55860 standard; DNA; 1954 BP.

ABA55860;

01-FEB-2002 (first entry)

Human foetal liver single exon nucleic acid probe #4165.

Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

Homo sapiens.

WO200157277-A2.

09-AUG-2001.

30-JAN-2001; 2001WO-US000669.

04-FEB-2000; 2000US-0180312P.

26-MAY-2000; 2000US-0207456P.

30-JUN-2000; 2000US-00608408.

03-AUG-2000; 2000US-00632366.

21-SEP-2000; 2000US-0234687P.

27-SEP-2000; 2000US-0236359P.

04-OCT-2000; 2000GB-00024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;

WPI; 2001-483447/52.

Human genome-derived single exon nucleic acid probes useful for analyzing

gene expression in human fetal liver.

Claim 1; SEQ ID NO 4165; 639pp + Sequence Listing; English.

The invention relates to a single exon nucleic acid probe for measuring

human gene expression in a sample derived from human foetal liver. The

single exon nucleic acid probes may be used for predicting, measuring and

displaying gene expression in samples derived from human fetal liver. The


```
ID  ABA25535 standard; DNA; 1954 BP.
XX  ABA25535;
AC
XX
XX  23-JAN-2002 (first entry)
DT
XX
XX  Probe #4001 for gene expression analysis in human heart cell sample.
DE
XX
XX  Human; gene expression; heart; microarray; vascular system; probe;
KW  cardiovascular disease; hypertension; cardiac arrhythmia;
KW  congenital heart disease; ss.
XX
XX  Homo sapiens.
OS
XX
XX  WO200157274-A2.
PN
XX
XX  09-AUG-2001.
PD
XX
XX  30-JAN-2001; 2001WO-US000666.
PF
XX
XX  04-FEB-2000; 2000US-0180312P.
PR  26-MAY-2000; 2000US-0207456P.
PR  30-JUN-2000; 2000US-00608408.
PR  03-AUG-2000; 2000US-00632366.
PR  21-SEP-2000; 2000US-0234687P.
PR  27-SEP-2000; 2000US-0236359P.
PR  04-OCT-2000; 2000GB-00024263.
XX
XX  (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX
XX  Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX  WPI; 2001-488899/53.
XX
XX  Single exon nucleic acid probes for analyzing gene expression in human
PT  hearts.
XX
XX  Claim 1; SEQ ID NO 4001; 530pp; English.
PS
XX  The present invention relates to single exon nucleic acid probes for
SS  measuring human gene expression in a sample derived from human heart. The
CC  present sequence is one such probe. The probes may be used for
CC  predicting, measuring and displaying gene expression in samples derived
CC  from the human heart via microarrays. By measuring gene expression, the
CC  probes are useful for predicting, diagnosing, grading, staging,
CC  monitoring and prognosing diseases of the human heart and vascular system
CC  e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC  congenital heart disease. Note: The sequence data for this patent did not
CC  form part of the printed specification, but was obtained in electronic
CC  format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX  Sequence 1954 BP; 410 A; 510 C; 444 G; 590 T; 0 U; 0 Other;
SQ
XX
XX  Query Match 73.6%; Score 16.2; DB 4; Length 1954;
XX  Best Local Similarity 85.7%; Pred. No. 6.9e+02;
XX  Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX  2 AAAGGCCTTTCGGGGTGCTC 22
QY  ||| ||||| ||| |||||
DB  394 AAATGCTTTGGGGAGTGCTC 374
XX
XX  RESULT 64
XX  AAK29561/c
XX  ID AAK29561 standard; DNA; 1954 BP.
XX
XX  AAK29561;
AC
XX
XX  06-NOV-2001 (first entry)
DT
XX
XX  Human bone marrow expressed single exon probe SEQ ID NO: 4118.
DE
XX  Human; bone marrow expressed exon; gene expression analysis; probe;
KW  Human; bone marrow expressed exon; gene expression analysis; probe;
XX
```

```
KW  microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX  Homo sapiens.
OS
XX  WO200157276-A2.
PN
XX  09-AUG-2001.
PD
XX
XX  30-JAN-2001; 2001WO-US000668.
PF
XX
XX  04-FEB-2000; 2000US-0180312P.
PR  26-MAY-2000; 2000US-0207456P.
PR  30-JUN-2000; 2000US-00608408.
PR  03-AUG-2000; 2000US-00632366.
PR  21-SEP-2000; 2000US-0234687P.
PR  27-SEP-2000; 2000US-0236359P.
PR  04-OCT-2000; 2000GB-00024263.
XX
XX  (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX
XX  Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX  WPI; 2001-488900/53.
XX
XX  Human genome-derived single exon nucleic acid probes useful for analyzing
PT  gene expression in human bone marrow.
XX
XX  Example 4; SEQ ID NO 4118; 658pp + Sequence Listing; English.
PS
XX
XX  The present invention provides a number of single exon nucleic acid
CC  probes which are derived from genomic sequences expressed in the human
CC  bone marrow. They can be used to measure gene expression in bone marrow
CC  samples, which may enable the improved diagnosis and treatment of cancers
CC  such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC  the probes of the invention
XX
XX  Sequence 1954 BP; 410 A; 510 C; 444 G; 590 T; 0 U; 0 Other;
SQ
XX
XX  Query Match 73.6%; Score 16.2; DB 4; Length 1954;
XX  Best Local Similarity 85.7%; Pred. No. 6.9e+02;
XX  Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX  2 AAAGGCCTTTCGGGGTGCTC 22
QY  ||| ||||| ||| |||||
DB  394 AAATGCTTTGGGGAGTGCTC 374
XX
XX  RESULT 65
XX  AAK04079/c
XX  ID AAK04079 standard; DNA; 1954 BP.
XX
XX  AAK04079;
AC
XX
XX  05-NOV-2001 (first entry)
DT
XX
XX  Human brain expressed single exon probe SEQ ID NO: 4070.
DE
XX
XX  Human; brain expressed exon; gene expression analysis; probe; microarray;
KW  Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
XX  ss.
XX
XX  Homo sapiens.
OS
XX
XX  WO200157275-A2.
PN
XX
XX  09-AUG-2001.
PD
XX
XX  30-JAN-2001; 2001WO-US000667.
PF
XX
XX  04-FEB-2000; 2000US-0180312P.
PR  26-MAY-2000; 2000US-0207456P.
PR  30-JUN-2000; 2000US-00608408.
PR  03-AUG-2000; 2000US-00632366.
XX
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PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-483446/52.
 XX
 XX Single exon nucleic acid probes for analyzing gene expression in human
 PT brains.
 PT
 PS Example 4; SEQ ID NO 4070; 650pp + Sequence Listing; English.
 CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is one of the probes of the
 CC invention
 XX
 SQ Sequence 1954 BP; 410 A; 510 C; 444 G; 590 T; 0 U; 0 Other;
 Query Match 73.6%; Score 16.2; DB 4; Length 1954;
 Best Local Similarity 85.7%; Pred. No. 6.9e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 AAAGGCTTTCGGGGTGCTC 22
 DB 394 AAATGCTTTGGGAGTGCTC 374
 ||| ||||| ||| |||||
 RESULT 66
 ABS29189/c
 ID ABS29189 standard; DNA; 1954 BP.
 AC ABS29189;
 XX
 XX Human liver single exon probe, SEQ ID No 4179.
 DT 25-FEB-2003 (first entry)
 DE
 DE Human; single exon nucleic acid probe; liver; cirrhosis;
 KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
 KW coronary heart disease; ss.
 XX Homo sapiens.
 OS
 XX WO200157273-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 30-JAN-2001; 2001WO-US000664.
 XX
 XX 04-FEB-2000; 2000US-0180312P.
 XX 26-MAY-2000; 2000US-0207456P.
 XX 30-JUN-2000; 2000US-00608408.
 XX 03-AUG-2000; 2000US-00632366.
 XX 21-SEP-2000; 2000US-0234687P.
 XX 27-SEP-2000; 2000US-0236359P.
 XX 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-488898/53.
 XX
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human adult liver.
 PT
 XX

PS Claim 1; SEQ ID NO 4179; 658pp; English.
 XX
 CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
 CC measuring human gene expression in a sample derived from human adult
 CC liver, comprising one of 13109 defined nucleotide sequences given in the
 CC specification (or complements/ fragments). The probe hybridises at high
 CC stringency to a nucleic acid molecule expressed in the human adult liver.
 CC (I) may be used for predicting, measuring and displaying gene expression
 CC in samples derived from human adult liver. The genes identified may be
 CC involved in genetic liver diseases such as cirrhosis,
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
 CC associated with coronary heart disease. ABS25011-ABS51005 represent human
 CC liver single exon nucleic acid probes of the invention. Note: The
 CC sequence information for this patent does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1954 BP; 410 A; 510 C; 444 G; 590 T; 0 U; 0 Other;
 Query Match 73.6%; Score 16.2; DB 4; Length 1954;
 Best Local Similarity 85.7%; Pred. No. 6.9e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 AAAGGCTTTCGGGGTGCTC 22
 DB 394 AAATGCTTTGGGAGTGCTC 374
 ||| ||||| ||| |||||
 RESULT 67
 AAI03983/c
 ID AAI03983 standard; DNA; 1954 BP.
 XX AAI03983;
 AC
 XX 09-OCT-2001 (first entry)
 DT
 DE Probe #3974 used to measure gene expression in human breast sample.
 DE
 XX Probe; human; breast disease; breast cancer; development disorder; ss;
 KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
 KW
 XX Homo sapiens.
 OS
 XX WO200157270-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 29-JAN-2001; 2001WO-US000661.
 XX
 XX 04-FEB-2000; 2000US-0180312P.
 XX 26-MAY-2000; 2000US-0207456P.
 XX 30-JUN-2000; 2000US-00608408.
 XX 03-AUG-2000; 2000US-00632366.
 XX 21-SEP-2000; 2000US-0234687P.
 XX 27-SEP-2000; 2000US-0236359P.
 XX 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-476286/51.
 XX
 XX Novel single exon nucleic acid probe used to measuring gene expression in
 PT a human breast.
 PT
 PS Claim 25; SEQ ID NO 3974; 322pp; English.
 XX
 XX The present invention relates to novel single exon nucleic acid probes.
 CC The present sequence is one such probe. The probes are useful for
 CC measuring human gene expression in a human breast sample, where the probe
 CC hybridises at high stringency to a nucleic acid expressed in the human
 CC breast. The probes are useful for predicting, diagnosing, grading,

CC staging, monitoring and prognosing diseases of the human breast,
 CC particularly those diseases with polygenic aetiology. The diseases
 CC include: breast cancer, disorders of development, inflammatory diseases
 CC of the breast, fibrocystic changes, proliferative breast disease and non-
 CC carcinoma tumours. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1954 BP; 410 A; 510 C; 444 G; 590 T; 0 U; 0 Other;
 Query Match 73.6%; Score 16.2; DB 5; Length 1954;
 Best Local Similarity 85.7%; Pred. No. 6.9e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 AAAGGCTTTGGGGGTGCTC 22
 DB 394 AAATGCTTTGGGGAGTGCTC 374
 RESULT 68
 ID ABS04116/c
 AC ABS04116;
 XX
 XX 19-AUG-2002 (first entry)
 DT
 DE Human genome-derived single exon probe from lung SEQ ID No 4107.
 KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.
 XX
 OS Homo sapiens.
 XX
 XX WO200186003-A2.
 XX
 XX 15-NOV-2001.
 XX
 XX 30-JAN-2001; 2001WO-US000665.
 XX
 XX 04-FEB-2000; 2000US-0180312P.
 XX 26-MAY-2000; 2000US-0207456P.
 XX 30-JUN-2000; 2000US-00608408.
 XX 03-AUG-2000; 2000US-00632366.
 XX 21-SEP-2000; 2000US-0234687P.
 XX 27-SEP-2000; 2000US-0236359P.
 XX 04-OCT-2000; 2000GB-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 XX WPI; 2002-114183/15.
 XX
 XX Spatially-addressable set of single exon nucleic acid probes, used to
 XX measure gene expression in human lung samples.
 XX
 XX Claim 1; SEQ ID NO 4107; 634pp; English.
 XX
 XX The invention relates to a spatially-addressable set of single exon
 XX nucleic acid probes for measuring gene expression in a sample derived
 XX from human lung comprising single exon nucleic acid probes having one of
 XX 12614 nucleic acid sequences mentioned in the specification, or their
 XX complements or the 12387 open reading frames derived from the 12614
 XX probes. Also included are a microarray comprising the novel set of probes
 XX ; the novel set of probes which hybridise at high stringency to a nucleic

CC acid expressed in the human lung; measuring gene expression in a sample
 CC derived from human lung, comprising (a) contacting the array with a
 CC collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of the
 CC array; identifying exons in a eukaryotic genome, comprising (a)
 CC algorithmically predicting at least one exon from genomic sequences of
 CC the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene expression
 CC analysis, and for identifying exons in a gene, particularly using human
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a single exon probe of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1954 BP; 410 A; 510 C; 444 G; 590 T; 0 U; 0 Other;
 Query Match 73.6%; Score 16.2; DB 6; Length 1954;
 Best Local Similarity 85.7%; Pred. No. 6.9e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 AAAGGCTTTGGGGGTGCTC 22
 DB 394 AAATGCTTTGGGGAGTGCTC 374
 RESULT 69
 AB054935
 ID AB054935 standard; cDNA; 2772 BP.
 XX
 XX AB054935;
 XX
 XX 22-AUG-2002 (first entry)
 XX
 XX Human ovarian antigen HFPHF52 cDNA, SEQ ID NO:815.
 XX
 XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 XX ovarian cancer; breast cancer; tumour; reproductive system disorder;
 XX infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 XX PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 XX inflammatory condition; immune disorder; blood disorder;
 XX cardiovascular disorder; respiratory disorder; neurological disorder;
 XX gastrointestinal disorder; urinary system disorder; drug screening;
 XX gene therapy; chromosome mapping; forensic analysis;
 XX antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 XX antiinflammatory; gynaecological; reproductive; chromosome 19q13.4; gene;
 XX ss.
 XX
 XX Homo sapiens.
 XX
 XX WO200200677-A1.
 XX
 XX 03-JAN-2002.
 XX
 XX 07-JUN-2001; 2001WO-US018569.
 XX
 XX

PR	07-JUN-2000; 2000US-0209467P.	
XX	(HUMA-) HUMAN GENOME SCI INC.	
PA		
XX		
PI	Birse CE, Rosen CA;	
XX		
DR	WPI; 2002-147878/19.	
DR	P-PSDB; ABP41858.	
XX		
XX	Isolated nucleic acid molecules encoding novel ovarian polypeptides,	
PT	useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian	
PT	cancer), immune disorders, cardiovascular disorders and neurological	
PT	diseases.	
XX		
PS	Claim 1; SEQ ID NO 815; 2922pp; English.	
XX		
CC	The invention relates to 2175 novel human ovarian antigens (ABP41054-	
CC	ABP4328) and to cDNAs encoding them (ABQ54131-ABQ56305), and also	
CC	encompasses polypeptides 90% identical and polynucleotides 95% identical	
CC	to the sequences of the invention. The invention additionally relates to	
CC	recombinant vectors and host cells comprising human ovarian antigen	
CC	polynucleotides, antibodies against human ovarian antigens, and the use	
CC	of ovarian antigen polynucleotides and polypeptides in diagnosing,	
CC	treating, prognosing or preventing various ovary and/or breast-related	
CC	disorders. Such conditions include ovarian cancer and breast cancer, and	
CC	metastatic tumours of ovarian or breast origin, reproductive system	
CC	disorders (e.g., infertility, disorders of pregnancy, anovulation,	
CC	polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine	
CC	disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic	
CC	shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and	
CC	vaginitis), immune disorders (e.g., congenital and acquired	
CC	immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),	
CC	blood-related disorders (e.g., anaemia), cardiovascular disorders,	
CC	respiratory disorders, neurological disorders, gastrointestinal disorders	
CC	and urinary system disorders. Ovarian antigen polypeptides and	
CC	polynucleotides may also be used in screening for compounds which	
CC	modulate ovarian antigen expression or activity. The polynucleotides may	
CC	further be used for gene therapy, chromosome mapping, in the	
CC	identification of individuals and in forensic analysis, and the	
CC	polypeptides may be used as food additives or to prepare antibodies	
CC	useful in disease diagnosis, drug targeting and phenotyping. The present	
CC	sequence represents a cDNA encoding a human ovarian antigen of the	
CC	invention. Note: The sequence data for this patent did not form part of	
CC	the printed specification, but was obtained in electronic format directly	
CC	from WIPO at ftp.wipo.int/pub/published_pat_sequences	
XX		
SQ	Sequence 2772 BP; 805 A; 590 C; 687 G; 680 T; 0 U; 10 Other;	
	Query Match 73.6%; Score 16.2; DB 6; Length 2772;	
	Best Local Similarity 85.7%; Pred. No. 7.1e+02;	
	Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
QY	2 AAAGGCCTTTCGGGGTGCTC 22	
Db	1526 AAATGCCCTTGGGAGTGCTC 1546	
RESULT 70		
ADV35075		
ID	ADV35075 standard; cDNA; 3135 BP.	
XX		
AC	ADV35075;	
XX		
DT	10-FEB-2005 (first entry)	
XX		
DE	Human cDNA differentially expressed in the presence of valproate Seq151.	
XX	human; valproate; ss; multi-parameter high throughput screening; MPHTS;	
KW	disease signature; neuropsychiatric; neurodegenerative; schizophrenia;	
KW	bipolar affective disorder; BAD; autism; Parkinson's;	
KW	Alzheimer's disease; neuroleptic; nootropic; antimanic; antidepressant.	
XX	Homo sapiens.	
OS		
XX		
PN	US2003096264-A1.	
XX		
PD	22-MAY-2003.	
XX		
PF	18-JUN-2002; 2002US-00175523.	
XX		
PR	18-JUN-2001; 2001US-0299151P.	
PR	07-SEP-2001; 2001US-0317828P.	
PR	25-SEP-2001; 2001US-0325150P.	
PR	14-NOV-2001; 2001US-033047P.	
PR	18-JAN-2002; 2002US-0349936P.	
PR	04-MAR-2002; 2002US-0361834P.	
XX		
PA	(PSYC-) PSYCHIATRIC GENOMICS INC.	
XX		
PI	Altar CA, Brockman JA, Evans D, Hook D, Klimczak LJ, Laeng P;	
PI	Palfreyman M, Rajan P;	
XX		
DR	WPI; 2004-118903/12.	
XX		
XX	Identifying a compound that can treat disease or disorders, such as, a	
PT	neuropsychiatric disorder e.g., schizophrenia, or autism, comprises	
PT	determining the expression of one or more efficacy genes in a cell	
PT	contacted with the test compound.	
XX		
PS	Claim 13; SEQ ID NO 151; 39pp; English.	
XX		
CC	This invention relates to a novel screening method identified as a multi-	
CC	parameter high throughput screening (MPHTS) assay. Specifically, it	
CC	refers to an assay that utilises the disease signature of a plurality of	
CC	specific genes associated with a particular disease, and identifies	
CC	differential expression between those cells taken from individuals	
CC	affected by that disease and those that are not affected. The present	
CC	invention then describes the screening of candidate pharmaceutical	
CC	compounds to identify those that have a potential therapeutic benefit for	
CC	the treatment of neuropsychiatric and neurodegenerative disorders	
CC	including schizophrenia, bipolar affective disorder (BAD) and autism, as	
CC	well as Parkinson's and Alzheimer's disease. Accordingly, the compounds	
CC	of this invention exhibit various activities including neuroleptic,	
CC	nootropic, antimanic and antidepressant. Furthermore, the screening	
CC	method used in MPHTS will be automated, such that a large number of test	
CC	compounds may be rapidly screened with a minimal amount of labour and	
CC	effort. This polynucleotide is a human cDNA sequence of a gene that is	
CC	differentially expressed in the presence of the therapeutic compound	
CC	valproate, given in an exemplification of the invention.	
XX		
SQ	Sequence 3135 BP; 919 A; 671 C; 730 G; 815 T; 0 U; 0 Other;	
	Query Match 73.6%; Score 16.2; DB 13; Length 3135;	
	Best Local Similarity 85.7%; Pred. No. 7.2e+02;	
	Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
QY	2 AAAGGCCTTTCGGGGTGCTC 22	
Db	1689 AAATGCCCTTGGGAGTGCTC 1709	
RESULT 71		
ADP65658		
ID	ADP65658 standard; DNA; 4258 BP.	
XX		
AC	ADP65658;	
XX		
DT	12-AUG-2004 (first entry)	
XX		
DE	Human mitochondrial benzodiazepine receptor (MBR) gene, complete DNA.	
XX	autoimmune disease; arthritis; gene expression analysis;	
KW	rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;	
KW	antiarthritic; osteopathic; antigen; antiinflammatory; dermatological;	
KW	immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;	
KW	fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;	

KW immune; ds; human.
 OS Homo sapiens.
 XX WO2003072827-A1.
 XX 04-SEP-2003.
 XX 31-OCT-2002; 2002WO-US035433.
 XX 31-OCT-2001; 2001US-0336220P.
 XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 XX Hirsch R, Thorton SL;
 XX WPI: 2003-712740/67.
 XX GENBANK; U12421.
 XX Diagnosing and analyzing autoimmune disease using gene expression
 PT profiles and microarray technology, useful for diagnosing and treating
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
 PT gout.
 XX Disclosure; Page; 56pp; English.
 XX The invention relates to a novel method for diagnosing and analysing
 CC autoimmune disease or arthritides. The method comprises obtaining a
 CC patient sample containing mRNA, analysing gene expression using the mRNA
 CC that results in a gene expression signature of the mRNA, and using that
 CC gene expression signature to diagnose or analyse the autoimmune disease
 CC or arthritides in the patient, where gene expression of at least 60% of
 CC the genes correlates with that of the gene signature. The invention
 CC further comprises: a treatment of rheumatoid arthritis; identification of
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the
 CC efficacy of a candidate drug in vitro for the treatment of collagen-
 CC induced arthritis; and reducing the symptoms associated with collagen-
 CC induced arthritis. The compositions of the invention have the following
 CC activities: immunosuppressive, anti-rheumatic, antiarthritic, osteopathic,
 CC antitumor, antiinflammatory, dermatological, and immunomodulatory. The
 CC methods and compositions of the present invention are useful for
 CC diagnosing and treating autoimmune disease or arthritides, such as
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
 CC immune disease caused by an infectious agent. This polynucleotide
 CC represents a DNA sequence relating to the genes used in the analysis and
 CC treatment of autoimmune diseases or arthritides. Note: This sequence is
 CC not shown in the specification. It has been supplied in an electronic
 CC format from WIPO.
 XX SQ Sequence 4258 BP; 794 A; 1246 C; 1221 G; 997 T; 0 U; 0 Other;
 Query Match 73.6%; Score 16.2; DB 11; Length 4258;
 Best Local Similarity 85.7%; Pred. No. 7.3e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GAGAGGCTTTCGGGGTGCT 21
 Db 12 GACAGGCTTTCGGGGTGCT 32
 RESULT 72
 AAC77830
 ID AAC77830 standard; cDNA; 4395 BP.
 XX AAC77830;
 XX AC
 XX 08-FEB-2001 (first entry)
 XX Human cancer associated gene sequence SEQ ID NO:224.
 XX
 KW Human; cancer associated gene; cancer antigen; detection; cancer;
 KW diagnosis; cytostatic; proliferative; vulnary; immunomodulator;
 KW antidiabetic; antiaesthetic; antirheumatic; antiarthritic; antiviral;
 KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
 KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
 KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
 KW immune disorder; haematopoietic cell disorder; autoimmune disorder;
 KW allergic reaction; graft versus host disease; organ rejection;
 KW haemostatic; thrombolytic; cardiovascular disorder; infection;
 KW neurological disease; drug screening; ss.
 XX Homo sapiens.
 OS WO200005350-A1.
 XX 21-SEP-2000.
 XX 08-MAR-2000; 2000WO-US005882.
 XX 12-MAR-1999; 99US-0124270P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Ruben SM;
 XX WPI: 2000-587533/55.
 XX P-PSDB; AAB43621.
 XX Novel isolated nucleic acids comprising sequences encoding peptides
 PT useful for treating or diagnosing e.g. cancer.
 XX Claim 1; Page 795-796; 2352pp; English.
 XX AAC77607 to AAC78448 encode the human cancer associated proteins given in
 CC AAB43398 to AAB44339. The proteins can have activities based on the
 CC tissues and cells the genes are expressed in. Example of activities
 CC include: cycostatic; proliferative; vulnary; immunomodulator;
 CC antidiabetic; antiaesthetic; antirheumatic; antiarthritic;
 CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
 CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
 CC nootropic; vasotropic; antipsoriatic and antiangiogenic. The
 CC polynucleotides and polypeptides can be used for preventing, treating or
 CC ameliorating medical conditions and diagnosing pathological conditions.
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
 CC the present invention may be used to treat immune disorders by activating
 CC or inhibiting the proliferation, differentiation or mobilisation of
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune
 CC disorders, allergic reactions, graft versus host disease and organ
 CC rejection, modulate haemostatic or thrombolytic activity, modulate
 CC inflammation, cancers, cardiovascular disorders, neurological diseases
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to
 CC AAC78457 and AAB44240 represent sequences used in the exemplification of
 CC the present invention
 XX SQ Sequence 4395 BP; 1364 A; 765 C; 923 G; 1335 T; 0 U; 8 Other;
 Query Match 73.6%; Score 16.2; DB 3; Length 4395;
 Best Local Similarity 85.7%; Pred. No. 7.4e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 AAAGGCTTTCGGGGTGCTC 22
 Db 603 AAATGCTTTCGGGGTGCTC 623
 RESULT 73
 ADL96632/c
 ID ADL96632 standard; DNA; 4415 BP.
 XX ADL96632;
 XX AC
 XX ADL96632;
 XX


```

ID ADY91665 standard; DNA; 4738 BP.
XX
AC ADY91665;
XX
XX
DT 16-JUN-2005 (first entry)
XX
DE Human prostatic cancer marker, PEG3 Kruppel-type zinc finger DNA.
XX
XX tumor marker; cytostatic; prostate tumor; andrology;
KW genitourinary disease; neoplasm; immunotherapy; ds; gene; PEG3.
XX
XX Homo sapiens.
XX
XX JP2005080524-A.
XX
XX 31-MAR-2005.
XX
XX 05-SEP-2003; 2003JP-00313565.
XX
XX 05-SEP-2003; 2003JP-00313565.
XX
XX (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
XX
XX WPI; 2005-266555/28.
DR P-PSDB; ADY91630.
XX
XX Novel prostatic-cancer marker polypeptide, useful for diagnosing
PT prostatic-cancer or androgen independent prostatic-cancer.
XX
XX Claim 23; SEQ ID NO 64; 43pp; Japanese.
XX
XX The invention relates to a novel prostatic cancer marker polypeptide
CC comprising any one of 35 fully defined amino acid sequences (SEQ ID NOS:1
CC -35) as given in specification. Prostate-specific antigen (PSA) is
CC currently widely used as a prostatic tumor marker. Certain problems are
CC associated with diagnosis using PSA, however, such as false positives and
CC ambiguity between benign and malignant results. The polypeptides of the
CC invention demonstrate cytostatic activity and may be useful for
CC diagnosing and treating prostatic cancer or androgen-independent
CC prostatic cancer. The polypeptides may be utilized for immunotherapy. The
CC current sequence is that of the human prostatic cancer marker, PEG3
CC Kruppel-type zinc finger DNA of the invention.
XX
XX Sequence 4738 BP; 1405 A; 1055 C; 1269 G; 1009 T; 0 U; 0 Other;
SQ
Query Match 73.6%; Score 16.2; DB 14; Length 4738;
Best Local Similarity 85.7%; Pred. No. 7.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGGCCTTTGGGGGTGCTC 22
Db 4582 AAATGCCTTTGGGGAGTGCTC 4602

RESULT 76
ABX93240
ID ABX93240 standard; cDNA; 4758 BP.
XX
XX
AC ABX93240;
XX
XX 30-MAY-2003 (first entry)
XX
XX Full-length cDNA encoding human zinc finger protein, PEG3.
XX
XX Human; paternally expressed gene 3; PEG3; zinc finger protein;
KW transcription factor; gene expression; body weight; obesity; Behaviour;
KW thermoregulation; thermoregulatory disorder; cell death; degeneration;
KW Alzheimer's disease; anorectic; gene therapy; gene; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH 5'UTR 1..363
FT
```

```

FT CDS /*tag= a
FT FT 364..4758
FT FT /*tag= b
FT FT /product= "PEG3"
XX
XX US2002182668-A1.
XX
XX 05-DEC-2002.
XX
XX 27-APR-2001; 2001US-00842777.
XX
XX 27-APR-2001; 2001US-00842777.
XX
XX (SURA/) SURANI A.
XX (SZET/) SZETO Y Y.
XX
XX Surani A, Szeto YY;
XX
XX WPI; 2003-340975/32.
DR P-PSDB; ABU08353.
XX
XX New cDNAs of the paternally expressed gene 3 (PEG3), useful in gene
PT therapy to increase or decrease the expression of PEG3 in cells of a
PT patient, particularly for modifying or controlling body weight or
PT behavior, or for thermoregulation.
XX
XX Claim 3; Page 13-15; 39pp; English.
XX
XX The present invention relates to the isolation of cDNA fragments and the
CC full-length cDNA sequence encoding human paternally expressed gene 3
CC (PEG3). PEG3 is a zinc finger protein thought to act as a transcription
CC factor. The polynucleotide sequences encoding PEG3 are useful in gene
CC therapy to increase or decrease (using the antisense form of the nucleic
CC acid) the expression of PEG3 in cells of a human patient, particularly
CC for modifying or controlling body weight (to treat obesity) or behaviour,
CC or for thermoregulation. The PEG3 polynucleotide sequence is also useful
CC in diagnostic assays, e.g. for testing an individual's susceptibility to
CC obesity or a thermoregulatory disorder, or for diagnosing and staging
CC diseases involving cell death and degeneration (e.g. Alzheimer's
CC disease). The PEG3 polypeptide is useful for prophylactic and/or
CC therapeutic treatment. The present sequence encodes human PEG3
XX
XX Sequence 4758 BP; 1410 A; 1055 C; 1281 G; 1012 T; 0 U; 0 Other;
SQ
Query Match 73.6%; Score 16.2; DB 10; Length 4758;
Best Local Similarity 85.7%; Pred. No. 7.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGGCCTTTGGGGGTGCTC 22
Db 4599 AAATGCCTTTGGGGAGTGCTC 4619

RESULT 77
ADK41009
ID ADK41009 standard; DNA; 4831 BP.
XX
XX
AC ADK41009;
XX
XX 06-MAY-2004 (first entry)
XX
XX Novel human kinase gene #29.
XX
XX Cytostatic; immunomodulator; cardiant; neuroprotective; nootropic;
KW antiparkinsonian; virucide; antibacterial; fungicide; ophthalmological;
KW analgesic; hypotensive; immunosuppressive; kinase inhibitor; kinase;
KW cancer; peripheral nervous system; central nervous system;
KW Alzheimer's disease; Parkinson's disease; multiple sclerosis;
KW amyotrophic lateral sclerosis; viral infection; prion infection;
KW ocular disease; migraine; pain; sexual dysfunction; mood disorder;
KW attention disorder; cognition disorder; hypotension; hypertension;
KW psychotic disorder; neurological disorder; dyskinesia;
KW metabolic disorder; organ transplant rejection; enzyme; gene; ds.
XX
```


14-JUN-1999 (first entry)
 DT XX Nucleic acid encoding a carcinogenesis-inhibiting protein.
 DE XX Carcinogenesis-inhibiting activity; genetic treatment; cerebral tumour;
 KW ds.
 KW ds.
 KW ds.
 OS Homo sapiens.
 FH Key
 FT CDS Location/Qualifiers
 FT 344..4732
 FT /*tag= a
 XX
 XX JF11075844-A.
 PN XX
 XX 23-MAR-1999.
 PD XX
 XX 01-SEP-1997; 97JP-00236208.
 PF XX
 XX 01-SEP-1997; 97JP-00236208.
 PR XX
 XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 PA XX
 DR WPI; 1999-257694/22.
 DR P-PSDB; AAY01519.
 DR XX
 XX A carcinogenesis-inhibiting gene - useful for genetic treatment of
 PT cerebral tumors.
 PT Claim 3; Page 9-15; 21pp; Japanese.
 PS XX
 CC The present sequence encodes a protein with carcinogenesis-inhibiting
 CC activity. The gene is useful for the genetic treatment of cerebral
 CC tumours
 CC XX
 SQ Sequence 5970 BP; 1745 A; 1297 C; 1502 G; 1426 T; 0 U; 0 Other;
 Query Match 73.6%; Score 16.2; DB 2; Length 5970;
 Best Local Similarity 85.7%; Pred. No. 7.5e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 AAAGGCTTTTCGGGGTGTCTC 22
 DB 4573 AAATGCCCTTTGGGGAGTGTCTC 4593
 RESULT 80
 ADB80558
 ID ADB80558 standard; DNA; 5994 BP.
 XX AC ADB80558;
 XX DT 04-DEC-2003 (first entry)
 XX DE Ovarian cancer-associated transcript #62.
 XX cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis;
 KW post-operative chemotherapy; radiation therapy; tumour prognosis;
 KW pre-cancerous lesion detection; ds; gene.
 XX Homo sapiens.
 OS Key
 FH Location/Qualifiers
 FT CDS 356..4750
 FT /*tag= a
 XX WO2002102235-A2.
 PN XX
 XX 27-DEC-2002.
 PD XX
 XX 18-JUN-2002; 2002WO-US019297.
 PF XX
 XX 18-JUN-2001; 2001US-0299234P.
 PR XX

27-AUG-2001; 2001US-0315287P.
 PR 03-SEP-2001; 2001US-0317544P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 12-APR-2002; 2002US-0372246P.
 XX
 XX (EOSB-) EOS BIOTECHNOLOGY INC.
 XX Mack DH, Gish KC;
 PI WPI; 2003-167431/16.
 XX P-PSDB; ADB80559.
 DR
 DR
 DR
 XX
 XX
 PT Detecting an ovarian cancer-associated transcript in a cell from a
 PT patient, comprises contacting a biological sample from the patient with a
 PT polynucleotide that hybridizes to an ovarian cancer gene.
 XX
 XX Claim 10; Page 316-317; 332pp; English.
 PS
 XX The invention relates to a method of detecting an ovarian cancer-
 CC associated transcript in a cell from a patient, by contacting a
 CC biological sample from the patient with a polynucleotide that selectively
 CC hybridizes to a sequence at least 80% identical to any of one of 80
 CC nucleic acid sequences given in the specification. The method is useful
 CC in diagnosing ovarian cancer and in identifying and using agents and/or
 CC targets that inhibit ovarian cancer. The nucleic acid molecule,
 CC polypeptide and the antibody may also be used in detecting ovarian
 CC cancers, monitoring and early detection of relapse following treatment,
 CC monitoring response to therapy, selecting patients for post-operative
 CC chemotherapy or radiation therapy, in selecting mode of therapy,
 CC determining tumour prognosis, early detection of pre-cancerous lesions,
 CC and as vaccines. This sequence corresponds to one of the nucleic acids
 CC used for the detection method of the invention.
 XX
 SQ Sequence 5994 BP; 1760 A; 1298 C; 1504 G; 1432 T; 0 U; 0 Other;
 Query Match 73.6%; Score 16.2; DB 10; Length 5994;
 Best Local Similarity 85.7%; Pred. No. 7.5e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 AAAGGCTTTTCGGGGTGTCTC 22
 DB 4591 AAATGCCCTTTGGGGAGTGTCTC 4611
 RESULT 81
 ADB79896
 ID ADB79896 standard; DNA; 5994 BP.
 XX AC ADB79896;
 XX DT 04-DEC-2003 (first entry)
 XX DE Human putative KIAA0287 coding sequence, SEQ ID 136.
 XX Analgesic; pain; streptozocin-induced diabetes; human; gene; ds.
 KW Homo sapiens.
 OS
 XX EP1279744-A2.
 PN
 XX 29-JAN-2003.
 PD
 XX 26-JUL-2002; 2002EP-00255249.
 PF
 XX 27-JUL-2001; 2001GB-00018354.
 PR
 XX 07-FEB-2002; 2002GB-00002910.
 XX
 XX (WARN) WARNER LAMBERT CO.
 XX Brooksbank RA, Dixon AK, Lee K, Pinnock RD;
 PI WPI; 2003-395407/38.
 DR P-PSDB; ADB79895.
 DR

CC carrier; an antibody directed against the polypeptide of (3); a method
 CC for detecting (1) in a sample; a method for detecting the polypeptide of
 CC (3) in a sample; a method for identifying a compound that binds to the
 CC polypeptide of (3); a method for producing the polypeptide of (3); and a
 CC collection of polynucleotides, where the collection comprising of at
 CC least one of SEQ ID NOS: 1-567. (1) is a polynucleotide comprising any of
 CC the sequences of SEQ ID NOS: 1-567 encoding a polypeptide with biological
 CC activity, which comprises any of the amino acid sequence of SEQ ID NOS:
 CC 568-1134. All sequences are fully defined in the specification. The
 CC sequences and methods are useful in diagnostics, forensic, and gene
 CC mapping, in identifying of mutations responsible for genetic disorders or
 CC other traits, in assessing biodiversity, and for producing many other
 CC types of data and products dependent on DNA and amino acid sequences. The
 CC composition and method are useful for treating a disease or disorder,
 CC e.g. osteoporosis, osteoarthritis, periodontal disease, burns, CNS and
 CC peripheral disease, Alzheimer's disease, Parkinson's disease, stroke,
 CC autoimmune disorders, viral infection, or cancer. This sequence encodes a
 CC novel polypeptide of the invention.

XX SQ Sequence 6315 BP; 1852 A; 1366 C; 1573 G; 1524 T; 0 U; 0 Other;

Query Match 73.6%; Score 16.2; DB 14; Length 6315;
 Best Local Similarity 85.7%; Pred. No. 7.6e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGGCCTTTTCGGGGTGCTC 22

Db 4899 AAATGCTTTGGGGAGTGCTC 4919

RESULT 84

ABA09565

ID ABA09565 standard; cDNA; 6332 BP.

AC ABA09565;

XX 11-JAN-2002 (first entry)

XX Human carcinogenesis inhibitor homologue-encoding cDNA, SEQ ID NO:1341.

XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
 KW cytosstatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 KW antifungal; vulnery; antiulcer; ss.

XX Homo sapiens.

XX WO200157188-A2.

XX 09-AUG-2001.

XX 05-FEB-2001; 2001WO-US003800.

XX 03-FEB-2000; 2000US-00496914.

XX 27-APR-2000; 2000US-00560875.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI: 2001-457740/49.

XX P-PSDB; ABB12321.

XX Human proteins and DNA encoding sequences useful for preventing, treating

PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
 and cancer.

PS Claim 1; Page 1002-1004; 1963pp; English.

XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA09225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis; cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.

XX Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a cDNA encoding a
 CC novel human polypeptide of the invention

XX SQ Sequence 6332 BP; 1860 A; 1378 C; 1582 G; 1512 T; 0 U; 0 Other;

Query Match 73.6%; Score 16.2; DB 4; Length 6332;
 Best Local Similarity 85.7%; Pred. No. 7.6e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGGCCTTTTCGGGGTGCTC 22

Db 4899 AAATGCTTTGGGGAGTGCTC 4919

RESULT 85

ADL12831

ID ADL12831 standard; cDNA; 8411 BP.

XX AC ADL12831;

XX 06-MAY-2004 (first entry)

XX Human steroid-induced C3A liver cell cDNA #560.

XX ss; gene; Hepatotropic; Gene therapy; Wilson disease; liver disorder;
 KW steroid therapy; cirrhosis; hepatitis; human; C3A liver cell.

XX Homo sapiens.

XX US6673549-B1.

XX 06-JAN-2004.

XX

PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216860P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226686P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227099P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 01-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232337P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
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PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 37745; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I) amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to

CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention
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SQ Sequence 14063 BP; 4698 A; 2703 C; 2660 G; 4002 T; 0 U; 0 Other;

Query Match 73.6%; Score 16.2; DB 4; Length 14063;
Best Local Similarity 85.7%; Pred. No. 8.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GAAAGGCTTTCGGGGTGCT 21
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Db 10020 GAAAGGCTTTCGAGATGCT 10040

RESULT 88

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ID AAK82934 standard; DNA; 14063 BP.

XX

AC AAK82934;

XX

DT 07-NOV-2001 (first entry)

XX

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37746.

XX

KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cystostatic; gene therapy; vaccine; metastasis; ds.

XX

OS Homo sapiens.

XX

PN WO200157182-A2.

XX

PD 09-AUG-2001.

XX

PF 17-JAN-2001; 2001WO-US0001354.

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PR

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PR 17-NOV-2000; 2000US-0249207P.
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PR 17-NOV-2000; 2000US-0249213P.
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PR 17-NOV-2000; 2000US-0249216P.
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PR 01-DEC-2000; 2000US-0250160P.
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PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
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PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX Disclosure; SEQ ID NO 37746; 3071pp + Sequence Listing; English.
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX SQ Sequence 14063 BP; 4696 A; 2705 C; 2660 G; 4002 T; 0 U; 0 Other;
Query March 73.6%; Score 16.2; DB 4; Length 14063;
Best Local Similarity 85.7%; Pred. No. 8.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GAAAGGCTTTCGGGGGTGCT 21
DB 10018 GAAAGGCTTTCGATGCT 10038

RESULT 89
ADW22177
ID ADW22177 standard; cDNA; 25759 BP.
XX AC ADW22177;
XX AC ADW22177;
DT 10-MAR-2005 (first entry)
XX XX
DE Rat hepatotoxicity marker gene, SEQ:556.
XX XX
KW Toxicology screening; drug screening; gene expression;
KW expression profile; hepatotoxicity; drug-induced; hepatitis;
KW liver disease; gastrointestinal disease; gene; ss.
XX OS Rattus norvegicus.
XX PN EP1344834-A2.
XX XX
PD 17-SEP-2003.
XX XX
XX 04-MAR-2003; 2003EP-00004810.
XX PF
XX 14-MAR-2002; 2002EP-00005336.
PR 17-JUL-2002; 2002EP-00015657.
XX XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX XX
XX Boess F, Suter-Dick L, Wolf D;
XX WPI; 2003-723475/69.
DR EMBL; X04267.
XX XX
PT Predicting toxicity of compounds, useful in development of safe drugs, by
PT measuring the differential expression of specific genes in cells exposed
PT to test compounds.
XX PS Claim 2; SEQ ID NO 556; 895pp; English.
XX CC The invention relates to methods of predicting at least one toxic effect
CC (or toxicity progression or the mechanism of toxicity) of a compound. The
CC methods involve detecting the level of expression of at least one of a
CC set of 680 genes ADW21622-ADW22301 or at least one of a set of 17 genes
CC (including ADW22362, ADW22414 and ADW22481-ADW22483) in a tissue or cell
CC exposed to the compound, and determining whether the gene is
CC differentially expressed compared with a control tissue or cell.
CC Differential expression of the gene in the presence of the compound is
CC indicative of a toxic effect, of toxicity progression or of a specific
CC mechanism of toxicity. The toxic effect is especially hepatotoxicity,
CC particularly hepatitis, liver necrosis, protein adduct formation or fatty
CC liver. The invention also relates to sets of primers and probes specific
CC for at least two genes selected from ADW21622-ADW22301; solid supports
CC (e.g., DNA chips) and kits containing the probes; and a database
CC containing DNA sequence information and expression information for at
CC least two of the 680 genes from hepatotoxin-exposed tissues. The
CC invention is based on the determination of global changes in gene
CC expression in tissues or cells exposed to known toxins, particularly
CC hepatotoxins, and the identification of individual genes (toxicity
CC markers) that are differentially expressed on toxin exposure. The changes
CC in gene expression can be characteristic of different mechanisms of
CC hepatotoxicity mediated by various classes of compounds. Such compounds
CC include: direct acting compounds which cause damage to macromolecules,
CC especially proteins and lipids by directly interacting with them;
CC steatotic compounds which cause an accumulation of fat in the liver; and
CC cholestatic compounds which impair bile flow or bile acid transport,
CC resulting in jaundice. The methods of the invention are useful in
CC toxicology screening for predicting the toxic effects (especially
CC hepatotoxic effects) of compounds for the development of safer drugs.
CC Sequences ADW21622-ADW22301 represent specifically claimed hepatotoxicity
CC marker genes of rat origin whose expression is altered on exposure to
CC hepatotoxins.
XX SQ Sequence 25759 BP; 6768 A; 5975 C; 6783 G; 6229 T; 0 U; 4 Other;

Query Match 73.6%; Score 16.2; DB 11; Length 25759;
 Best Local Similarity 85.7%; Pred. No. 8.5e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGCT 21
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 Db 21445 GAAAGGCATTAGTGGTGCT 21465

RESULT 90
 AEB96542
 ID AEB96542 standard; DNA; 104932 BP.

XX AC AEB96542;
 XX 06-OCT-2005 (first entry)
 DT Human STAT5A gene, SEQ ID 26.
 DE hepatitis C virus infection; antiinflammatory; hepatotropic; virucide;
 KW liver cirrhosis; fibrosis; hepatoma; SNP detection; STAT5A; ds.
 XX Homo sapiens.

XX Key Location/Qualifiers
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 FT /tag= a
 FT /standard_name= "Single nucleotide polymorphism"
 FT 4403
 FT variation
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 FT /standard_name= "Single nucleotide polymorphism"
 FT 4414
 FT variation
 FT /tag= c
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 FT 4481
 FT variation
 FT /tag= d
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 FT 4607
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variation
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Db      37462 GATATGCCTTTCGGGTGCTC 37442

RESULT 92
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Continuation (31 of 45) of AAI99682 from base 3000001 (Mycobacterium tuberculosis strain
WP Sequence split into 45 fragments LOCUS AAI99682 Accession Aai99682
WP Fragment Name Begin End
WP AAI99682_00 1 110000
WP AAI99682_01 100001 310000
WP AAI99682_02 200001 310000
WP AAI99682_03 300001 410000
WP AAI99682_04 400001 510000
WP AAI99682_05 500001 610000
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WP AAI99682_07 700001 810000
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WP AAI99682_09 900001 1010000
WP AAI99682_10 1000001 1110000
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Query Match 73.6%; Score 16.2; DB 4; Length 110000;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      2 AAAGCCCTTCGGGGTGCTC 22
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Db      101041 AAAGCCGTCGCGGTGCTC 101021

RESULT 93
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WP AAI99682_16 1600001 1710000
WP AAI99682_17 1700001 1810000
WP AAI99682_18 1800001 1910000
WP AAI99682_19 1900001 2010000
WP AAI99682_20 2000001 2110000
WP AAI99682_21 2100001 2210000
WP AAI99682_22 2200001 2310000
WP AAI99682_23 2300001 2410000
WP AAI99682_24 2400001 2510000
WP AAI99682_25 2500001 2610000
WP AAI99682_26 2600001 2710000
WP AAI99682_27 2700001 2810000
WP AAI99682_28 2800001 2910000
WP AAI99682_29 2900001 3010000
WP AAI99682_30 3000001 3110000
WP AAI99682_31 3100001 3210000
WP AAI99682_32 3200001 3310000
WP AAI99682_33 3300001 3410000
WP AAI99682_34 3400001 3510000
WP AAI99682_35 3500001 3610000
WP AAI99682_36 3600001 3710000
WP AAI99682_37 3700001 3810000
WP AAI99682_38 3800001 3910000
WP AAI99682_39 3900001 4010000
WP AAI99682_40 4000001 4110000
WP AAI99682_41 4100001 4210000
WP AAI99682_42 4200001 4310000
WP AAI99682_43 4300001 4410000
WP AAI99682_44 4400001 4411529

Query Match 73.6%; Score 16.2; DB 4; Length 110000;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      2 AAAGCCCTTCGGGGTGCTC 22
        ||||| ||| |||||
Db      101041 AAAGCCGTCGCGGTGCTC 101021

RESULT 94
AAI99683_30/c
Continuation (31 of 44) of AAI99683 from base 3000001 (Mycobacterium tuberculosis strain
WP Sequence split into 44 fragments LOCUS AAI99683 Accession Aai99683
WP Fragment Name Begin End
WP AAI99683_00 1 110000
WP AAI99683_01 100001 210000
WP AAI99683_02 200001 310000
WP AAI99683_03 300001 410000
WP AAI99683_04 400001 510000
WP AAI99683_05 500001 610000
WP AAI99683_06 600001 710000
WP AAI99683_07 700001 810000
WP AAI99683_08 800001 910000
WP AAI99683_09 900001 1010000
WP AAI99683_10 1000001 1110000
WP AAI99683_11 1100001 1210000
WP AAI99683_12 1200001 1310000
WP AAI99683_13 1300001 1410000
WP AAI99683_14 1400001 1510000
WP AAI99683_15 1500001 1610000
WP AAI99683_16 1600001 1710000
WP AAI99683_17 1700001 1810000

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WP      AAI99682_05 500001 610000
WP      AAI99682_06 600001 710000
WP      AAI99682_07 700001 810000
WP      AAI99682_08 800001 910000
WP      AAI99682_09 900001 1010000
WP      AAI99682_10 1000001 1110000
WP      AAI99682_11 1100001 1210000
WP      AAI99682_12 1200001 1310000
WP      AAI99682_13 1300001 1410000
WP      AAI99682_14 1400001 1510000
WP      AAI99682_15 1500001 1610000
WP      AAI99682_16 1600001 1710000
WP      AAI99682_17 1700001 1810000
WP      AAI99682_18 1800001 1910000
WP      AAI99682_19 1900001 2010000
WP      AAI99682_20 2000001 2110000
WP      AAI99682_21 2100001 2210000
WP      AAI99682_22 2200001 2310000
WP      AAI99682_23 2300001 2410000
WP      AAI99682_24 2400001 2510000
WP      AAI99682_25 2500001 2610000
WP      AAI99682_26 2600001 2710000
WP      AAI99682_27 2700001 2810000
WP      AAI99682_28 2800001 2910000
WP      AAI99682_29 2900001 3010000
WP      AAI99682_30 3000001 3110000
WP      AAI99682_31 3100001 3210000
WP      AAI99682_32 3200001 3310000
WP      AAI99682_33 3300001 3410000
WP      AAI99682_34 3400001 3510000
WP      AAI99682_35 3500001 3610000
WP      AAI99682_36 3600001 3710000
WP      AAI99682_37 3700001 3810000
WP      AAI99682_38 3800001 3910000
WP      AAI99682_39 3900001 4010000
WP      AAI99682_40 4000001 4110000
WP      AAI99682_41 4100001 4210000
WP      AAI99682_42 4200001 4310000
WP      AAI99682_43 4300001 4410000
WP      AAI99682_44 4400001 4411529

Query Match 73.6%; Score 16.2; DB 4; Length 110000;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      2 AAAGCCCTTCGGGGTGCTC 22
        ||||| ||| |||||
Db      1041 AAAGCCGTCGCGGTGCTC 1021

RESULT 94
AAI99683_30/c
Continuation (31 of 44) of AAI99683 from base 3000001 (Mycobacterium tuberculosis strain
WP Sequence split into 44 fragments LOCUS AAI99683 Accession Aai99683
WP Fragment Name Begin End
WP AAI99683_00 1 110000
WP AAI99683_01 100001 210000
WP AAI99683_02 200001 310000
WP AAI99683_03 300001 410000
WP AAI99683_04 400001 510000
WP AAI99683_05 500001 610000
WP AAI99683_06 600001 710000
WP AAI99683_07 700001 810000
WP AAI99683_08 800001 910000
WP AAI99683_09 900001 1010000
WP AAI99683_10 1000001 1110000
WP AAI99683_11 1100001 1210000
WP AAI99683_12 1200001 1310000
WP AAI99683_13 1300001 1410000
WP AAI99683_14 1400001 1510000
WP AAI99683_15 1500001 1610000
WP AAI99683_16 1600001 1710000
WP AAI99683_17 1700001 1810000

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WP AA199683_18 1800001 1910000
 WP AA199683_19 1900001 2010000
 WP AA199683_20 2000001 2110000
 WP AA199683_21 2100001 2210000
 WP AA199683_22 2200001 2310000
 WP AA199683_23 2300001 2410000
 WP AA199683_24 2400001 2510000
 WP AA199683_25 2500001 2610000
 WP AA199683_26 2600001 2710000
 WP AA199683_27 2700001 2810000
 WP AA199683_28 2800001 2910000
 WP AA199683_29 2900001 3010000
 WP AA199683_30 3000001 3110000
 WP AA199683_31 3100001 3210000
 WP AA199683_32 3200001 3310000
 WP AA199683_33 3300001 3410000
 WP AA199683_34 3400001 3510000
 WP AA199683_35 3500001 3610000
 WP AA199683_36 3600001 3710000
 WP AA199683_37 3700001 3810000
 WP AA199683_38 3800001 3910000
 WP AA199683_39 3900001 4010000
 WP AA199683_40 4000001 4110000
 WP AA199683_41 4100001 4210000
 WP AA199683_42 4200001 4310000
 WP AA199683_43 4300001 4403765

Query Match 73.6%; Score 16.2; DB 4; Length 110000;
 Best Local Similarity 85.7%; Pred. No. 9.4e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGGCTTTTCGGGGTGCTC 22
 ||||| ||| |||||
 Db 95717 AAAGCGGTCGCGGTGCTC 95697

RESULT 95
 ID ADB82110/c
 AC ADB82110;
 XX
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Human cDNA sequence useful for the treatment of cancer (SegID 422).
 XX
 XX human; prostate; cancer; cytostatic; gene therapy; vaccine;
 KW immune response; gene; ss.
 KW Homo sapiens.
 OS
 XX WO2003050236-A2.
 XX
 XX 19-JUN-2003.
 XX
 XX 04-SEP-2002; 2002WO-US028214.
 XX
 XX 07-DEC-2001; 2001US-00012697.
 XX
 XX (CHIR) CHIRON CORP.
 PA (HYSE-) HYSEQ INC.
 XX
 XX Escobedo J, Garcia PD, Kassam A, Lamson G, Drmanac R;
 PI Crkvenjakov R, Dickson M, Drmanac S, Labat I, Leshkowitz D, Kita D;
 PI Garcia V, Jones LW, Stache-Crain B, Scott EM;
 XX WPI; 2003-513972/48.
 DR
 XX New polynucleotides derived from human prostate, useful for modulating
 PT immune response to prevent or treat cancer.
 PT
 XX
 XX Claim 1; SEQ ID NO 422; 188pp; English.

CC This invention relates to novel isolated polynucleotides of human origin,
 CC particularly isolated from the human prostate. Specifically, it refers to
 CC the diagnostics and therapeutics comprising these novel human
 CC polynucleotides, and includes the derived probes, antisense
 CC oligonucleotides and antibodies thereof. The identification of these
 CC human prostate genes that can inhibit tumour growth is useful for
 CC understanding the progression and nature of complex diseases such as
 CC cancer, and hence they are important in the drug discovery process. The
 CC present invention describes these polynucleotides and encoded
 CC polypeptides as exhibiting cytostatic activity, and through gene therapy
 CC and/or vaccines they can be used to modulate the immune response for the
 CC prevention or treatment of cancers, particularly of the prostate, but
 CC also for breast, lung and colon cancer. This polynucleotide sequence is a
 CC human cDNA sequence useful for the treatment of cancer, used in an
 CC exemplification of the invention. NOTE: These sequences are not given in
 CC the specification but are provided on the WIPO website.

SQ Sequence 297 BP; 56 A; 72 C; 76 G; 72 T; 0 U; 21 Other;
 Query Match 72.7%; Score 16; DB 9; Length 297;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTTCGGGG 16
 ||||| ||||| |||||
 Db 74 GAAAGGCTTTTCGGGG 59

RESULT 96
 ABQ89167/c
 ID ABQ89167 standard; cDNA; 331 BP.
 XX
 AC ABQ89167;
 XX
 XX
 DT 27-SEP-2002 (first entry)
 XX
 DE Human prostate expressed polynucleotide SEQ ID NO 423.
 XX
 XX Human; prostate; cytostatic; tumour; cancer; vaccine; gene therapy; gene;
 KW ss.
 KW Homo sapiens.
 OS
 XX WO200255700-A2.
 PN
 XX 18-JUL-2002.
 XX
 XX 07-DEC-2001; 2001WO-US047349.
 XX
 XX 07-DEC-2000; 2000US-0254648P.
 PR 13-MAR-2001; 2001US-0275688P.
 XX
 XX (CHIR) CHIRON CORP.
 PA (HYSE-) HYSEQ INC.
 XX
 XX Escobedo J, Garcia PD, Kassam A, Lamson G, Drmanac R;
 PI Crkvenjakov R, Dickson M, Drmanac S, Labat I, Leshkowitz D, Kita D;
 PI Garcia V, Jones WL, Stache-Crain B, Scott EM;
 XX WPI; 2002-557824/59.
 DR
 XX New genes and gene products isolated from human prostate, useful for
 PT treating or diagnosing tumor or cancer (e.g. prostate cancer or breast
 PT cancer), or as vaccines for treating or preventing these diseases.
 PT
 XX Claim 1; SEQ ID NO 423; 186pp + Sequence Listing; English.
 PS
 CC The invention relates to an isolated polynucleotide comprising any of
 CC 1477 sequences or its fragment, degenerate variant, antisense or
 CC complement. The polynucleotides and gene products are useful for treating
 CC or diagnosing tumor or cancer (e.g. prostate cancer, breast cancer, lung
 CC cancer or medullary carcinoma) in a subject (e.g. cattle, dogs, cats,
 CC rabbits, horse or human). The polynucleotides and polypeptides are also

CC useful as vaccines for treating or preventing these diseases. The
 CC polynucleotides are useful for gene therapy. The present sequence is that
 CC of one of a group of polynucleotides (ABQ8745-ABQ90015) disclosed
 CC electronically as sequences of the invention. However only 1271
 CC polynucleotide sequences are given, whereas 1477 polynucleotides and 91
 CC proteins are claimed. Note: The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 331 BP; 74 A; 77 C; 85 G; 74 T; 0 U; 21 Other;
 Query Match 72.7%; Score 16; DB 6; Length 331;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAAAGGCTTTCGGG 16
 Db 99 GAAAGGCTTTCGGG 84
 RESULT 97
 ABX64840
 ID ABX64840 standard; cDNA; 132 BP.
 XX AC ABX64840;
 DT 03-MAR-2003 (first entry)
 XX
 DE Human gene trapped sequence (GTS) cDNA SEQ ID NO 447.
 XX Human; gene trapped sequence; GTS; gene discovery; forensic; mapping;
 KW gene therapy; antisense therapy; prenatal analysis; autoimmune disease;
 KW developmental disorder; aging; cancer; Crohn's disease; schizophrenia;
 KW multiple sclerosis; skin disorder; rheumatoid arthritis; skeletal system;
 KW atherosclerosis; cardiovascular disease; degenerative disease; neural;
 KW Alzheimer's disease; osteoporosis; asthma; infection; ss.
 XX Homo sapiens.
 XX US2002110809-A1.
 XX 15-AUG-2002.
 PD 28-APR-2000; 2000US-00560863.
 PF 30-APR-1999; 99US-0132408P.
 XX (NEHL/) NEHLS M C.
 PA (ZAMB/) ZAMBROWICZ B.
 PA (SAND/) SANDS A T.
 XX Nehls MC, Zambrowicz B, Sands AT;
 XX WPI; 2003-090170/08.
 DR Novel human polynucleotides that correspond to human gene trapped
 PT sequences useful for gene discovery, gene therapy, as markers for gene
 PT expression analysis, forensic analysis and determining genetic basis of
 PT diseases.
 XX Claim 1; SEQ ID NO 447; 36pp; English.
 PS This invention describes isolated or purified polynucleotides
 CC corresponding to human gene trapped sequence (GTS) comprising a sense or
 CC antisense sequence chosen from 1000 sequences or its fragment of 8
 CC contiguous nucleotides. GTSs are useful for gene discovery and as markers
 CC for gene expression analysis, identifying and mapping the coding regions
 CC of the mammalian and particularly human, genome, forensic analysis, for
 CC cross species hybridisation analysis, genetic manipulation, antisense
 CC inhibition, gene targeting, identification or generation of full-length
 CC cDNA, mapping the human genome, gene or antisense therapy, gene delivery
 CC and determining the genetic basis of human disease. Portion of the GTS
 CC sequences are useful as a hybridisation probe or for chromosome mapping,

CC and can be incorporated into phage display system that can be used to
 CC screen for proteins, or other ligands, that are capable of binding an
 CC amino acid sequence encoded by the GTS sequences. The GTS sequences are
 CC also useful to regulate gene expression, as a part of ribozyme and/or
 CC triple helix sequences that can be used to regulate gene expression, as
 CC components of diagnostic methods, for analysing single nucleotide
 CC polymorphisms, and also as genetic markers for prenatal analysis of
 CC congenital traits or defects. The polynucleotides of the invention are
 CC useful for diagnosis, prognosis of disorders involving developmental and
 CC differentiation processes and for the identification of subjects having a
 CC predisposition to such disorders. Diseases or natural processes that can
 CC be correlated with the expression of mutant or normal, variants of GTSs
 CC include, aging, cancer, autoimmune disease, Crohn's disease, multiple
 CC sclerosis, immune disorders, schizophrenia, skin disorders, rheumatoid
 CC arthritis, atherosclerosis, cardiovascular disease, degenerative diseases
 CC of the neural or skeletal systems, Alzheimer's disease, osteoporosis,
 CC asthma, and infections. GTSs can also be used to identify the specific
 CC locations of exon splice junctions, which are important in the study of
 CC disease and cancer. Modulating the level of expression of one or more
 CC genes and/or regulating activity of one or more peptides or proteins is
 CC useful for modifying development and cell differentiation and treating
 CC development and cell differentiation disorders. ABX64402-ABX65401
 CC represent the human gene trapped cDNA sequences described in the
 CC disclosure of the invention. NOTE: The sequence data for this patent did
 CC not form part of the printed specification but was obtained in electronic
 CC format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20020110809
 XX
 SQ Sequence 132 BP; 41 A; 24 C; 33 G; 34 T; 0 U; 0 Other;
 Query Match 71.8%; Score 15.8; DB 8; Length 132;
 Best Local Similarity 89.5%; Pred. No. 8.8e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GAAAGGCTTTCGGGGTG 19
 Db 21 GGAAGGGCTTTCGGGGTG 39
 RESULT 98
 ADQ50381/c
 ID ADQ50381 standard; DNA; 362 BP.
 XX AC ADQ50381;
 DT 21-OCT-2004 (first entry)
 XX
 DE Novel canine microarray-related DNA sequence SeqID1683.
 XX canine microarray; drug screening; toxicity assay;
 KW environmental pollutant; cellular response; gene expression profile;
 KW toxic response; liver necrosis; fatty liver disease;
 KW protein adduct formation; hepatitis; dog; ds.
 XX Canis familiaris.
 OS WO2004063324-A2.
 PN 29-JUL-2004.
 XX 05-MAY-2003; 2003WO-US013853.
 PF 03-MAY-2002; 2002US-0377240P.
 XX (GENE-) GENE LOGIC INC.
 PA (PFIZ) PFIZER PROD INC.
 XX Diggins JC, Porter M, Wei T;
 XX WPI; 2004-561890/54.
 DR New isolated nucleic acid molecule, useful for drug screening and
 XX toxicity assays or for assessing the impact, including toxicity, of a

PT compound, pharmaceutical agent or environmental pollutant on a cell or
 XX living organism.
 PS Claim 1; SEQ ID NO 1683; 41pp; English.
 XX
 CC This invention is related to a novel isolated canine nucleic acid
 CC sequences and the construction of canine microarrays containing a
 CC significant portion of the canine genome. The isolated canine nucleic
 CC acid sequences of the invention may be useful for drug screening and
 CC toxicity assays. The invention is therefore useful for assessing the
 CC impact, including toxicity, of a compound, pharmaceutical agent or
 CC environmental pollutant on a cell or living organism. The methods are
 CC useful for detecting genes that are up- or down-regulated in canines in a
 CC disease state. The sequences are useful as diagnostic agents or markers
 CC to detect a cellular response in a sample individually or as part of a
 CC gene expression profile. It is also useful as a target for agents that
 CC modulate gene expression or activity. The database is useful for
 CC producing electronic Northern blots that allow the user to determine the cell
 CC type or tissue in which a given gene is expressed and to allow
 CC determination of the abundance or expression level of a given gene in a
 CC particular tissue or cell. The methods are useful for determining the
 CC similarity of a toxic response to one or more individual compounds. The
 CC methods are useful for predicting at least one toxic response or the
 CC likelihood that a compound or test agent will induce various specific
 CC pathologies such as those of the liver (liver necrosis, fatty liver
 CC disease, protein adduct formation or hepatitis), those of the kidney,
 CC heart, brain or testes, or other pathologies associated with at least one
 CC of the toxins. The methods are also useful for predicting or elucidating
 CC the potential cellular pathways influenced, induced or modulated by the
 CC compound or test agent due to the similarity of the expression profile
 CC compared to the profile induced by a known toxin. The present profile is
 CC that of a canine DNA sequence which was claimed for use during the
 CC production of a canine microarray of the invention.
 XX
 SQ Sequence 362 BP; 76 A; 99 C; 92 G; 71 T; 0 U; 24 Other;
 Query Match 71.8%; Score 15.8; DB 13; Length 362;
 Best Local Similarity 89.5%; Pred. No. 9.5e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 AAGGCCCTTCGGGGTGCT 21
 |||||
 DB 271 AAGGCCCTTCGGGGTGCT 253
 RESULT 99
 ADA28874
 ID ADA28874 standard; DNA; 579 BP.
 XX
 AC ADA28874;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE DNA encoding Acinetobacter baumannii protein #161.
 XX
 KW ds; gene; Acinetobacter baumannii; bacterial disease; antibacterial;
 KW vaccine; plant biocontrol agent.
 XX
 OS Acinetobacter baumannii.
 XX
 EN US6562958-B1.
 XX
 PD 13-MAY-2003.
 XX
 PF 04-JUN-1999; 99US-00328352.
 XX
 PR 09-JUN-1998; 98US-0088701P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Breton G, Bush D;
 XX
 XX WPI; 2003-576092/54.

DR P-PSDB; ADA33000.
 XX
 PT New Acinetobacter baumannii proteins and nucleic acids, useful as reagents
 PT for diagnosing a bacterial disease, as components of antibacterial
 PT vaccines, as targets for antibacterial drugs, or as biocontrol agents for
 PT plants.
 PS Example; SEQ ID NO 161; 328pp; English.
 XX
 CC The invention relates to isolated Acinetobacter baumannii nucleic acids.
 CC The A. baumannii nucleic acids and polypeptides are useful as reagents
 CC for diagnosing a bacterial disease, as components of antibacterial
 CC vaccines, as targets for antibacterial drugs, to detect the presence of
 CC A. baumannii and other Acinetobacter species in a sample, in screening
 CC compounds for the ability to interfere with the A. baumannii life cycle
 CC or to inhibit A. baumannii infection, and as biocontrol agents for
 CC plants. The present sequence represents DNA encoding an A. baumannii
 CC protein.
 XX
 SQ Sequence 579 BP; 137 A; 99 C; 132 G; 211 T; 0 U; 0 Other;
 Query Match 71.8%; Score 15.8; DB 9; Length 579;
 Best Local Similarity 89.5%; Pred. No. 9.8e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 AGGCCTTCGGGGTGCTC 22
 |||||
 DB 327 AGGCCTTCGGGGTGCTC 345
 RESULT 100
 ABZ54797
 ID ABZ54797 standard; cDNA; 665 BP.
 XX
 AC ABZ54797;
 XX
 DT 28-MAR-2003 (first entry)
 XX
 DE Aspergillus oryzae polynucleotide SEQ ID NO 3910.
 XX
 KW Aspergillus oryzae; fermentation; fungus; industrial; EST;
 KW expressed sequence tag; gene; ss.
 XX
 OS Aspergillus oryzae.
 XX
 EN WO200279476-A1.
 XX
 PD 10-OCT-2002.
 XX
 PF 22-MAR-2002; 2002WO-1B000890.
 XX
 PR 30-MAR-2001; 2001JP-00098371.
 XX
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (NARE-) NAT RES INST BREWING.
 PA (NORE-) NAT FOOD RES INST MIN AGRIC.
 XX
 PI Machida M, Akita O, Kashiwagi Y, Kitamoto K, Horiuchi H;
 PI Takeuchi M, Kobayashi T, Kitamoto N, Gomi K, Abe K;
 XX
 DR WPI; 2003-046817/04.
 XX
 PT Detection of expression of specific Aspergillus genes for monitoring the
 PT fermentation and growth conditions of the fungus, using DNA probes.
 XX
 PS Claim 1; SEQ ID NO 3910; 48pp + Sequence Listing; Japanese.
 XX
 CC The invention relates to a polynucleotide having any of 6006 specific
 CC sequences (ABZ50888-ABZ56893), which are expressed by a fungus under
 CC specific culture conditions including one or more of eutrophic,
 CC oligotrophic, solid, early germination, alkaline, high temperature, low
 CC temperature or maltose culture or polynucleotides stringently hybridising
 CC to these sequences. The polynucleotides are useful for monitoring the

CC progress of fermentation and the growth conditions of a fungus,
CC especially of Aspergillus oryzae which is widely used in industrial
CC fermentation. Also monitoring for fungal contamination. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 665 BP; 143 A; 196 C; 154 G; 172 T; 0 U; 0 Other;

Query Match 71.8%; Score 15.8; DB 8; Length 665;
Best Local Similarity 89.5%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGCGCTTTCGGGGTG 19
||| ||||| ||||| |||||
Db 640 GAAAGCGCTTTCGGGGTG 658

Search completed: May 19, 2006, 04:19:21
Job time : 271.361 secs

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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 02:24:46 ; Search time 1471.35 Seconds
(without alignments)
836.120 Million cell updates/sec

Title: US-10-665-708-25

Perfect score: 22
Sequence: 1 gaaagcccttcgggggtgctc 22

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

- EST:*
- 1: gb_est1.*
 - 2: gb_est3.*
 - 3: gb_est4.*
 - 4: gb_est5.*
 - 5: gb_est6.*
 - 6: gb_estc.*
 - 7: gb_est2.*
 - 8: gb_est7.*
 - 9: gb_est8.*
 - 10: gb_est9.*
 - 11: gb_gses1.*
 - 12: gb_gses2.*
 - 13: gb_gses3.*
 - 14: gb_gses4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19.4	88.2	369	12	CC794955
C 2	19.4	88.2	741	7	BB660584
C 3	19.4	88.2	1266	6	AK052580
C 4	19.4	88.2	3468	6	AK036537
C 5	18.8	85.5	514	9	DR082998
C 6	18.8	85.5	583	2	BM344289
C 7	18.8	85.5	927	14	CNS06S86
C 8	18.8	85.5	1078	14	CNS06Q72
C 9	18.8	81.8	794	5	CJ485936
C 10	17.8	80.9	221	10	DV692385
C 11	17.8	80.9	236	8	C0308813
C 12	17.8	80.9	267	5	CF045077
C 13	17.8	80.9	288	5	CF044432
C 14	17.8	80.9	510	8	CO711127
C 15	17.8	80.9	536	5	CD277478
C 16	17.8	80.9	598	4	CB754809
C 17	17.8	80.9	658	2	BT215331
C 18	17.8	80.9	664	5	CK133302
C 19	17.8	80.9	683	11	BH385770

BB634710	BB634710	687	7	BB634710
BI104420	BI104420	753	2	BI104420
CX343351	JGI_X2T22	847	9	CX343351
CK425517	AUF_Ipfes	950	5	CK425517
BF162561	601770203	977	7	BF162561
BN907310	AGENCOURT	994	3	BN907310
CF376920	AGENCOURT	1016	5	CF376920
DM665607	CNB332-C1	1045	10	DM665607
DT956623	CFW146-D1	1371	10	DT956623
DR985203	JGI_AOKG4	373	10	DR985203
T56721	va71a03_s2	408	10	T56721
BB157276	BB157276	658	7	BB157276
EX926884	EX926884	694	4	EX926884
AG463060	Mus muscu	765	14	AG463060
HS_5538_A	HS_5538_A	843	11	AQ746955
BO689861	AGENCOURT	893	3	BQ689861
BN179-H0	BN179-H0	1413	10	DT995647
DT995647	DT995647	270	5	CD377892
PTMM03061	PTMM03061	353	8	CN690130
E0289B09-	E0289B09-	363	7	AW854955
PMO-CTO26	PMO-CTO26	371	5	CD383045
PTMM08215	PTMM08215	378	12	CG548494
CG548494	CG548494	386	7	AW854998
OST150127	OST150127	390	12	CG548510
PM3-CTO26	PM3-CTO26	394	12	CG545039
OST150188	OST150188	405	1	AA555150
CG545039	CG545039	413	12	CG548505
nl07g10.8	nl07g10.8	417	12	CG662443
OST150171	OST150171	432	10	DT596565
CG548505	CG548505	434	12	CG505758
OST446019	OST446019	436	7	BF392844
wmi03-11m	wmi03-11m	442	5	CJ145102
OST54874	OST54874	444	10	DT598769
UI-R-CA0-	UI-R-CA0-	462	4	BY370180
CJ145102	CJ145102	525	4	CB426198
wmi03-12m	wmi03-12m	525	4	CB426543
BY370180	BY370180	535	4	CA886724
601354_MA	601354_MA	553	8	CN695093
601738_MA	601738_MA	554	4	CB462716
80131G09-	80131G09-	555	4	CB464162
E0360A01-	E0360A01-	556	10	DY385738
723046_MA	723046_MA	562	2	BG804845
725350_MA	725350_MA	566	4	CA888697
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0273-08_M	0273-08_M	594	1	AI663484
04907cc.r	04907cc.r	597	7	BE534580
a4907cc.r	a4907cc.r	600	2	BG804780
uk33d10.Y	uk33d10.Y	603	8	CV562959
601233510	601233510	608	4	CA163213
0272-28_M	0272-28_M	609	8	CK975625
UI-M-FC0-	UI-M-FC0-	614	14	LBAF055F03
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4106617_B	4106617_B	632	12	CE758231
Leishmani	Leishmani	638	5	CF902767
TM1-GSS00	TM1-GSS00	638	7	BB614371
tigr-g88-	tigr-g88-	638	9	CX768159
A0345F09-	A0345F09-	644	11	BH091738
BB614371	BB614371	652	5	CD406831
UI-M-HU0-	UI-M-HU0-	652	8	CK976084
RPIC1-24-2	RPIC1-24-2	659	7	BB619260
Gm_Ck3178	Gm_Ck3178	673	8	CO426515
4107001_B	4107001_B	674	5	CJ252013
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UI-M-HU0-	UI-M-HU0-	674	10	DR749476
C1252013	C1252013	682	3	BU654491
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tigr-g88-	tigr-g88-	749	4	BX326765
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1470678_M	1470678_M			
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1391525_M	1391525_M			

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C 94	17.2	78.2	780	9	CX887509 JGI CAAML	C 167	16.8	76.4	674	13	CW323036	CW323036 104_817_1
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96	17.2	78.2	800	9	DN524756	C 169	16.8	76.4	682	1	AL697364	AL697364 AL697364
97	17.2	78.2	806	4	CA315865	C 170	16.8	76.4	682	1	CW057016	CW057016 104_299_1
C 98	17.2	78.2	829	3	BP434131 BP434131	C 171	16.8	76.4	682	13	CT186330	CT186330 104_scrof
C 99	17.2	78.2	848	12	BZ654405	C 172	16.8	76.4	689	14	AM044576	AM044576 IS0012_B2
C 100	17.2	78.2	849	8	CV069365	C 173	16.8	76.4	692	8	CO203656	CO203656 AM044576
C 101	17.2	78.2	855	3	BQ885105	C 174	16.8	76.4	707	4	BX609637	BX609637 BX609637
C 102	17.2	78.2	874	3	BQ953912	C 175	16.8	76.4	713	8	CO201435	CO201435 RYCN12_5
C 103	17.2	78.2	874	13	CZ228082	C 176	16.8	76.4	720	13	CW451938	CW451938 fbb0001f1
C 104	17.2	78.2	891	10	DV918769	C 177	16.8	76.4	727	13	CW405695	CW405695 fbb0001f0
C 105	17.2	78.2	903	3	BQ931621	C 178	16.8	76.4	737	1	AM022377	AM022377 AM022377
C 106	17.2	78.2	915	3	BQ730676	C 179	16.8	76.4	744	8	CO369073	CO369073 RTK1_44_F
C 107	17.2	78.2	916	13	CW702244	C 180	16.8	76.4	756	1	AM046636	AM046636
C 108	17.2	78.2	921	14	AG894822	C 181	16.8	76.4	763	10	DR469521	DR469521 WS00948_B
C 109	17.2	78.2	923	13	CL238970	C 182	16.8	76.4	767	8	CR531122	CR531122 CR531122
C 110	17.2	78.2	930	13	CZ519583	C 183	16.8	76.4	775	13	CW413553	CW413553 fbb0001f1
C 111	17.2	78.2	933	3	BU512781	C 184	16.8	76.4	776	3	BU178253	BU178253 AGENCOURT
C 112	17.2	78.2	933	3	BU5131985	C 185	16.8	76.4	784	12	CG275138	CG275138 OG1AX02TH
C 113	17.2	78.2	940	3	BQ963681	C 186	16.8	76.4	789	11	BH733665	BH733665 BOHVR73TF
C 114	17.2	78.2	941	12	CC727409	C 187	16.8	76.4	798	12	CG702034	CG702034 ZMMBC011
C 115	17.2	78.2	948	12	CC836602	C 188	16.8	76.4	803	10	DV133910	DV133910 CV03107A1
C 116	17.2	78.2	963	12	CC374402	C 189	16.8	76.4	822	8	CV036037	CV036037 RTNACL1_4
C 117	17.2	78.2	988	3	BU520184	C 190	16.8	76.4	826	3	BU532058	BU532058 AGENCOURT
C 118	17.2	78.2	1008	12	CC733494	C 191	16.8	76.4	832	4	BX625372	BX625372
C 119	17.2	78.2	1048	14	CNS06ROE	C 192	16.8	76.4	832	12	CG179864	CG179864 PUIGG05TB
C 120	17.2	78.2	1074	3	BU179665	C 193	16.8	76.4	837	10	DT629302	DT629302 EST115587
C 121	17.2	78.2	1113	3	BQ230435	C 194	16.8	76.4	861	12	BZ656570	BZ656570 OGCAW04TM
C 122	17.2	78.2	1114	7	BH897150	C 195	16.8	76.4	864	14	CT286132	CT286132 US scrof
C 123	17.2	78.2	1179	12	CC280442	C 196	16.8	76.4	881	3	BQ917467	BQ917467 AGENCOURT
C 124	17.2	78.2	1256	1	AJ924334	C 197	16.8	76.4	881	14	CNS01016	AL152939 Anopheles
C 125	17.2	78.2	1313	9	DN667985	C 198	16.8	76.4	882	4	CA979418	CA979418 AGENCOURT
C 126	17.2	78.2	2345	6	AK159080	C 199	16.8	76.4	902	8	CN162201	CN162201 931567 MA
C 127	17.2	78.2	3040	6	AK132703	C 200	16.8	76.4	932	12	CG322551	CG322551 OG0CX67TV
C 128	17	77.3	610	1	AA042746	C 201	16.8	76.4	943	3	BU538391	BU538391 AGENCOURT
C 129	17	77.3	850	9	DR105288	C 202	16.8	76.4	955	10	DR472833	DR472833 WS00957_B
C 130	16.8	76.4	154	10	R58318	C 203	16.8	76.4	994	12	CL499651	CL499651 SAIL_671
C 131	16.8	76.4	196	10	DV894214	C 204	16.8	76.4	994	12	CG462884	CG462884 PUKE80TB
C 132	16.8	76.4	205	7	AW010105	C 205	16.8	76.4	1050	5	CK231117	CK231117 ILLUMIGEN
C 133	16.8	76.4	246	4	BX613093	C 206	16.8	76.4	1055	2	BM475890	BM475890 AGENCOURT
C 134	16.8	76.4	286	4	BX610825	C 207	16.8	76.4	1182	12	CC280354	CC280354 CH261-24X
C 135	16.8	76.4	302	7	AW010059	C 208	16.8	76.4	1217	13	CL495019	CL495019 SAIL_604
C 136	16.8	76.4	366	12	CE086808	C 209	16.8	76.4	1368	10	DT949410	DT949410 CFML03-D0
C 137	16.8	76.4	405	11	BH618083	C 210	16.8	76.4	1381	9	DN716077	DN716077 CNB110-G0
C 138	16.8	76.4	437	4	BH790538	C 211	16.8	76.4	1423	9	DN693573	DN693573 CX889-C02
C 139	16.8	76.4	437	9	DR180795	C 212	16.4	74.5	277	7	BE906962	BE906962 601500767
C 140	16.8	76.4	493	11	AZ503760	C 213	16.4	74.5	329	11	BH788475	BH788475 fzm0202F0
C 141	16.8	76.4	515	4	BX610657	C 214	16.4	74.5	347	12	CC607962	CC607962 OGUCV42TH
C 142	16.8	76.4	543	10	DR467635	C 215	16.4	74.5	360	4	C39785	C39785 C39785 Yuji
C 143	16.8	76.4	552	8	CV628596	C 216	16.4	74.5	360	4	C39832	C39832 C39832 Yuji
C 144	16.8	76.4	564	9	DN628521	C 217	16.4	74.5	427	11	BZ246325	BZ246325 CH230-314
C 145	16.8	76.4	564	9	DN632287	C 218	16.4	74.5	435	11	BZ244283	BZ244283 CH230-314
C 146	16.8	76.4	565	9	DN630032	C 219	16.4	74.5	437	10	H37136	H37136 15265 Lambd
C 147	16.8	76.4	570	9	DN632166	C 220	16.4	74.5	500	2	BI775641	BI775641 468309 MA
C 148	16.8	76.4	571	9	DN632042	C 221	16.4	74.5	534	2	BI346258	BI346258 375325 MA
C 149	16.8	76.4	582	3	BU775076	C 222	16.4	74.5	579	7	BE284320	BE284320 601087428
C 150	16.8	76.4	588	3	BQ81172	C 223	16.4	74.5	631	4	BX666423	BX666423 BX666423
C 151	16.8	76.4	591	11	AZ856127	C 224	16.4	74.5	658	12	CG992786	CG992786 CH240_152
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C 153	16.8	76.4	608	8	CO665914	C 226	16.4	74.5	667	7	BD066580	BD066580 B806580
C 154	16.8	76.4	609	8	CR394054	C 227	16.4	74.5	687	12	CC432179	CC432179 PUER587TD
C 155	16.8	76.4	614	13	CW398950	C 228	16.4	74.5	699	2	BI247626	BI247626 602960092
C 156	16.8	76.4	631	5	CF448920	C 229	16.4	74.5	735	12	CC160643	CC160643 lg10b05.9
C 157	16.8	76.4	633	8	CO476243	C 230	16.4	74.5	745	5	CD511623	CD511623 AGENCOURT
C 158	16.8	76.4	638	10	DV994366	C 231	16.4	74.5	771	14	CR485289	CR485289 mth2-1540
C 159	16.8	76.4	638	10	DR742857	C 232	16.4	74.5	796	3	BU749503	BU749503 CH3#027_C
C 160	16.8	76.4	638	10	DY368013	C 233	16.4	74.5	800	8	CN167783	CN167783 AGENCOURT
C 161	16.8	76.4	641	4	CB944804	C 234	16.4	74.5	818	12	CG844554	CG844554 Ynhw5168
C 162	16.8	76.4	642	1	AM048474	C 235	16.4	74.5	824	3	BU190398	BU190398 AGENCOURT
C 163	16.8	76.4	642	13	CW172666	C 236	16.4	74.5	835	11	AZ681554	AZ681554 ENT1E24TR
C 164	16.8	76.4	643	7	BE660337	C 237	16.4	74.5	843	4	CA791265	CA791265 AGENCOURT
C 165	16.8	76.4	647	8	CR531123	C 238	16.4	74.5	845	5	CF552602	CF552602 AGENCOURT

239	16.4	74.5	846	3	B0860887
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261	16.4	74.5	1130	2	BG328715
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265	16.4	74.5	1203	9	DN689440
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269	16.2	73.6	158	3	BQ096009
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272	16.2	73.6	201	3	BP590460
273	16.2	73.6	208	12	CEY11502
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278	16.2	73.6	268	5	CF043572
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294	16.2	73.6	371	8	CO000303
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ALIGNMENTS

RESULT 1
CC794955 369 bp DNA linear GSS 01-JUL-2003
LOCUS SALK_059534.25.55.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_059534.25.55.x, genomic survey sequence.

ACCESSION CC794955
VERSION GI:32390178
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi
1 (bases 1 to 369)
REFERENCE Alonzo,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At3g21150.
Class: TDNA tagged.
FEATURES
Location/Qualifiers
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/notes="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
ORIGIN
Query Match 88.2%; Score 19.4; DB 12; Length 369;
Best Local Similarity 95.2%; Pred. No. 2.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GAAAGCCCTTTTCGGGGTCT 21
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Db 70 GAAAGCCCTTTTCGGGGTCT 90
RESULT 2
LOCUS BB660584/c
DEFINITION BB660584 RIKEN full-length enriched, 13 days embryo stomach Mus musculus cDNA clone D53003C13 5', mRNA sequence.
ACCESSION BB660584
VERSION BB660584.1 GI:16494381
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 741)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toyota,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
TITLE Unpublished (2001)
JOURNAL

Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/.

FEATURES

source

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1. 1266
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misc_feature

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   74.3%ID, 86.1%length, match=1026)"
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ORIGIN

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Query Match      88.2%; Score 19.4; DB 6; Length 1266;
Best Local Similarity 95.2%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAGAGCCTTCGGGGTGCT 21
    |||||
Db 543 GAAGAGCCTTCGGGTGCT 523
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RESULT 4

AK036537/c

LOCUS AK036537 3468 bp mRNA linear HTC 02-SEP-2005
DEFINITION Mus musculus adult male bone cDNA, RIKEN full-length enriched library, clone:9830131G07 product:similar to BOMAPIN (PROTEASE INHIBITOR 10) (SERPIN B10) [Homo sapiens], full insert sequence.

ACCESSION

AK036537 GI:26085290

VERSION

HTC; CAP trapper.

SOURCE

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

1 Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

PUBMED

10349636

AUTHORS

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL

PUBMED

11042159

REFERENCE

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,

Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861

PUBMED

11076861

REFERENCE

4

AUTHORS

FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

TITLE

Nature 409, 685-690 (2001)

REFERENCE

5

The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

TITLE

Nature 420, 563-573 (2002)

REFERENCE

6

RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the FANTOM Consortium.

Antisense transcription in the Mammalian Transcriptome

Science 309, 1564-1566 (2005)

TITLE

Science 309, 1564-1566 (2005)

REFERENCE

7

The FANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group).

The Transcriptional Landscape of the Mammalian Genome

Science 309, 1559-1563 (2005)

TITLE

Science 309, 1559-1563 (2005)

REFERENCE

8

(bases 1 to 3468)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yaeunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/.

COMMENT

Location/Qualifiers

1. 3468

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="FANTOM,DB:9830131G07"

/db_xref="taxon:10090"

/clone="9830131G07"

/sex="male"

/tissue_type="bone"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev_stage="adult"

1. 3468

/note="putative

similar to BOMAPIN (PROTEASE INHIBITOR 10) (SERPIN B10)

[Homo sapiens] (SWISSPROT|P48595, evidence: FASTY,

74.8%ID, 100%length, match=1191)"

FEATURES

source

misc_feature

1. 3468

/note="putative

similar to BOMAPIN (PROTEASE INHIBITOR 10) (SERPIN B10)

[Homo sapiens] (SWISSPROT|P48595, evidence: FASTY,

74.8%ID, 100%length, match=1191)"

ORIGIN

Query Match 88.2%; Score 19.4; DB 6; Length 3468;
 Best Local Similarity 95.2%; Pred. No. 2.9e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGCT 21
 |||||
 Db 696 GAAAGGCTTTCGGGTGCT 676

RESULT 5
 DR082998
 LOCUS PMUS1-020CE07.yl_#0634.1 DIAS_PMUS Sus scrofa cDNA 5', mRNA
 DEFINITION
 sequence.
 ACCESSION DR082998
 VERSION DR082998.1 GI:67206801
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 Sus.
 1 (bases 1 to 514)
 Panitz,F. and Bendixen,C.
 Unpublished (Panitz,F., Bendixen,C.)
 TITLE Unpublished (2005)
 JOURNAL Unpublished (2005)
 COMMENT Contact: Bendixen C
 Molecular Genetics and Systems Biology, Department Genetics and
 Biotechnology
 Danish Institute of Agricultural Sciences
 P.O.Box 50, DK 8830-Tjele, Denmark
 Tel: +45 8999 1351
 Fax: +45 8999 1300
 Email: Christian.Bendixen@agrsci.dk.

FEATURES
 source Location/Qualifiers
 1..514
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /tissue_type="muscle"
 /clone_lib="DIAS PMUS"
 /notes="Vector: pT7T3D-PacI; Site 1: EcoRI; Site 2: NotI;
 Normalised cDNA library, adult muscle (longissimus dors).
 Single pass sequencing."

ORIGIN
 Query Match 85.5%; Score 18.8; DB 9; Length 514;
 Best Local Similarity 90.9%; Pred. No. 5e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGCTC 22
 |||||
 Db 171 GAAAGGCTTTCGGGGTGCTC 192

RESULT 6
 BM344289/c
 LOCUS
 DEFINITION
 rr49b02.y1 Globodera rostochiensis J2 pCDNAII Smant v1 Globodera
 rostochiensis cDNA 5', similar to TR:Q21420 Q21420 K10D6.1 PROTEIN.
 [1] ; mRNA sequence.
 ACCESSION BM344289
 VERSION BM344289.1 GI:18081204
 KEYWORDS EST.
 SOURCE Globodera rostochiensis
 ORGANISM Globodera rostochiensis
 Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
 Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
 1 (bases 1 to 583)
 McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
 Wyllie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
 Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,

TITLE JOURNAL COMMENT

Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
 Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,
 Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
 McCann,R., Waterson,R. and Wilson,R.
 The Washington Univ. Nematode EST Project, 1999
 Unpublished (1999)
 Contact: McCarter JP
 The Washington Univ. Nematode EST Project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 The library was contributed by Dr. Geert Smant of the Laboratory of
 Nematology at Wageningen University, Wageningen,
 Netherlands(Geert.smant@wur.nl). DNA Sequencing by:
 Washington University Genome Sequencing Center
 Seq primer: -40RP from Gibco
 High quality sequence stop: 421.

FEATURES
 source Location/Qualifiers
 1..583
 /organism="Globodera rostochiensis"
 /mol_type="mRNA"
 /db_xref="taxon:31243"
 /dev_stage="J2"
 /lab_host="DH10B"
 /clone_lib="Globodera rostochiensis J2 pCDNAII Smant v1"
 /notes="Vector: pCDNAII (Invitrogen); Site 1: BstXI;
 Site 2: EcoRI; The library was donated for sequencing by
 Geert Smant from Wageningen University, Laboratory of
 Nematology, The Netherlands."

ORIGIN
 Query Match 85.5%; Score 18.8; DB 2; Length 583;
 Best Local Similarity 90.9%; Pred. No. 5.1e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGCTC 22
 |||||
 Db 192 GAAAGGCTTTCGGGGTGCTC 171

RESULT 7
 CNS06SS6/c
 LOCUS
 DEFINITION
 T7 end of clone AW0AA026A05 of library AW0AA from strain CLIB 89 of
 Yarrowia lipolytica, genomic survey sequence.
 AL413644
 AL413644.1 GI:12185773
 GSS.
 Yarrowia lipolytica
 Yarrowia lipolytica
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; Dipodascaceae; Yarrowia.
 1 (bases 1 to 927)
 Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
 Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
 de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
 Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
 Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
 Wincker,P. and Weissenbach,J.
 Genomic exploration of the hemiascomycetous yeasts: 1. A set of
 yeast species for molecular evolution studies
 FEBS Lett. 487 (1), 3-12 (2000)

TITLE
 JOURNAL
 PUBMED
 REFERENCE
 2 (bases 1 to 927)
 Casaregola,S., Neuveglise,C., Lepingle,A., Bon,E., Feynrol,C.,
 Artiguenave,F., Wincker,P. and Gaillardin,C.
 Genomic exploration of the hemiascomycetous yeasts: 17. Yarrowia
 lipolytica
 FEBS Lett. 487 (1), 95-100 (2000)

TITLE
 JOURNAL
 PUBMED
 REFERENCE
 3 (bases 1 to 927)

sites of pME18S-FL3. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Libraries were constructed by oligo-capping method."

ORIGIN

Query Match 81.8%; Score 18; DB 5; Length 794;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGT 18
|||||
Db 767 GAAAGGCTTTCGGGGT 784
|||||

RESULT 10

DV692385/c 221 bp mRNA linear EST 16-NOV-2005
LOCUS CGN-36297 Leaf Coffea canephora cDNA clone cccl12b3 5', mRNA
DEFINITION sequence.

ACCESSION

VERSION DV692385

KEYWORDS

SOURCE DV692385.1 GI:82472213

ORGANISM

Coffea canephora
Coffea canephora
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicotyledons;
asterids; lamiids; Gentianales; Rubiaceae; Ixoroideae; Coffeae;
Coffea.

REFERENCE

1. (bases 1 to 221)
Lin, C., Mueller, L.A., McCarthy, J., Crouzillat, D., Petiard, V. and
Tankeley, S.D.

TITLE

Coffee and Tomato Share Common Gene Repertoires as Revealed by Deep

JOURNAL

Theoretical and Applied Genetics (2005) In press

COMMENT

Contact: Steven D. Tanksley
Department of Plant Breeding
Cornell University
248 Emerson Hall, Ithaca, NY 14853
Tel: 607 255 1673
Fax: 607 255 6683
Email: sdt@cornell.edu
The sequence provided is trimmed of vector and low quality regions.
Full sequence and original trace file are available from the Sol
Genome Network website (<http://www.sgn.cornell.edu>)
Plate: 12 row: b column: 3
Seq primer: M13r
High quality sequence stop: 221.

FEATURES

source
Location/Qualifiers
1. .221
/organism="Coffea canephora"
/mol_type="mRNA"
/db_xref="taxon:49390"
/clone="cccl12b3"
/tissue_type="leaf"
/dev_stage="young"
/clone_lib="Leaf"
/note="Vector: pBSSK-; Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Query Match 80.9%; Score 17.8; DB 10; Length 221;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAAGGCTTTCGGGGTGCTC 22
|||

Db 61 AAAAGGCTTTCGAGGGTGCTC 41
|||||

RESULT 11

CO308813/c 236 bp mRNA linear EST 25-JUN-2004
LOCUS EK259430.5prime Exelixis Flytag CK01 pCDNA-SK+ Drosophila
DEFINITION melanogaster cDNA clone EK259430 5', mRNA sequence.

ACCESSION

VERSION CO308813.1 GI:49230691

KEYWORDS

SOURCE EST.

ORGANISM

Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

1 (bases 1 to 236)

AUTHORS

Kopczynski, C., Platt, D., Campbell, J., Muzong, C., Laufer, A.,
Peterson, E. and Swimmer, C.

TITLE

Exelixis Flytag EST Project CK01 Library

JOURNAL

Unpublished (2004)

COMMENT

Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
Based upon one or more reads of this clone where vector sequence
was present at both ends, this clone has been determined to contain
contain a cDNA insert on the order of 600-1000 bases.
Plate: EK.2594 row: C column: 6
High quality sequence stop: 157.

FEATURES

source
Location/Qualifiers

1. .236
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="EK259430"
/clone_lib="Exelixis Flytag CK01 pCDNA-SK+"
/note="Organ: mixed stage embryos, imaginal disks, and
adult heads; Vector: pCDNA-SK+; Site_1: NotI; Site_2:
XhoI; Random primed, normalized library from mixed stage
embryos, imaginal disks, and adult heads."

ORIGIN

Query Match 80.9%; Score 17.8; DB 8; Length 236;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAAGGCTTTCGGGGTGCTC 22
|||||

Db 109 ACAGGCTTTCGGTGCTC 89
|||||

RESULT 12

CF045077 267 bp mRNA linear EST 17-JUL-2003
LOCUS QCJ8all.yg QCU Zea mays cDNA clone QCJ8all, mRNA sequence.
DEFINITION
ACCESSION CF045077
VERSION CF045077.1 GI:32940258

KEYWORDS

SOURCE EST.

ORGANISM

Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 267)

AUTHORS

Genoplante, a major partnership french program in plant genomics

TITLE

Unpublished (2003)

JOURNAL

Contact: Genoplante

COMMENT

Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>)
and <http://genoplante-info.infobiogen.fr>.

FEATURES

source
Location/Qualifiers

1. .267
/organism="Zea mays"

```

/mol_type="mRNA"
/cultivar="F2"
/db_xref="taxon:4577"
/clone="QCJ8a11"
/tissue_type="cell lignification part of the 6th leaf"
/clone_lib="QCJ"

ORIGIN
Query Match      80.9%; Score 17.8; DB 5; Length 267;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGCT 21
    |||||
Db 193 GAAAGGCTTTCGGGGTGCT 213

RESULT 13
CF044432
LOCUS      288 bp mRNA linear EST 17-JUL-2003
DEFINITION QJ29g07.yg QCJ Zea mays cDNA clone QJ29g07, mRNA sequence.
ACCESSION  CF044432
VERSION     CF044432.1 GI:32939613
KEYWORDS    EST.
SOURCE      Zea mays
ORGANISM    Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
            1 (bases 1 to 288)
REFERENCE   Genoplante, a major partnership french program in plant genomics
AUTHORS     Genoplante.
TITLE       Unpublished (2003)
JOURNAL     Contact: Genoplante
COMMENT     Genoplante
            93, rue Henri Rochefort 91025 EVRY CEDEX France
            Tel: 33 1 69 47 54 00
            Fax: 33 1 69 47 54 10
            This sequence has been generated in the framework of the french
            plant genomics programme 'Genoplante' (http://www.genoplante.com
            and http://genoplante-info.infobiogen.fr).

FEATURES             source
    source
    1..288
        /organism="Zea mays"
        /mol_type="mRNA"
        /cultivar="F2"
        /db_xref="taxon:4577"
        /clone="QCJ29g07"
        /tissue_type="cell lignification part of the 6th leaf"
        /clone_lib="QCJ"

ORIGIN
Query Match      80.9%; Score 17.8; DB 5; Length 288;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGCT 21
    |||||
Db 214 GAAAGGCTTTCGGGGTGCT 234

RESULT 14
CO711127
LOCUS      510 bp mRNA linear EST 27-JUL-2004
DEFINITION DG14-163c22 DG14-muscle Canis familiaris cDNA 3', mRNA sequence.
ACCESSION  CO711127
VERSION     CO711127.1 GI:50678849
KEYWORDS    EST.
SOURCE      Canis familiaris (dog)
ORGANISM    Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.

/mol_type="mRNA"
/db_xref="taxon:4577"
/clone="QCJ8a11"
/tissue_type="cell lignification part of the 6th leaf"
/clone_lib="QCJ"

ORIGIN
Query Match      80.9%; Score 17.8; DB 8; Length 510;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAAGGCTTTCGGGGTGCTC 22
    |||||
Db 471 AAAGGCTTTCGGGGTGCTC 491

RESULT 15
CD277478/c
LOCUS      536 bp mRNA linear EST 01-SEP-2003
DEFINITION TL43C03271F (FHIG:C) Axenic plate culture Betula pendula cDNA 5',
            mRNA sequence.
ACCESSION  CD277478
VERSION     CD277478.1 GI:34389524
KEYWORDS    EST.
SOURCE      Betula pendula (European white birch)
ORGANISM    Betula pendula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fagales; Betulaceae; Betula.
            1 (bases 1 to 536)
REFERENCE   Johansson, T., Le Quere, A., Ahren, D., Soderstrom, B., Erlandsson, R.,
AUTHORS     Lundeborg, J., Uhlen, M. and Funlid, A.
TITLE       Transcriptional responses of Paxillus involutus and Betula pendula
            during formation of ectomycorrhizal root tissue
JOURNAL     Mol. Plant Microbe Interact. 17 (2), 202-215 (2004)
PUBMED     14964534
COMMENT     Contact: Johansson, T.
            Fungal-Host Interaction Group (FHIG)
            Microbial Ecology, Institution of Ecology
            Ecology Building, Lund University, SE-223 62 Lund, Sweden
            Tel: +46 46 222 45 49
            Fax: +46 46 222 41 58
            Email: tomas.johansson@bioekol.lu.se
            PCR Primers
            FORWARD: P104 (5'-GGGAAGCGCGCATTTGTGT-3')
            BACKWARD: P105 (5'-AGTGAGCTCGAATTCGGGC-3')
            Seq primer: P104
            High quality sequence stop: 536.
            Location/Qualifiers
                1..536
                    /organism="Betula pendula"
                    /mol_type="mRNA"
                    /strain="Skuleskogen, Skogsforsk, Sweden"
                    /db_xref="taxon:3505"
                    /tissue_type="Root tissue"
                    /dev_stage="25 days of growth after transfer"

REFERENCE   Schluter, T., Hermanns, J., Weindel, M., Schuette, D., Kranz, H.,
AUTHORS     Henrich, J. and Loeber, R.
TITLE       Dog arrayTAG cDNA clone collection
JOURNAL     Unpublished (2004)
COMMENT     Contact: Thomas Schluter
            LiON bioscience AG
            Walhoferstrasse 98, D-69123 Heidelberg, Germany
            Tel: +49 6221 4038 150
            Fax: +49 6221 4038 290
            Email: Thomas.Schluter@lionbioscience.com.

FEATURES             source
    source
    1..510
        /organism="Canis familiaris"
        /mol_type="mRNA"
        /strain="Beagle"
        /db_xref="taxon:9615"
        /tissue_type="muscle"
        /dev_stage="adult"
        /lab_host="DH10B"
        /clone_lib="DG14-muscle"
        /note="Organ: muscle; Vector: Dog pBluescript LION"

ORIGIN
Query Match      80.9%; Score 17.8; DB 8; Length 510;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAAGGCTTTCGGGGTGCTC 22
    |||||
Db 471 AAAGGCTTTCGGGGTGCTC 491
```

```

/lab_host="Escherichia coli BM25.8"
/clone_lib="(FHIG:C) Axenic plate culture"
/notes="Vector: pTriplEx2; Site_1: SfilI; Site_2: SfilI; This
EST clone is originating from one of three cDNA libraries,
constructed for transcript profiling of the mycorrhizal
interaction between the basidiomycete Paxillus involutus
and Betula pendula (birch). One library represents the
developed and functional mycorrhizal root tissue
('FHIG:A) Ectomycorrhiza plate culture'), a second
library represents axenically grown fungus ('FHIG:B)
Axenic plate culture') and a third library represents
axenically grown plants ('FHIG:C) Axenic plate culture'.
Libraries were analyzed in parallel and 3855 (FHIG:A),
3964 (FHIG:B), and 2532 (FHIG:C) high-quality (PHRED 20)
ESTs of >99bp have been deposited. The cDNA libraries were
constructed from total RNA using the SMART cDNA library
Construction kit (HK1051-1, Clontech, Palo Alto, CA, USA)
according to the manufacturer's instructions. Full-length
cDNAs were trimmed by SfilI, fractionated and directionally
ligated into (lambda)TriplEx2 arms. The lambda library was
converted to a plasmid library via site-specific
recombination at loxP sites in a Cre+ strain (E. coli
BM25.8). Plasmid clones were randomly collected and
analysed by DNA sequencing using a plasmid-specific
forward primer (P104)."
```

ORIGIN

```

Query Match      80.9%; Score 17.8; DB 5; Length 536;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAAGGCTTTTCGGGGTGCTC 22
    ||||| ||||| ||||| |||||
Db 151 AAAGGCTTTTCGGGGTGCTC 131
```

RESULT 16

```

CB754809
LOCUS CB754809
DEFINITION CB754809 598 bp mRNA linear EST 11-APR-2003
TgESTzy11lc07.y1 TgME49 3 day invitro bradyzoite Toxoplasma gondii
cDNA clone TgESTzy11lc07.y1 5', mRNA sequence.
ACCESSION CB754809
VERSION CB754809.1 GI:29822101
KEYWORDS EST.
SOURCE Toxoplasma gondii
ORGANISM Toxoplasma gondii
```

REFERENCE

```

AUTHORS Tang,K., Cole,R., Fogarty,S., Sibley,L.D., Ajioke,J.A., White,M.,
Clifton,S., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M.,
Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M.,
Ritter,E., Bennett,J., Franklin,C., Teagareishvili,R., Ronko,I.,
Kennedy,S., Maguire,L., Waterston,R. and Wilson,R.
Toxoplasma EST Project
Unpublished (2001)
Contact: Clifton, S.
```

TITLE

```

JOURNAL Toxoplasma EST Project
COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: toxo@watson.wustl.edu
Contact David Sibley (toxoe@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Seq primer: -40RP from Gibco.
```

FEATURES

```

source
1. .598
/organism="Toxoplasma gondii"
/mol_type="mRNA"
/db_xref="taxon:5811"
/clone="TgESTzy11lc07.y1"
/dev_stage="3 day"
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ORIGIN

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Query Match      80.9%; Score 17.8; DB 4; Length 598;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAAGGCTTTTCGGGGTGCTC 22
    ||||| ||||| ||||| |||||
Db 371 AAAGGCTTTTCGGGGTGCTC 391
```

RESULT 17

```

B1215331/c
LOCUS B1215331
DEFINITION B1215331 658 bp mRNA linear EST 16-JAN-2004
Drosophila melanogaster cDNA clone RE21703 5, mRNA sequence.
ACCESSION B1215331
VERSION B1215331
KEYWORDS EST.
SOURCE B1215331.1 GI:14693055
ORGANISM Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 658)
```

REFERENCE

```

AUTHORS Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B.,
Carlson,J., Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E.,
George,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G.,
Misra,S., Mungall,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S.,
Phouanavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and
Rubin,G.M.
BDGP/HMI RE Drosophila EST Project
Unpublished (2001)
Other ESTs: RE21703.3prime
Contact: Stapleton, M.
```

TITLE

```

JOURNAL BDGP/HMI RE Drosophila EST Project
COMMENT Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AB003172: arm:U [6931003,6963876] estimated-cyto?:
04/12/2001
Plate: RE.217 row: A column: 3
High quality sequence stop: 600.
```

FEATURES

```

source
1. .658
Location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="RE21703"
/sex="male and female"
/lab_host="DHS-alpha Tona"
/clone_lib="RE Drosophila melanogaster normalized Embryo
pFlc-1"
/note="Organ: embryo; Vector: pFlc1; Site_1: XhoI; Site_2:
BamHI; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
```

[illegible]

Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

1 (bases 1 to 687)
 Arakawa.T., Carninci.P., Fukuda.S., Furuno.M., Hanagaki.T., Hara.A., Hiramoto.K., Hori.F., Ishii.Y., Ito.M., Kawai.J., Konno.H., Kouda.M., Koya.S., Matsuyama.T., Miyazaki.A., Nomura.K., Ohno.M., Okazaki.Y., Okido.T., Saito.R., Sakai.C., Sakai.K., Sano.H., Sasaki.D., Shibata.K., Shinagawa.A., Shiraki.T., Sogabe.Y., Suzuki.H., Tagami.M., Tagawa.A., Takahashi.F., Takeda.Y., Tanaka.T., Toya.T., Muramatsu.M. and Hayashizaki.Y.
 RIKEN Mouse ESTs (Arakawa.T., et al. 2001)
 Unpublished (2001)
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suenro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/
 Carninci.P., Shibata.Y., Hayatsu.N., Sugahara.Y., Shibata.K., Itoh.M., Konno.H., Okazaki.Y., Muramatsu.M. and Hayashizaki.Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi.K., Fujiwaki.S., Inoue.K., Togawa.Y., Izawa.M., Ohara.E., Watabiki.M., Yoneda.Y., Ishikawa.T., Ozawa.K., Tanaka.T., Matsura.S., Kawai.J., Okazaki.Y., Muramatsu.M., Inoue.Y., Kira.A. and Hayashizaki.Y.
 RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
 Konno.H., Fukunishi.Y., Shibata.K., Itoh.M., Carninci.P., Sugahara.Y. and Hayashizaki.Y.
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Kondo.S., Shinagawa.A., Saito.T., Kiyosawa.H., Yamanaka.I., Aizawa.K., Fukuda.S., Hara.A., Itoh.M., Kawai.J., Shibata.K. and Hayashizaki.Y.
 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
 Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
 e mouse tissues.
 Location/Qualifiers
 1..687
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="A430041D14"
 /tissue_type="thymus"
 /dev_stage="0 day neonate"
 /lab_host="DH108"
 /clone_lib="RIKEN full-length enriched, 0 day neonate thymus"
 /note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
 GAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATCTCGAGTTAATTAATCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

REFERENCE
 AUTHORS
 JOURNAL
 COMMENT

ORIGIN
 Query Match 80.9%; Score 17.8; DB 7; Length 687;
 Best Local Similarity 90.5%; Pred. No. 1.5e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAAGGCTTTTCGGGGGTGCT 22
 |||||
 Db 591 AAAGGCTTTTCGGGGGTGTC 571
 |||||

RESULT 21
 BI104420/c
 LOCUS
 DEFINITION
 602890015F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5035202 5', mRNA sequence.
 ACCESSION
 VERSION
 BI104420.1 GI:14555313
 EST.
 KEYWORDS
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.
 1 (bases 1 to 753)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM11097 row: n column: 03
 High quality sequence stop: 745.
 Location/Qualifiers
 1..753
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="Czech II"
 /db_xref="taxon:10090"
 /clone="IMAGE:5035202"
 /tissue_type="spontaneous tumor, metastatic to mammary. Stem cell origin."
 /lab_host="DH108"
 /clone_lib="NCI CGAP Lu29"
 /note="Organ: lung; Vector: pCMV-SPORT6; Site 1: Sali; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

FEATURES
 source
 Query Match 80.9%; Score 17.8; DB 2; Length 753;
 Best Local Similarity 90.5%; Pred. No. 1.5e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGGTGCT 21
 |||||
 Db 705 GAAAGGCTTTTCGGGGGTGCT 685
 |||||

RESULT 22
 CX343351
 LOCUS
 DEFINITION
 JGI_XZ722789.fwd NIH XGC tropTad5 Xenopus tropicalis cDNA clone IMAGE:7599083 5', mRNA sequence.
 ACCESSION
 VERSION
 CX343351.2 GI:74078928
 EST.
 KEYWORDS

SOURCE
ORGANISM Xenopus tropicalis (western clawed frog)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus; Silurana.

REFERENCE
AUTHORS Richardson, P., Lucas, S., Rokhsar, D., Dettler, J.C., Ng, D.C., Brokstein, P. and Lindquist, E.A.
TITLE DOE Joint Genome Institute Xenopus tropicalis EST project
JOURNAL Unpublished (2004)
COMMENT On Jan 4, 2005 this sequence version replaced gi:57079823. Other ESTs: JGI_X2722789 rev
 Contact: Lindquist, E.A., Richardson, P.
 DOE Joint Genome Institute
 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 Tel: 925 296 5600
 Fax: 925 296 5710
 Email: cdna@jgi-psf.org
 Tissue Procurement: Richard M. Harland Laboratory, University of California, Berkeley: <http://tropicalis.berkeley.edu/home>
 cDNA Library Preparation: Richard M. Harland Laboratory, University of California, Berkeley
 DNA Sequencing: DOE Joint Genome Institute: <http://www.jgi.doe.gov>
 Clone Distribution: I.M.A.G.E. Consortium/LLNL:
<http://image.llnl.gov>
 Naming Conventions: EST name is generated by the concatenation of the JGI Clone id and the direction of sequencing. The suffix '.fwd' indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.
 Plate: X27 0237 row: j column: 9
 High quality sequence stop: 814.
 Location/Qualifiers
 1..847
 /organism="Xenopus tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clone="IMAGE:7599083"
 /tissue_type="whole embryo"
 /dev_stage="Tadpole (st. 36-41)"
 /lab_host="E. coli XL1-Blue derivative, Stratagene ElectroTen-Blue"
 /clone_lib="NIH_XGC_tropTad5"
 /note="vector: PCS108; Site 1: SalI; Site 2: NotI; Tadpole library constructed by Russell B. Fletcher in R. Harland's lab using poly A RNA and oligo dT primers (Invitrogen SuperScript Plasmid System for cDNA Synthesis and Cloning) SalI (5' end) -NotI (3' end) cDNA was inserted into vector PCS108
 (http://mcb.berkeley.edu/labs/harland/pages/plasmids.html)"

ORIGIN
 Query Match 80.9%; Score 17.8; DB 9; Length 847;
 Best Local Similarity 90.5%; Pred. No. 1.6e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAAGGCTCTCGGGGTGCTC 22
 |||||
 401 AAAGGCTCTCGGGGTGCC 421

Db

RESULT 23
 CK425517/c 950 bp mRNA linear EST 06-JAN-2004
LOCUS AUF IpTes 22 k01 Testis cDNA library Ictalurus punctatus cDNA 5', similar to ribosomal protein l18, mRNA sequence.
DEFINITION
VERSION CK425517.1 GI:40667220
KEYWORDS EST.
SOURCE Ictalurus punctatus (channel catfish)
ORGANISM Ictalurus punctatus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Siluriformes;

REFERENCE
AUTHORS Ictaluridae; Ictalurus.
 1 (bases 1 to 950)
 Liu, Z., Li, P., Liu, L., He, C., Kucuktas, H., Feng, J., Chen, L., Peatman, E., Baoprasertkul, P., Simmons, M., Muir, W., Grizzle, J., Dunham, R. and Brady, Y.
TITLE 30,000 new catfish ESTs: new resources for functional analysis of genes involved in aquaculture performance traits
JOURNAL Unpublished (2004)
COMMENT Contact: Liu ZJ
 The Fish Molecular Genetics and Biotechnology Laboratory,
 Department of Fisheries and Allied Aquacultures and Program of Cell and Molecular Biosciences
 Auburn University
 203 Swingle Hall, Auburn University, Auburn, AL 36849, USA
 Tel: 334 844 4054
 Fax: 334 844 9208
 Email: zliu@acesag.auburn.edu
 Seq primer: T7.
 Location/Qualifiers
 1..950
 /organism="Ictalurus punctatus"
 /mol_type="mRNA"
 /db_xref="taxon:7998"
 /clone_lib="Testis cDNA library"
 /note="Organ: Testis; Vector: pSport1; Site 1: NotI; Site 2: SalI"

ORIGIN
 Query Match 80.9%; Score 17.8; DB 5; Length 950;
 Best Local Similarity 90.5%; Pred. No. 1.6e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGTGCT 21
 |||||
 924 GAAAGCCATTCGGGGTCT 904

Db

RESULT 24
 BF162561/c 977 bp mRNA linear EST 30-OCT-2000
LOCUS G01770203F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3989377 5', mRNA sequence.
DEFINITION
ACCESSION BF162561.1 GI:11042781
VERSION EST.
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
 1 (bases 1 to 977)
 NIH-MGC <http://mgc.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM9199 row: f column: 02
 High quality sequence stop: 706.
 Location/Qualifiers
 1..977
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="Czech II"
 /db_xref="taxon:10090"
 /clone="IMAGE:3989377"
 /tissue_type="spontaneous tumor, metastatic to mammary."


```

Stem cell origin."
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu29"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

ORIGIN
Query Match      80.9%; Score 17.8; DB 7; Length 977;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGTGCT 21
|||||
Db 653 GAAAGGCTTTTCGGGTGTT 633

RESULT 25
BM907310
LOCUS
DEFINITION
AGENCOURT_6638575 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:5735530
5', mRNA sequence.
ACCESSION
BM907310
VERSION
BM907310.1 GI:19357689
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 (bases 1 to 994)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12742 row: j column: 11
High quality sequence stop: 652.
Location/Qualifiers
1. .994
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5735530"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 68"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

ORIGIN
Query Match      80.9%; Score 17.8; DB 3; Length 994;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAAGGCTTTTCGGGGTGCTC 22
|||||
Db 912 AATGGCTTTTCGGGGTGCTC 932

RESULT 26
CF376920
LOCUS
DEFINITION
AGENCOURT_15348767 NICHD_XGC_Swb1N Xenopus tropicalis cDNA clone
IMAGE:7006248 5', mRNA sequence.
CF376920
VERSION
CF376920.1 GI:34314364
KEYWORDS
EST.
SOURCE
Xenopus tropicalis (western clawed frog)
ORGANISM
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus; Silurana.
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Rob Granger, University of Virginia
CDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14706 row: h column: 22
High quality sequence stop: 565.
Location/Qualifiers
1. .1016
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:7006248"
/tissue_type="whole body"
/clone_lib="NICHD_XGC_Swb1N"
/notes="Vector: pExpress-1; Site 1: EcoRV; Site 2: NotI;
Bulk tissue was collected from a whole 10 month old male
from the F6 strain. 1st strand cDNA was primed with a Not
I - oligo(dT) primer, double-stranded cDNA was cloned into
the Not I and EcoRV sites of pExpress-1. Library was
size-selected for >1.5 kb fragments for an average insert
size of 1.92 kb. Library was normalized to Cot5 with a
180-fold reduction of actin. A non-normalized version of
this library is also available (NICHD_XGC_Swb1). Library
was constructed by Open Biosystems (Huntsville, AL).
PLEASE NOTE: This library contains high level of
contamination by worm"

ORIGIN
Query Match      80.9%; Score 17.8; DB 5; Length 1016;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAAGGCTTTTCGGGGTGCTC 22
|||||
Db 308 AAAGGCTTCTCGGGTGCTCC 328

RESULT 27
DW665607/c
LOCUS
DEFINITION
CNB332-C11_xld-t SHGC-CNB2 Gasterosteus aculeatus cDNA clone
CNB332-C11 3', mRNA sequence.
DW665607
VERSION
DW665607.1 GI:85458785
KEYWORDS
EST.
SOURCE
Gasterosteus aculeatus (three spined stickleback)
ORGANISM
Gasterosteus aculeatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
Gasterosteidae; Gasterosteus.

```

REFERENCE 1 (bases 1 to 1045)
 AUTHORS Kingsley,D.M., Peichel,C., Knecht,A., Balabhadra,S., Grimwood,J.,
 Dickson,M., Schmutz,J. and Myers,R.M.
 TITLE Expressed sequence tags from *Gasterosteus aculeatus* (2004)
 JOURNAL Unpublished (2004)
 COMMENT Contact: Grimwood, Jane
 Stanford Human Genome Center
 Stanford University School of Medicine
 975 S California Ave, Palo Alto, CA 94304, USA
 Tel: 650 320 5917
 Fax: 650 320 5801
 Email: jane@hgsc.stanford.edu
 Plate: 332
 High quality sequence stop: 821.

FEATURES
 source
 Location/Qualifiers
 1..1045
 /organism="Gasterosteus aculeatus"
 /mol_type="mRNA"
 /strain="Conner Creek sticklebacks, WA USA"
 /db_xref="taxon:69293"
 /clone="CNB332-C11"
 /sex="mixed male and female"
 /tissue_type="brain"
 /dev_stage="adult"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="SHGC-CNB2"
 /notes="Vector: Express 1; Total and poly A+ RNA was isolated from the indicated stickleback tissue, and a cDNA library was constructed in the Express 1 plasmid vector by Open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceded by a synthetic NotI site (first strand primer: 5'-GACTAGTCTAGATCGGCGGCC(T)25-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5 prime end of mRNA, and cloned directionally into the NotI and EcoRV sites of Express 1. Note that the EcoRV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxxATC' (where is ATC is the second half of the EcoRV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at: http://www.openbiosystems.com/cdna_library_construction_fa q.php#8 The primary library was transformed and amplified in DH10B (T1 phage resistant) bacteria."

ORIGIN
 Query Match 80.9%; Score 17.8; DB 10; Length 1045;
 Best Local Similarity 90.5%; Pred.No.1.6e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTCGGGGTGCTC 22
 |||||
 Db 953 AAAGGCCTTTCGGGTGGTTC 933

RESULT 28
 DT956623/c
 LOCUS CFW146-D12 yld-s SHGC-CFW Gasterosteus aculeatus cDNA clone
 DEFINITION CFW146-D12 5', mRNA sequence.
 ACCESSION DT956623
 VERSION DT956623.1 GI:76029447
 KEYWORDS EST.
 SOURCE Gasterosteus aculeatus (three spined stickleback)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes; Gasterosteidae; Gasterosteus.
 REFERENCE 1 (bases 1 to 1371)
 AUTHORS Kingsley,D.M., Peichel,C., Balabhadra,S., Grimwood,J., Dickson,M., Schmutz,J. and Myers,R.M.
 TITLE Expressed sequence tags from *Gasterosteus aculeatus*

JOURNAL COMMENT Unpublished (2003)
 Contact: Grimwood, Jane
 Stanford Human Genome Center
 Stanford University School of Medicine
 975 S California Ave, Palo Alto, CA 94304, USA
 Tel: 650 320 5917
 Fax: 650 320 5801
 Email: jane@hgsc.stanford.edu
 Plate: 146
 High quality sequence start: 29
 High quality sequence stop: 875.

FEATURES
 source
 Location/Qualifiers
 1..1371
 /organism="Gasterosteus aculeatus"
 /mol_type="mRNA"
 /strain="Conner Creek sticklebacks, WA USA"
 /db_xref="taxon:69293"
 /clone="CFW146-D12"
 /sex="mixed male and female"
 /tissue_type="gills"
 /dev_stage="adult"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="SHGC-CFW"
 /notes="Vector: Express 1; Total and poly A+ RNA was isolated from the indicated stickleback tissue, and a cDNA library was constructed in the Express 1 plasmid vector by Open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceded by a synthetic NotI site (first strand primer: 5'-GACTAGTCTAGATCGGCGGCC(T)25-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5 prime end of mRNA, and cloned directionally into the NotI and EcoRV sites of Express 1. Note that the EcoRV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxxATC' (where is ATC is the second half of the EcoRV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at: http://www.openbiosystems.com/cdna_library_construction_fa q.php#8 The primary library was transformed and amplified in DH10B (T1 phage resistant) bacteria. Clones available from Open Biosystems: http://www.openbiosystems.com/stickleback"

ORIGIN
 Query Match 80.9%; Score 17.8; DB 10; Length 1371;
 Best Local Similarity 90.5%; Pred.No.1.6e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTCGGGGTGCTC 22
 |||||
 Db 1184 AAAGGCCTTTCGGGGTGCCC 1164

RESULT 29
 DR985203
 LOCUS JGI_AOKG417, rev AOKG Acropora palmata spawned eggs Acropora palmata
 DEFINITION cDNA clone AOKG417 3', mRNA sequence.
 ACCESSION DR985203
 VERSION DR985203.1 GI:71779909
 KEYWORDS EST.
 SOURCE Acropora palmata
 ORGANISM Acropora palmata
 Eukaryota; Metazoa; Cnidaria; Anthozoa; Hexacorallia; Scleractinia; Asterozoa; Acroporidae; Acropora.
 REFERENCE 1 (bases 1 to 373)
 AUTHORS Schwarz,J.A., Brokstein,P., Manohar,C., Coffroth,M.A., Szmant,A. and Medina,M.
 TITLE Coral-Symbiodinium EST Project
 JOURNAL Unpublished (2005)
 COMMENT Other_ESTs: JGI_AOKG417.fwd
 Contact: Schwarz, JA, Medina, M.

Evolutionary Genomics
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925-296-5823
Email: jaschwarz@lbl.gov
CDNA Library Preparation: DOE Joint Genome Institute:
http://www.jgi.doe.gov
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.rev' indicates a reverse sequencing read of the insert. It does not necessarily reflect the orientation of the insert.
Poly-T: A run of 14 or more T residues at the beginning of this sequence has been removed.
Plate: AOKG 0005 row: a column: 9
High quality sequence stop: 200.
Location/Qualifiers
1. .373
/organism="Acropora palmata"
/mol_type="mRNA"
/db_xref="taxon:6131"
/clone="AOKG417"
/dev_stage="Freshly spawned eggs"
/lab_host="ElectroMAX DH10B"
/clone_lib="AOKG Acropora palmata spawned eggs"
/notes="Vector: pDNR-LIB; Site 1: Sfil; Site 2: Sfil; The library was prepared from total RNA using the Creator SMART cDNA Library Construction Kit with the LD-PCR method to amplify the cDNA. Amplified cDNA was digested with Sfil, size selected for >1000bp, and ligated into the pDNR-LIB vector."

FEATURES
source
Query Match 79.1%; Score 17.4; DB 10; Length 373;
Best Local Similarity 94.1%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 AAAGGCTTTCGGGGGTGC 20
|||||
Db 9 AAAGGCTTTCGGGGGGC 27
|||||
RESULT 30
T56721
LOCUS
DEFINITION
Ya71a03.s2 Stratagene placenta (#937225) Homo sapiens cDNA clone
IMAGE:67084 3', mRNA sequence.
T56721
T56721.1 GI:658582
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 408)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
Trevaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.,
and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
8889549
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estowatson.wustl.edu
High quality sequence stops: 277

Source: IMAGE Consortium, L1NL
This clone is available royalty-free through L1NL; contact the
IMAGE Consortium (info@image.l1nl.gov) for further information.
Seq primer: -21ml3
High quality sequence stop: 277.
Location/Qualifiers
1. .408
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:67084"
/sex="male"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene placenta (#937225)"
/notes="Organ: Placenta; Vector: pBluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Caucasian. Average insert size: 1.2 kb; Uni-ZAP
XR Vector; ~5' adaptor sequence: 5' GAATTCGGACGAG 3' ~3'
adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

FEATURES
source
Query Match 79.1%; Score 17.4; DB 10; Length 408;
Best Local Similarity 90.0%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 AAAGGCTTTCGGGGGTGCT 21
|||||
Db 367 AAAGGCTTTCGGGGGTGCT 386
|||||
RESULT 31
BB157276/c
LOCUS
DEFINITION
BB157276 RIKEN full-length enriched, 16 days neonate thymus Mus
musculus cDNA clone Al30035115 3', mRNA sequence.
BB157276
BB157276.2 GI:16268376
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 658)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
On Jun 29, 2000 this sequence version replaced gi:8813206.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: http://genome-gsc.riken.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res. .

10 (11), 1757-1771 (2000)
 Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
 Sugahara,Y. and Hayashizaki,Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I.,
 Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
 Hayashizaki,Y.
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp/>) for
 further details.
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN,
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Location/Qualifiers
 1. 658
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="A130035115"
 /tissue_type="thymus"
 /dev_stage="16 days neonate"
 /lab_hosts="DH10B"
 /clone_lib="RIKEN full-length enriched, 16 days neonate
 thymus"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. cDNA went through one round of normalization
 to Rot = 10.0 and subtraction to Rot = 185.0. Second
 strand cDNA was prepared with the primer adapter of
 sequence [5' GAGAGAGATTCGAGTTAATAATATCCCCCCCCCCCC
 3']. cDNA was cleaved with XhoI and BamHI. Vector: a
 modified pBluescript KS(+) after bulk excision from Lambda
 FLC I."

ORIGIN
 Query Match 79.1%; Score 17.4; DB 7; Length 658;
 Best Local Similarity 94.7%; Pred. No. 2.4e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AAGGCCTTCGGGGTGCT 21
 |||||
 Db 89 AAGGCCTTCGGGGTGCT 71
 |||||

RESULT 32
 BX926884
 LOCUS BX926884 694 bp mRNA linear EST 07-MAY-2004
 DEFINITION BX926884 Sus Scrofa library (scan) Sus scrofa cDNA clone
 scan0010d.o.07 5prim, mRNA sequence.
 ACCESSION BX926884.1 GI:41143732
 VERSION EST.
 KEYWORDS Sus scrofa (pig)
 SOURCE Sus scrofa
 ORGANISM Sus scrofa
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 Sus.
 1 (bases 1 to 694)
 Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villegier,S.,
 Soares,M., Bonaldo,F. and Hatey,F.

10 (11), 1757-1771 (2000)
 Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
 Sugahara,Y. and Hayashizaki,Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I.,
 Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
 Hayashizaki,Y.
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp/>) for
 further details.
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN,
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Location/Qualifiers
 1. 694
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /clone="scan0010d.o.07"
 /tissue_type="mixed"
 /dev_stage="from embryos to adults"
 /clone_lib="Sus Scrofa library (scan)"
 /note="Tissues: adipose tissue, brain, kidney, liver,
 muscle, ovary, testis, heart, hypothalamus, pancreas,
 skin, spleen, thymus, placenta, pituitary gland, seminal
 vesicle, small intestine, uterus, adrenals, bulbo urethral
 gland, cerebral trunk, epididymis, female gonad,
 gall-bladder, hippocampus, large intestine, male gonad,
 melanocytes, stomach, udder"

ORIGIN
 Query Match 79.1%; Score 17.4; DB 4; Length 694;
 Best Local Similarity 94.7%; Pred. No. 2.4e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAAGCCCTTCGGGGGTG 19
 |||||
 Db 516 GAAAGCCCTTCGGGGGTG 534
 |||||

RESULT 33
 AG463060/c
 LOCUS AG463060 765 bp DNA linear GSS 22-DEC-2004
 DEFINITION Mus musculus molossinus DNA, clone:MSMg01-351M07.TJ, genomic survey
 sequence.
 ACCESSION AG463060
 VERSION AG463060.1 GI:48160316
 KEYWORDS GSS.
 SOURCE Mus musculus molossinus (Japanese wild mouse)
 ORGANISM Mus musculus molossinus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1
 Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,
 Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriaki,K. and
 Shiroishi,T.
 Contribution of Asian mouse subspecies Mus musculus molossinus to
 genomic constitution of strain C57BL/6J, as defined by BAC-end
 sequence-SNP analysis
 Genome Res. 14 (12), 2439-2447 (2004)
 15574823
 2 (bases 1 to 765)
 Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
 Direct Submission
 Submitted (17-NOV-2003) Mashira Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suehiro-chou,Tsuri-ku, Yokohama, Kanagawa, 230-0045, Japan
 [E-mail:hattori@gsc.riken.jp, URL:<http://hgp.gsc.riken.go.jp/>,
 Tel:81-45-503-9111, Fax:81-45-503-9170]
 Clones are derived from the mouse BAC library MSMg01. For BAC
 library availability, please contact Kuniya Abe (abe@rtc.riken.jp).

TITLE A Pig Normalised Multi-Tissue cDNA Library
 JOURNAL Unpublished (2003)
 COMMENT Contact: Tosser-Klopp G
 Genetique Animale
 Institut National de la Recherche Agronomique
 Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
 cedex, FRANCE
 Tel: 33 (0) 5.61.28.51.14
 Fax: 33 (0) 5.61.28.53.08
 Email: tosser@coulouse.inra.fr
 Sequence cleaned of vector, adaptor and repetitions. Contact us
 at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
 sequence.
 Plate: 0010 row: 0 column: 7.
 Location/Qualifiers
 1. 694
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /tissue_type="mixed"
 /dev_stage="from embryos to adults"
 /clone_lib="Sus Scrofa library (scan)"
 /note="Tissues: adipose tissue, brain, kidney, liver,
 muscle, ovary, testis, heart, hypothalamus, pancreas,
 skin, spleen, thymus, placenta, pituitary gland, seminal
 vesicle, small intestine, uterus, adrenals, bulbo urethral
 gland, cerebral trunk, epididymis, female gonad,
 gall-bladder, hippocampus, large intestine, male gonad,
 melanocytes, stomach, udder"

ORIGIN
 Query Match 79.1%; Score 17.4; DB 4; Length 694;
 Best Local Similarity 94.7%; Pred. No. 2.4e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAAGCCCTTCGGGGGTG 19
 |||||
 Db 516 GAAAGCCCTTCGGGGGTG 534
 |||||

RESULT 33
 AG463060/c
 LOCUS AG463060 765 bp DNA linear GSS 22-DEC-2004
 DEFINITION Mus musculus molossinus DNA, clone:MSMg01-351M07.TJ, genomic survey
 sequence.
 ACCESSION AG463060
 VERSION AG463060.1 GI:48160316
 KEYWORDS GSS.
 SOURCE Mus musculus molossinus (Japanese wild mouse)
 ORGANISM Mus musculus molossinus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1
 Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,
 Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriaki,K. and
 Shiroishi,T.
 Contribution of Asian mouse subspecies Mus musculus molossinus to
 genomic constitution of strain C57BL/6J, as defined by BAC-end
 sequence-SNP analysis
 Genome Res. 14 (12), 2439-2447 (2004)
 15574823
 2 (bases 1 to 765)
 Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
 Direct Submission
 Submitted (17-NOV-2003) Mashira Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suehiro-chou,Tsuri-ku, Yokohama, Kanagawa, 230-0045, Japan
 [E-mail:hattori@gsc.riken.jp, URL:<http://hgp.gsc.riken.go.jp/>,
 Tel:81-45-503-9111, Fax:81-45-503-9170]
 Clones are derived from the mouse BAC library MSMg01. For BAC
 library availability, please contact Kuniya Abe (abe@rtc.riken.jp).

Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: ab@rtc.riken.jp
PRIMERS
Sequencing : TJ
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
Location/Qualifiers
1. .765
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-351M07.TJ"
/sex="male"
/tissue types="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN
Query Match 79.1%; Score 17.4; DB 14; Length 765;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTG 19
||||| |||||||
Db 723 GAAAGGCTTTCGGGGTG 705

RESULT 34
LOCUS
DEFINITION
A0746955 HS 5538 Al_C11_T7A RPCI-11 Human Male BAC Library Homo sapiens
Genomic clone Plate=1114 Col=21 Row=E, genomic survey sequence.
ACCESSION
A0746955
VERSION
A0746955.1 GI:5534113
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 843)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieterdejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Research Genetics (Info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 1114 row: E column: 21
Seq primer: T7
Class: BAC ends
High quality sequence stop: 843.
Location/Qualifiers
1. .843
/organism="Homo sapiens"

FEATURES
source

/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=1114 Col=21 Row=E"
/sex="male"
/clone_lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"

ORIGIN
Query Match 79.1%; Score 17.4; DB 11; Length 843;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTG 19
||||| |||||||
Db 716 GAAAGGCTTTCGGGGTG 734

RESULT 35
BQ689861/c
LOCUS
DEFINITION
BQ689861 AGENCOURT 8047009 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6207361
5', mRNA sequence.
ACCESSION
BQ689861
VERSION
BQ689861.1 GI:21815177
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 893)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2363 row: f column: 02
High quality sequence stop: 714.

FEATURES
Location/Qualifiers
1. .893
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6207361"
/tissue type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_110"
/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 79.1%; Score 17.4; DB 3; Length 893;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTG 19

```

Db      845 GAAAGGCCCTTCTGGGGTG 827
|||||
RESULT 36
DT995647      1413 bp      mRNA      linear      EST 22-SEP-2005
LOCUS      CNB179-H01.y1d-s SHGC-CNB Gasterosteus aculeatus cDNA clone
DEFINITION      DT995647
ACCESSION      DT995647
VERSION      DT995647.1 GI:76119457
KEYWORDS      EST.
SOURCE      Gasterosteus aculeatus (three spined stickleback)
ORGANISM      Gasterosteus aculeatus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
              Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
              Gasterosteidae; Gasterosteus.
REFERENCE      1 (bases 1 to 1413)
AUTHORS      Kingsley,D.M., Peichel,C., Balabhadra,S., Grimwood,J., Dickson,M.,
              Schmutz,J. and Myers,R.M.
TITLE      Expressed sequence tags from Gasterosteus aculeatus
JOURNAL      Unpublished (2003)
COMMENT      Contact: Grimwood, Jane
              Stanford Human Genome Center
              Stanford University School of Medicine
              975 S California Ave, Palo Alto, CA 94304, USA
              Tel: 650 320 5917
              Fax: 650 320 5801
              Email: jane@shgc.stanford.edu
              Plate: 179
              High quality sequence start: 20
              High quality sequence stop: 848.

FEATURES             source
    Location/Qualifiers
        1..1413
            /organism="Gasterosteus aculeatus"
            /mol_type="mRNA"
            /strain="Conner Creek sticklebacks, WA USA"
            /db_xref="taxon:69293"
            /clone="CNB179-H01"
            /sex="mixed male and female"
            /tissue_type="brain"
            /dev_stage="adult"
            /lab_host="DH10B (T1 phage resistant)"
            /clone_lib="SHGC-CNB"
            /notes="Vector: Express 1; Total and poly A+ RNA was
              isolated from the indicated stickleback tissue, and a cDNA
              library was constructed in the Express 1 plasmid vector by
              Open Biosystems. First strand cDNA synthesis was primed
              with an 54 bp linker primer containing an oligodt sequence
              preceded by a synthetic NotI site (first strand primer:
              5'-GACTAGTCTAGATCGGAGCGGCCGCTT)25-3'. Following
              second strand synthesis, cDNAs were made blunt at the end
              corresponding to the original 5 prime end of mRNA, and
              cloned directionally into the NotI and EcoRV sites of
              Express 1. Note that the EcoRV site is typically destroyed
              in the blunt end cloning, leaving a junction of the form
              'xxxATC' (where is ATC is the second half of the EcoRV
              site, and xxx is derived from the cDNA sequence). A map of
              the Express 1 vector is available at:
              http://www.openbiosystems.com/cdna_library_construction_fa
              q.php#8 The primary library was transformed and amplified
              in DH10B (T1 phage resistant) bacteria. Clones available
              from Open Biosystems:
              http://www.openbiosystems.com/stickleback"

ORIGIN
Query Match      79.1%; Score 17.4; DB 10; Length 1413;
Best Local Similarity 94.7%; Pred. No. 2.5e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GAAAGGCCCTTCTGGGGTG 19
|||||

```

```

Db      1230 GAAAGGCCCTTTCAGGGGTG 1248
|||||
RESULT 37
CD377892      270 bp      mRNA      linear      EST 31-MAY-2003
LOCUS      PTM03081 Phaeodactylum tricornutum Uni-Zap XR Phaeodactylum
DEFINITION      CD377892
ACCESSION      CD377892
VERSION      CD377892.1 GI:31253506
KEYWORDS      EST.
SOURCE      Phaeodactylum tricornutum
ORGANISM      Phaeodactylum tricornutum
              Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;
              Bacillariophycidae; Naviculales; Phaeodactylaceae; Phaeodactylum.
              1 (bases 1 to 270)
AUTHORS      Scala,S., Carls,N., Falciatore,A., Chiusano,M.L. and Bowler,C.
TITLE      Genome properties of the diatom Phaeodactylum tricornutum
JOURNAL      Plant Physiol. 129 (3), 993-1002 (2002)
COMMENT      Contact: Bowler C
              Laboratory of Molecular Plant Biology
              Stazione Zoologica 'Anton Dohrn'
              Villa Comunale, I-80121, Napoli, Italy
              Tel: 39 081 583 3268/3211
              Fax: 39 081 764 1355
              Email: chris@alpha.szn.it
              Diatom EST Database(http://aves.thagen.sznbowler.com)
              Seq primer: T3 backward
              POLYA=No.

FEATURES             source
    Location/Qualifiers
        1..270
            /organism="Phaeodactylum tricornutum"
            /mol_type="mRNA"
            /db_xref="taxon:2850"
            /cell_line="CCMP632"
            /clone_lib="Phaeodactylum tricornutum Uni-Zap XR"
            /notes="Vector: Uni-Zap XR vector; Site_1: Eco RI; Site_2:
              Xho I"

ORIGIN
Query Match      78.2%; Score 17.2; DB 5; Length 270;
Best Local Similarity 86.4%; Pred. No. 2.8e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GAAAGGCCCTTTCGGGGTGCTC 22
|||||
Db      59 GAAAGGCCCTTTCGCGAGTGCTC 80
|||||
RESULT 38
CN690130      353 bp      mRNA      linear      EST 17-MAY-2004
LOCUS      E0289B09-5 NIA Mouse Embryonic Stem (ES) cell (Lif-, 48 h, high
DEFINITION      density) cDNA library (Long) Mus musculus cDNA clone NIA:E0289B09
              IMAGE:30857876 5', mRNA sequence.
ACCESSION      CN690130
VERSION      CN690130.1 GI:47456576
KEYWORDS      EST.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
              Sciurognathi; Muroidea; Muridae; Murinae; Mus.
              1 (bases 1 to 353)
AUTHORS      Sharov,A.A., Piao,Y., Matoba,R., Dudekula,D.B., Qian,Y.,
              VanBuren,V., Falco,G., Martin,P.R., Staggs,C.A., Basseey,U.C.,
              Wang,Y., Carter,M.G., Hamatani,T., Aiba,K., Akutsu,H., Sharova,L.,
              Tanaka,T.S., Kimber,W.L., Yoshikawa,T., Jaradat,S.A., Pantano,S.,
              Nagaraja,R., Boheler,K.R., Taub,D., Hodes,R.J., Longo,D.L.,
              Schlessinger,D., Keller,J., Klotz,E., Kelsae,G., Umazawa,A.,
              Vescovi,A.L., Rossant,J., Kunath,T., Hogan,B.L., Curci,A.,
              D'Urso,M., Kelson,J., Hide,W. and KO,M.S.

```


Villa Comunale, I-80121, Napoli, Italy
 Tel: 39 081 583 3288/3211
 Fax: 39 081 764 1355
 Email: chris@alpha.szn.it
 Dlatom EST database (<http://avesthagen.sznbowler.com>)
 Seq primer: T3 backward
 POLYA=No.

FEATURES

source Location/Qualifiers
 1. .371
 /organism="Phaeodactylum tricornutum"
 /mol_type="mRNA"
 /db_xref="taxon:2850"
 /call_line="CCMP632"
 /clone_lib="Phaeodactylum tricornutum Uni-Zap XR"
 /note="vector: Uni-Zap XR vector; Site_1: Eco RI; Site_2: Xho I"

ORIGIN

Query Match 78.2%; Score 17.2; DB 5; Length 371;
 Best Local Similarity 86.4%; Pred. No. 2.9e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTTCGGGGTGCTC 22

Db 161 GAAAGGCTTTTCGCAGTGCTC 182

RESULT 41

CG548494 378 bp mRNA linear GSS 01-OCT-2003
 LOCUS OST150127 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST150127,
 mRNA sequence.
 CG548494
 CG548494.1 GI:37335081
 GSS.
 Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 378)

AUTHORS Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
 Piggott, J., Beltrandeiro, H., Buxton, E.C., Edwards, J., Finch, R.A.,
 Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
 Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
 Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
 Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
 Zhu, Q., Person, C. and Sands, A.T.

TITLE Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
 screen to identify potential targets for therapeutic intervention
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
 14610273

CONTACT: Zambrowicz BP

OmniBank

Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: materials@lexgen.com
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as
 described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
 Class: Gene Trap.

FEATURES

source Location/Qualifiers
 1. .378
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129Sv/Ev"
 /db_xref="taxon:10090"
 /clone="OST150127"
 /cell_type="embryonic stem cell"
 /clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match 78.2%; Score 17.2; DB 12; Length 378;
 Best Local Similarity 86.4%; Pred. No. 2.9e+03;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTTCGGGGTGCTC 22

Db 288 GAAAGGCTTTTCGATGAGCTC 309

RESULT 42

AW854998 386 bp mRNA linear EST 19-MAY-2000
 LOCUS PM3-CT0263-091299-007-c06 CT0263 Homo sapiens cDNA, mRNA sequence.
 DEFINITION AW854998
 ACCESSION AW854998
 VERSION AW854998.1 GI:7950691
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE 1 (bases 1 to 386)

AUTHORS Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.,
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?ttl=et2=PM3-CT0263-091>)
 299-007-c06&tt3=1999-12-09&tt4=1

Seq primer: puc 18 forward

High quality sequence start: 18

High quality sequence stop: 386.

FEATURES

source Location/Qualifiers
 1..386
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="CT0263"
 /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
 SmaI; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No.
 196,716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

ORIGIN

Query Match 78.2%; Score 17.2; DB 7; Length 386;

Best Local Similarity 86.4%; Pred. No. 2.9e+03;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTTCGGGGTGCTC 22

Db 64 GACAAGCATTTCGGGGTGCTC 85

RESULT 43

CG548510 390 bp mRNA linear GSS 01-OCT-2003
 LOCUS

DEFINITION OST150188 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST150188, mRNA sequence.

ACCESSION CG548510

VERSION CG548510.1 GI:37335097

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 390)

Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J., Piggott,J., Beltrando,Rio,H., Buxton,E.C., Edwards,J., Finch,R.A., Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C., Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparks,M.J., Van Slightenhorst,I., Vogel,P., Walke,W., Xu,N., Zhu,Q., Person,C. and Sands,A.T.

TITLE Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

PUBMED 14610273

COMMENT Contact: Zambrowicz BP

Omnibank

Lexicon Genetics Incorporated

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene Trap.

Location/Qualifiers

1. .390

/organism="Mus musculus"

/mol_type="mRNA"

/strain="129Sv/Ev"

/db_xref="taxon:10090"

/clone="OST150188"

/cell_type="embryonic stem cell"

/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

source

1. .390

Query Match 78.2%; Score 17.2; DB 12; Length 390;

Best Local Similarity 86.4%; Pred. No. 2.9e+03;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCCCTTCGGGGTGCTC 22

Db 288 GAAAGCCCTTCGGATGAGCTC 309

FEATURES

LOCUS AA555150 394 bp mRNA linear GSS 01-OCT-2003

DEFINITION OST142970 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST142970, mRNA sequence.

ACCESSION CG545039

VERSION CG545039.1 GI:37331626

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 394)

Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J., Piggott,J., Beltrando,Rio,H., Buxton,E.C., Edwards,J., Finch,R.A., Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C., Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparks,M.J., Van Slightenhorst,I., Vogel,P., Walke,W., Xu,N., Zhu,Q., Person,C. and Sands,A.T.

TITLE Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

PUBMED 14610273

COMMENT Contact: Zambrowicz BP

Omnibank

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Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene Trap.

Location/Qualifiers

1. .390

/organism="Mus musculus"

/mol_type="mRNA"

/strain="129Sv/Ev"

/db_xref="taxon:10090"

/clone="OST150188"

/cell_type="embryonic stem cell"

/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

source

1. .390

Query Match 78.2%; Score 17.2; DB 12; Length 390;

Best Local Similarity 86.4%; Pred. No. 2.9e+03;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCCCTTCGGGGTGCTC 22

Db 288 GAAAGCCCTTCGGATGAGCTC 309

FEATURES

LOCUS AA555150 405 bp mRNA linear EST 09-SEP-1997

DEFINITION nt07g10.s1 NCI CGAP_Prl1 Homo sapiens cDNA clone IMAGE:1029666 similar to TR:G168081 G168081 UNIDENTIFIED GENE. ;, mRNA sequence.

ACCESSION AA555150

VERSION AA555150.1 GI:2325689

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

AUTHORS 1 (bases 1 to 405)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Rodrigo F. Chuqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Arrayed by: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/hbrp/image/image.html

Insert Length: 910 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 400.

Location/Qualifiers

1. .405

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1029666"

/sex="male"

/tissue_type="normal prostatic epithelial cells"

/lab_host="DH10B"

/clone_lib="NCI-CGAP Prl1"

/note="Organ: prostate; Vector: pAMP10; mRNA made from normal prostatic epithelial cells, cDNA made by oligo-dt

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

PUBMED 14610273

COMMENT Contact: Zambrowicz BP

Omnibank

Lexicon Genetics Incorporated

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene Trap.

Location/Qualifiers

1. .394

/organism="Mus musculus"

/mol_type="mRNA"

/strain="129Sv/Ev"

/db_xref="taxon:10090"

/clone="OST142970"

/cell_type="embryonic stem cell"

/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

source

1. .394

Query Match 78.2%; Score 17.2; DB 12; Length 394;

Best Local Similarity 86.4%; Pred. No. 2.9e+03;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCCCTTCGGGGTGCTC 22

Db 288 GAAAGCCCTTCGGATGAGCTC 309

FEATURES

LOCUS AA555150 405 bp mRNA linear EST 09-SEP-1997

DEFINITION nt07g10.s1 NCI CGAP_Prl1 Homo sapiens cDNA clone IMAGE:1029666 similar to TR:G168081 G168081 UNIDENTIFIED GENE. ;, mRNA sequence.

ACCESSION AA555150

VERSION AA555150.1 GI:2325689

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

AUTHORS 1 (bases 1 to 405)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Rodrigo F. Chuqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Arrayed by: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/hbrp/image/image.html

Insert Length: 910 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 400.

Location/Qualifiers

1. .405

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1029666"

/sex="male"

/tissue_type="normal prostatic epithelial cells"

/lab_host="DH10B"

/clone_lib="NCI-CGAP Prl1"

/note="Organ: prostate; Vector: pAMP10; mRNA made from normal prostatic epithelial cells, cDNA made by oligo-dt

priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Library made by D. Krizman, NIH."

ORIGIN

Query Match 78.2%; Score 17.2; DB 1; Length 405;
Best Local Similarity 86.4%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTCGGGGGTGCTC 22

|||||

Db 45 GAAAGGCTTCGGATGTCAC 24

RESULT 46

CG548505 413 bp mRNA linear GSS 01-OCT-2003
LOCUS OST150171 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST150171,
mRNA sequence.

ACCESSION

CG548505

VERSION

CG548505.1 GI:37335092

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 413)

Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,

Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,

Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,

Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,

Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,

Sparks, M.J., Van Slightenhorst, I., Vogel, P., Walke, W., Xu, N.,

Zhu, Q., Person, C. and Sands, A.T.

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap

screen to identify potential targets for therapeutic intervention

Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

14610273

Contact: Zambrowicz BP

OmniBank

Lexicon Genetics Incorporated

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as

described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene Trap.

Location/Qualifiers

1. .413

/organism="Mus musculus"

/mol_type="mRNA"

/strain="129Sv/Ev"

/db_xref="taxon:10090"

/clone="OST150171"

/cell_type="embryonic stem cell"

/clone_lib="Mus musculus 129Sv/Ev"

78.2%; Score 17.2; DB 12; Length 413;

Best Local Similarity 86.4%; Pred. No. 2.9e+03;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTCGGGGGTGCTC 22

|||||

Db 258 GAAAGGCTTCGGATGCTC 279

|||||

RESULT 47

CG562443 417 bp mRNA linear GSS 02-OCT-2003

LOCUS OST446019 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST446019,

mRNA sequence.

CG562443

VERSION

CG662443.1

GI:37486292

GSS.

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 417)

Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,

Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,

Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,

Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,

Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,

Sparks, M.J., Van Slightenhorst, I., Vogel, P., Walke, W., Xu, N.,

Zhu, Q., Person, C. and Sands, A.T.

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap

screen to identify potential targets for therapeutic intervention

Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

14610273

Contact: Zambrowicz BP

OmniBank

Lexicon Genetics Incorporated

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as

described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene Trap.

Location/Qualifiers

1. .417

/organism="Mus musculus"

/mol_type="mRNA"

/strain="129Sv/Ev"

/db_xref="taxon:10090"

/clone="OST446019"

/cell_type="embryonic stem cell"

/clone_lib="Mus musculus 129Sv/Ev"

78.2%; Score 17.2; DB 12; Length 417;

Best Local Similarity 86.4%; Pred. No. 2.9e+03;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTCGGGGGTGCTC 22

|||||

Db 289 GAAAGGCTTCGGATGCTC 310

|||||

RESULT 48

DT596565

LOCUS

DEFINITION

wmi03-11ms2-a04 Wmi03 Welwitschia mirabilis cDNA clone

wmi03-11ms2-a04 5', mRNA sequence.

DT596565

ACCESSION

DT596565

VERSION

DT596565.1

KEYWORDS

EST.

SOURCE

ORGANISM

Welwitschia mirabilis

Welwitschia mirabilis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Gnastophyta; Gnastophyta; Gnastophyta; Gnastophyta;

Welwitschiaceae; Welwitschia.

1 (bases 1 to 432)

Oppenheimer, D., Frohlich, M., Doyle, J., Tanksley, S., Webb, M.,

Leebens-Mack, J., McNeal, J., Landherr, L., Ilut, D. and Wall, K.

Generation of ESTs from early flower buds of Welwitschia mirabilis

Unpublished (2003)

Contact: Claude dePamphilis or James Leebens-Mack

Mueller Laboratory

Penn State University

208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn

State University, University Park, PA 16802, USA

Tel: 814 863 6413

Fax: 814 865 9131

Email: cwd3@psu.edu or jhl10@psu.edu
The sequence provided is trimmed of vector and low quality regions.
Full sequence and original trace file are available from the Plant
Genome Network website (<http://pgn.cornell.edu>)
Plate: wmi03-llms2 row: a column: 04
Seq primer: M13F.
Location/Qualifiers
1. .432
/organism="Welwitschia mirabilis"
/mol_type="mRNA"
/db_xref="PGN:wmi03-llms2-a04"
/db_xref="taxon:3377"
/clone="wmi03-llms2-a04"
/tissue_type="young female strobili"
/lab_host="SOLR"
/clone_lib="wmi03"
/notes="Vector: pBluescript; Site 1: EcoRI; Site 2: XhoI;
This is a directionally cloned, non-normalized library.
This library has been generated by the Floral Genome
Project (FGP). The Floral Genome Project is funded by
NSF's Plant Genome Research Program (DBI-0115684). More
information about the project can be obtained at
<http://fgp.bio.psu.edu>"

FEATURES

source

ORIGIN

Query Match 78.2%; Score 17.2; DB 10; Length 432;
Best Local Similarity 86.4%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCGCTTCGGGGTGCTC 22
| | | | | | | | | | | | | | | | | | | | | |
DB 209 GTAAGGCTTACGGCGTGCTC 230

RESULT 49

CG505758 434 bp mRNA linear GSS 01-OCT-2003
OST54874 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST54874,
mRNA sequence.
CG505758 GI:37284175
GSS.
Mus musculus (house mouse)
Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 434)
Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,W.J., Van Slightenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

JOURNAL

PUBMED

COMMENT

TITLE

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
14610273
Contact: Zambrowicz BP
OmiBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
Location/Qualifiers
1. .434
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"

FEATURES

source

ORIGIN

Query Match 78.2%; Score 17.2; DB 12; Length 434;
Best Local Similarity 86.4%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCGCTTCGGGGTGCTC 22
| | | | | | | | | | | | | | | | | | | | | |
DB 287 GAAAGCGCTTCGGATGAGCTC 308

RESULT 50

BF392844/c

LOCUS

DEFINITION

BF392844

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

BF392844 436 bp mRNA linear EST 27-NOV-2000
UI-CAO-bfo-h-03-0-UI.s1 UI-R-CAO Rattus norvegicus cDNA clone
UI-CAO-bfo-h-03-0-UI 3', mRNA sequence.

BF392844

BF392844.1 GI:11377698

EST.

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 436)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

8889548

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

The sequence contained an oligo-dT track that was present in the

oligonucleotide that was used to prime the synthesis of first

strand cDNA and therefore this may represent a bonafide poly A

tail. The sequence tag present in the cDNA between the NotI site

and the oligo-dT track served to identify it as a clone from the

normalized thalamus library cDNA library Preparation: M.B. Soares

Lab Clone distribution: clones will be available through Research

Genetics (www.resgen.com)

Seq primer: M13 Forward

POLYA=Yes.

FEATURES

source

1. .436

/organism="Rattus norvegicus"

/mol_type="mRNA"

/strain="Sprague-Dawley"

/db_xref="taxon:10116"

/clone="UI-R-CAO-bfo-h-03-0-UI"

/lab_host="DH10B (Life Technologies)"

/clone_lib="UI-R-CAO"

/note="Vector: pT7T3D-PacI; Site 1: Not I; Site 2: Eco RI;

The UI-R-CAO library is a subtracted library derived from

the following tissues: thalamus, cerebellum,

hypothalamus, medulla, pons, midbrain, cerebral cortex,

corpus striatum, testis, and hippocampus. For a detailed

description of the library from which this clone was

derived, please visit our web site at

rateg.eng.uiowa.edu. The subtraction has been

previously described in (Bonaldo, Lennon and Soares,

Genome Research 6:791-806, 1996)

Genome Research 6:791-806, 1996)

Genome Research 6:791-806, 1996)

Genome Research 6:791-806, 1996)

ORIGIN

```

Query Match      78.2%; Score 17.2; DB 7; Length 436;
Best Local Similarity 86.4%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCCGGGGTGCTC 22
    |||||
Db 156 GAAAGGCTTTCCGATGAGCTC 135

RESULT 51
CJ145102/c
LOCUS CJ145102 RIKEN full-length enriched mouse cDNA library, C57BL/6J
DEFINITION visual cortex Mus musculus cDNA clone K230305107 5', mRNA sequence.
ACCESSION CJ145102
VERSION CJ145102.1 GI:76245430
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 442)
AUTHORS The FANTOM Consortium and RIKEN Genome Exploration Research Group
and Genome Science Group (Genome Network Project Core Group).
TITLE The transcriptional landscape of the mammalian genome
JOURNAL Science 309 (5740), 1559-1563 (2005)
PUBMED 16141072
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues. Tissues were provided by Michela Fagiolini
and Takao K. Hensch (Laboratory for Neuronal Circuit Development
Brain Science Institute RIKEN 2-1 Hirotsawa, Wako-shi, Saitama
351-0198 Japan) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/.

FEATURES             Location/Qualifiers
     source           1..442
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="K230305107"
                     /tissue_type="visual cortex"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library,
                     C57BL/6J visual cortex"

ORIGIN
Query Match      78.2%; Score 17.2; DB 5; Length 442;
Best Local Similarity 86.4%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCCGGGGTGCTC 22
    |||||
Db 239 GTAAGGCTTCCTGGGTGCTC 218

RESULT 52
DT598769
LOCUS DT598769 444 bp mRNA linear EST 02-SEP-2005
DEFINITION wmi03-12ms3-b04 Wmi03 Welwitschia mirabilis cDNA clone
wmi03-12ms3-b04 5', mRNA sequence.

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```

DT598769
VERSION DT598769.1 GI:74110042
KEYWORDS Welwitschia mirabilis
SOURCE Welwitschia mirabilis
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetales; Welwitschiaceae; Welwitschia.
REFERENCE 1 (bases 1 to 444)
AUTHORS dePamphilis, C., Carlson, J., Ma, H., Soltis, D., Soltis, P.,
Oppenheimer, D., Frohlich, M., Doyle, J., Tanksley, S., Webb, M.,
Leebens-Mack, J., McNeal, J., Landherr, L., Ilut, D., and Wall, K.
Generation of ESTs from early flower buds of Welwitschia mirabilis
Unpublished (2003)
COMMENT Contact: Claude dePamphilis or James Leebens-Mack
Mueller Laboratory
Penn State University
208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn
State University, University Park, PA 16802, USA
Tel: 814 863 6413
Fax: 814 865 9131
Email: cwd3@psu.edu or jhl10@psu.edu
The sequence provided is trimmed of vector and low quality regions.
Full sequence and original trace file are available from the Plant
Genome Network website (http://pgn.cornell.edu)
Plate: wmi03-12ms3 row: b column: 04
Seq primer: M13F.

FEATURES             Location/Qualifiers
     source           1..444
                     /organism="Welwitschia mirabilis"
                     /mol_type="mRNA"
                     /db_xref="PGN:wmi03-12ms3-b04"
                     /db_xref="taxon:3377"
                     /clone="wmi03-12ms3-b04"
                     /tissue_type="young female strobili"
                     /lab_host="SOLR"
                     /clone_lib="wmi03"
                     /notes="Vector: pBluescript; Site 1: EcoRI; Site 2: XhoI;
                     This is a directionally cloned, non-normalized library.
                     This library has been generated by the Floral Genome
                     Project (FGP). The Floral Genome Project is funded by
                     NSF's Plant Genome Research Program (DBI-0115884). More
                     information about the project can be obtained at
                     http://fgp.bio.psu.edu"

ORIGIN
Query Match      78.2%; Score 17.2; DB 10; Length 444;
Best Local Similarity 86.4%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCCGGGGTGCTC 22
    |||||
Db 221 GTAAGGCTTACGGGGTGCTC 242

RESULT 53
BY370180
LOCUS BY370180 462 bp mRNA linear EST 12-DEC-2002
DEFINITION BY370180 RIKEN full-length enriched, pooled tissues, 16 days
embryo, etc. Mus musculus cDNA clone GI30001F17 3', mRNA sequence.
ACCESSION BY370180
VERSION BY370180.1 GI:26599668
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 462)
AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Ose, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Tagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,

```


Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE

1 (bases 1 to 525)

AUTHORS

Smith, T.P.L., Roberts, A.J., Echteknamp, S.E., Chitko-McKown, C.G.,

Wray, J.E., and Keel, J.W. 2003. Bases called with phred v0.020425.c and

trimmed with the aid of the trim_alt option. Vector identified with

cross match v0.990329.

Plate: FQY8029 row: L column: 13

Seq primer: TAGAGGACACATCGAGG.

Location/Qualifiers

1. 525

/organism="Bos taurus"

/mol_type="mRNA"

/db_xref="taxon:9913"

/tissue_type="pooled"

/lab_host="DH10B"

/clone_lib="MARC 6BOV"

/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;

Library made with RNA pooled from multiple tissues

including liver, lung, hypothalamus, pituitary, and

placenta/endometrium."

FEATURES

source

ORIGIN

Query Match 78.2%; Score 17.2; DB 4; Length 525;

Best Local Similarity 86.4%; Pred. No. 2.9e+03;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTCGGGGTGCTC 22

|||||

Db 426 GAAGGACCTTTCGGGGTGCTC 447

RESULT 56

CA886724

LOCUS

DEFINITION B0131G09-5N NIA Mouse Neural Stem Cell (Differentiated) cDNA

Library (Long) Mus musculus cDNA clone NIA:B0131G09 IMAGE:30096848

5', mRNA sequence.

CA886724

VERSION CA886724.1 GI:27338273

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 549)

Piao, Y., Dudekula, D.B., Qian, Y., Martin, P.R., Alba, K., Vescovi, A.L.

and Ko, M.S.H. 2002.

Systematic Analyses of NIA Mouse Neural Stem Cell (Differentiated)

cDNA Library (Long)

Unpublished (2002)

Contact: Dawood B. Dudekula

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

Email: cdna@lgsun.grc.nia.nih.gov

Plate: B0131 row: G column: 09

Seq primer: -21M13 Reverse

High quality sequence stop: 549

POLYA-No.

Location/Qualifiers

1. 549

FEATURES

source

/organism="Mus musculus"

/mol_type="mRNA"

/strain="CD1"

/db_xref="niaEST:B0131G09-5N"

/db_xref="taxon:10090"

/clone="NIA:B0131G09 IMAGE:30096848"

/dev_stage="Adult"

/lab_host="DH10B"

/clone_lib="NIA Mouse Neural Stem Cell (Differentiated)

cDNA Library (Long)"

/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:

NotI; Mouse cDNA project by the Laboratory of Genetics,

National Institute on Aging (NIA), Intramural Research

Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is

a long-transcript enriched cDNA library (Ref. Genome Res.

11: 1553-1558 (2001). [PMID: 11544199]. Total RNAs were

obtained from Dr. Angelo L. Vescovi (Institute for Stem

Cell Research, Italy). Double-stranded cDNAs were

synthesized with an Oligo(dT) primer [Invitrogen:

5'-pGACTAGTTCTAGATCGCGCGCCCTTTT-3'] from

2.0 Microgram of total RNA, treated with T4 DNA

polymerase, and purified by ethanol-precipitation. The

cDNAs were ligated to lone-linker L1-Sal4, purified by

phenol/chloroform, and separated from free linkers by

Centricon 100. Then, the cDNAs were amplified by

long-range high fidelity PCR using Ex Taq polymerase

(Takara) with a primer Sal4-S. The products were purified

by phenol/chloroform and Centricon 100. The cDNAs were

digested with SalI and NotI enzymes and cloned into

SalI/NotI site of pSPORT1 plasmid vector. The DH10B E.

coli host was transformed with the ligation mixture by the

standard chemical method. The average insert size is about

3.2 kb. The library was constructed by Yulan Piao."

ORIGIN

Query Match 78.2%; Score 17.2; DB 4; Length 549;

Best Local Similarity 86.4%; Pred. No. 2.9e+03;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTCGGGGTGCTC 22

|||||

Db 526 GAAAGGCTTTCGGATGAGCTC 547

RESULT 57

CN695093

LOCUS

DEFINITION

musculus cDNA clone NIA:E0360A01 IMAGE:30864672 5', mRNA sequence.

CN695093

VERSION

CN695093.1 GI:47463842

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 553)

Sharov, A.A., Piao, Y., Matoba, R., Dudekula, D.B., Qian, Y.,

VanBuren, V., Falco, G., Martin, P.R., Staggs, C.A., Bassey, J.C.,

Wang, Y., Carter, M.G., Hamatani, T., Alba, K., Akutsu, H., Sharova, L.,

Nagata, T.S., Kimber, W.L., Yoshikawa, T., Jaradat, S.A., Pantano, S.,

Tanaraja, R., Boheler, K.R., Taub, D., Hodes, R.J., Longo, D.L.,

Schlessinger, D., Keller, J., Klotz, E., Kelsae, G., Umezawa, A.,

Vescovi, A.L., Rossant, J., Kunath, T., Hogan, B.L., Curci, A.,

D'Urso, M., Kelsae, J., Hide, W., and Ko, M.S.

Transcriptome analysis of mouse stem cells and early embryos

PLoS Biol. 1 (3), 410-419 (2003)

Contact: Dawood B. Dudekula

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

Email: cdna@lgsun.grc.nia.nih.gov

Plate: E0360 row: A column: 01
Seq primer: M13 Reverse
High quality sequence stop: 553
POLYA=No.

Location/Qualifiers
1. .553
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="niaEST:E0360A01-5"
/db_xref="taxon:10090"
/clone="NIA:E0360A01 IMAGE:30864672"
/tissue_type="whole embryo including extraembryonic
tissues at 10.5-days postcoitum"
/dev_stage="E10.5"
/lab_host="DH10B"
/clone_lib="NIA Mouse E10.5 whole embryo cDNA library
(Long)"
/notes="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI;
Site 2: NotI; Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (<http://lgsun.grc.nia.nih.gov/cDNA>).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001)). [PMID: 11544199]. Total
RNAs were extracted from a pool of 8 embryos at 10.5-days
postcoitum. Double-stranded cDNAs were synthesized with an
Oligo(dT) primer (Invitrogen).
5'-PGACTGTTCTAGTCGCGAGCGCGCCCTTTTCTTTT-3' from
2ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to Lone-linker LL-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by the standard chemical method. The
average insert size is about 3.4Kb. The library was
constructed by Yulan Piao."

ORIGIN
Query Match 78.2%; Score 17.2; DB 8; Length 553;
Best Local Similarity 86.4%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCGCTTTCGGGGTGCTC 22
|||||
Db 515 GAAAGCGCTTTCGGAGCTC 536

RESULT 58
CB462716/c
LOCUS 555 bp mRNA linear EST 26-MAR-2003
DEFINITION 723046 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION CB462716
VERSION
KEYWORDS
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 555)
Smith, T.P.L., Roberts, A.J., Echtenkamp, S.E., Chitko-McKown, C.G.,
Wray, J.E. and Keefe, J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries
Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329.
Plate: LAM8002 row: M column: 8
Seq primer: TAGAAGGCACACTCGAGG.

FEATURES
source
1. .555
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 6BOV"
/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."

ORIGIN
Query Match 78.2%; Score 17.2; DB 4; Length 555;
Best Local Similarity 86.4%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCGCTTTCGGGGTGCTC 22
|||||
Db 129 GAAGGACCTTCGGGATGCTC 108

RESULT 59
CB464162
LOCUS 555 bp mRNA linear EST 26-MAR-2003
DEFINITION 725350 MARC 6BOV Bos taurus cDNA 3', mRNA sequence.
ACCESSION CB464162
VERSION
KEYWORDS
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 555)
Smith, T.P.L., Roberts, A.J., Echtenkamp, S.E., Chitko-McKown, C.G.,
Wray, J.E. and Keefe, J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries
Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329.
Plate: LAM8002 row: M column: 8
Seq primer: TAGAAGGCACACTCGAGG.

FEATURES
source
1. .555
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 6BOV"
/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."

ORIGIN
Query Match 78.2%; Score 17.2; DB 4; Length 555;
Best Local Similarity 86.4%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCGCTTTCGGGGTGCTC 22
|||||
Db 129 GAAGGACCTTCGGGATGCTC 108


```

Best Local Similarity 86.4%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGGTGCTC 22
    |||||
Db 427 GAAGGACCTTCGGGGGTGCTC 448

RESULT 60
DY385738/c
LOCUS
DEFINITION CL_Ea0005L09.r CL_Ea Curcuma longa cDNA clone CL_Ea0005L09 3',
mRNA sequence.
ACCESSION DY385738
VERSION DY385738.1 GI:87141127
KEYWORDS EST.
SOURCE Curcuma longa
ORGANISM Curcuma longa
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales;
Zingiberaceae; Curcuma.
REFERENCE 1 (bases 1 to 556)
AUTHORS Ma, X.Q., Koo, H.J., Haller, K.P., Soderlund, C.A. and Gang, D.R.
TITLE Comparative Analysis of Expressed Sequence Tags from Different
Organs of Ginger and Turmeric. Insights into Specialized Metabolism
in Traditional Medicinal Plants
JOURNAL Unpublished (2006)
COMMENT Contact: David R. Gang
Department of Plant Sciences
The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 621 7154
Fax: 520 621 7186
Email: gang@ag.arizona.edu
Plate: 0005 row: L column: 09.

FEATURES
    source
    1..556
        /organism="Curcuma longa"
        /mol_type="mRNA"
        /cultivar="Orange Turmeric"
        /db_xref="taxon:136217"
        /clone="CL_Ea0005L09"
        /tissue_type="young leaves"
        /lab_host="TJC 121"
        /clone_lib="CL_Ea"
        /note="Vector: BluescriptIIISK-; Site_1: EcoRI; Site_2:
        XhoI; Greenhouse, soil grown"

ORIGIN

Query Match 78.2%; Score 17.2; DB 10; Length 556;
Best Local Similarity 86.4%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGGTGCTC 22
    |||||
Db 502 GAAAGGCTTTTCGGATGAGTC 523

RESULT 62
CA888697
LOCUS
DEFINITION B0147H08-5N NIA Mouse Neural Stem Cell (Differentiated) cDNA
Library (Long) Mus musculus cDNA clone NIA:B0147H08 IMAGE:30098395
5', mRNA sequence.
ACCESSION CA888697
VERSION CA888697.1 GI:27340246
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 566)
AUTHORS Piao, Y., Dudekula, D.B., Qian, Y., Martin, P.R., Aiba, K., Vescovi, A.L.
and Ko, M.S.H.
TITLE Systematic Analyses of NIA Mouse Neural Stem Cell (Differentiated)
cDNA Library (long)
JOURNAL Unpublished (2002)
COMMENT Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: B0147 row: H column: 08
Seq primer: -21M13 Reverse
High quality sequence stop: 566
POLYA=No.

FEATURES
    source
    1..566
        /organism="Mus musculus"
        /mol_type="mRNA"
        /strain="CD1"
        /db_xref="niaEST:B0147H08-5N"
        /clone="NIA:B0147H08 IMAGE:30098395"
        /dev_stage="Adult"
        /lab_host="DH10B"
        /clone_lib="NIA Mouse Neural Stem Cell (Differentiated)
        cDNA Library (Long)"
        /note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2:
        NotI; Mouse cDNA project by the Laboratory of Genetics,

```

```

White, R.A., Beremand, P.D., Thomas, T.L., Gan, L. and Klein, W.H.
Gene expression in the developing mouse retina by EST sequencing
and microarray analysis
Nucleic Acids Res. 29 (24), 4983-4993 (2001)
11812828
COMMENT Contact: Klein WH
Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
Tel: 713 792 3646
Fax: 713 790 0329.

FEATURES
    source
    1..562
        /organism="Mus musculus"
        /mol_type="mRNA"
        /db_xref="taxon:10090"
        /tissue_type="neural retina"
        /dev_stage="embryonic day 14.5 post-fertilization"
        /clone_lib="Mouse E14.5 retina lambda ZAP II Library"

ORIGIN

Query Match 78.2%; Score 17.2; DB 2; Length 562;
Best Local Similarity 86.4%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGGTGCTC 22
    |||||
Db 502 GAAAGGCTTTTCGGATGAGTC 523

RESULT 62
CA888697
LOCUS
DEFINITION B0147H08-5N NIA Mouse Neural Stem Cell (Differentiated) cDNA
Library (Long) Mus musculus cDNA clone NIA:B0147H08 IMAGE:30098395
5', mRNA sequence.
ACCESSION CA888697
VERSION CA888697.1 GI:27340246
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 566)
AUTHORS Piao, Y., Dudekula, D.B., Qian, Y., Martin, P.R., Aiba, K., Vescovi, A.L.
and Ko, M.S.H.
TITLE Systematic Analyses of NIA Mouse Neural Stem Cell (Differentiated)
cDNA Library (long)
JOURNAL Unpublished (2002)
COMMENT Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: B0147 row: H column: 08
Seq primer: -21M13 Reverse
High quality sequence stop: 566
POLYA=No.

FEATURES
    source
    1..566
        /organism="Mus musculus"
        /mol_type="mRNA"
        /strain="CD1"
        /db_xref="niaEST:B0147H08-5N"
        /clone="NIA:B0147H08 IMAGE:30098395"
        /dev_stage="Adult"
        /lab_host="DH10B"
        /clone_lib="NIA Mouse Neural Stem Cell (Differentiated)
        cDNA Library (Long)"
        /note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2:
        NotI; Mouse cDNA project by the Laboratory of Genetics,

```


National Institute on Aging (NIA), Intramural Research Program, NIH (<http://lgsun.grc.nia.nih.gov/cDNA>). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were obtained from Dr. Angelo L. Vescovi (Institute for Stem Cell Research, Italy). Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTTCTAGATCGGAGCGCGCCCTTTTTTT-3'] from 2.0 microgram of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker L1-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 3.2 kb. The library was constructed by Yulan Piao."

ORIGIN

Query Match 78.2%; Score 17.2; DB 4; Length 566;
Best Local Similarity 86.4%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCCCTTCGGGGTGCTC 22
|||||

Db 526 GAAAGCCCTTCGGATGATC 547
|||||

RESULT 63

DN591849/c

LOCUS DN591849 591 bp mRNA linear EST 15-MAR-2005
DEFINITION a4g07cc.r1 Coprinus cinereus fruit body cap cDNAs in meiotic
prophase (K+6) Coprinopsis cinerea CDNA 3', mRNA sequence.

ACCESSION DN591849

VERSION DN591849.1 GI:61242453

KEYWORDS EST.

SOURCE Coprinopsis cinerea (Coprinus cinereus)

ORGANISM Coprinopsis cinerea
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Pezizyrellaceae; Coprinopsis.

REFERENCE 1 (bases 1 to 591)

AUTHORS Zolan,M.E., Roe B., Kupfer, D., Palmerini,H., Ramesh,M.A.,

Gathman,A.C., Lilly,W.W. and Pukkila,P.J.

TITLE Expressed sequence tags from Coprinus cinereus (Coprinopsis

cinerea) cDNAs, 2002

JOURNAL Unpublished (2002)

COMMENT Contact: Gathman AC

Biologiy Department

Southeast Missouri State University

1 University Plaza, Cape Girardeau, MO 63701, USA

Tel: 5736512361

Fax: 573 651 2382

Email: agathman@semo.edu

Seq primer: T7.

Location/Qualifiers

source

1. 591

/organism="Coprinopsis cinerea"

/mol_type="mRNA"

/strain="Dikaryon - strains backcrossed into Okayama7#130

thru 5 gens"

/db_xref="taxon:5346"

/dev_stage="Fruit body caps harvested six hours after

karyogamy (nuclear fusion)"

/lab_host="E. coli DH10B"

/clone_lib="Coprinus cinereus fruit body cap cDNAs in

meiotic prophase (K+6)"

/note="Vector: pAD-Gal 4-2.1; Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

QY 1 GAAAGCCCTTCGGGGTGCTC 22

|||||

Db 168 GAAAGACCTGCTGGGTGCTC 147

|||||

RESULT 64

AI663484

LOCUS AI663484

DEFINITION

AI663484

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Murioidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 594)

AUTHORS

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,

Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,

Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,

Ritter,B., Kohn,S., Shin,T., Jackson,F., Cardenas,M., McCann,R.,

Waterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999

Unpublished (1999)

Other ESTs: uk33d10.x1

Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:987543

Seq primer: custom primer used

High quality sequence stop: 515.

Location/Qualifiers

source

1. 594

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL"

/db_xref="taxon:10090"

/clone="IMAGE:1970803"

/sex="female"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="Sugano mouse kidney mkia"

/note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII

(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA

was primed with an oligo(dT) primer

[ATGGGCTTTTCTTTTCTTTT]

ligated to a DraIII adaptor [TGTGGCTTACTGG], digested

and cloned into distinct DraIII sites of the pME18S-FL3

vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should

be used to isolate the cDNA insert. Size selection was

performed to exclude fragments <1.5kb. Library

constructed by Dr. Sumio Sugano (University of Tokyo

Institute of Medical Science). Custom primers for

sequencing: 5' end primer CTTCGTCTCTAAAGCTGG and 3' end

primer CGACCTGCAGCTCGAGACA."

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

```

QY 1 GAAAGGCTTTTCGGGGTGTCTC 22
    |||||
Db 543 GAAAGGCTTTTCGGATGAGCTC 564

RESULT 65
BE534580
LOCUS BE534580 597 bp mRNA linear EST 09-AUG-2000
DEFINITION 601233510F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:3597243 5',
mRNA sequence.
ACCESSION BE534580
VERSION BE534580.1 GI:9763134
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 597)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM8776 row: c column: 04
High quality sequence stop: 597.
Location/Qualifiers
FEATURES
source
1..597
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3597243"
/sex="female; virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mam6"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Salt;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

ORIGIN
Query Match 78.2%; Score 17.2; DB 7; Length 597;
Best Local Similarity 86.4%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGTGTCTC 22
    |||||
Db 523 GAAAGGCTTTTCGGATGAGCTC 544

RESULT 66
BG804780
LOCUS BG804780 600 bp mRNA linear EST 20-DEC-2001
DEFINITION 0272-28 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
mRNA sequence.
ACCESSION BG804780
VERSION BG804780.1 GI:17951704
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

```

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REFERENCE 1 (bases 1 to 600)
AUTHORS Mu, X., Zhao, S., Pershad, R., Hsieh, T.-F., Scarpa, A., Wang, S.W.,
White, R.A., Beremand, P.D., Thomas, T.L., Gan, L. and Klein, W.H.
TITLE Gene expression in the developing mouse retina by EST sequencing
and microarray analysis
JOURNAL Nucleic Acids Res. 29 (24), 4983-4993 (2001)
PUBMED 11812828
COMMENT Contact: Klein WH
Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
Tel: 713 792 3646
Fax: 713 790 0329.
Location/Qualifiers
FEATURES
source
1..600
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="neural retina"
/dev_stage="embryonic day 14.5 post-fertilization"
/clone_lib="Mouse E14.5 retina lambda ZAP II Library"

ORIGIN
Query Match 78.2%; Score 17.2; DB 2; Length 600;
Best Local Similarity 86.4%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGTGTCTC 22
    |||||
Db 515 GAAAGGCTTTTCGGATGAGCTC 536

RESULT 67
CV562959
LOCUS CV562959 603 bp mRNA linear EST 22-OCT-2004
DEFINITION UI-M-FC0-ctx-g-16-0-UI.r1 NIH_BMAP_F00 Mus musculus cDNA clone
IMAGE:6734729 5', mRNA sequence.
ACCESSION CV562959
VERSION CV562959.1 GI:54454174
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 603)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5.
Location/Qualifiers
FEATURES
source
1..603
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/tissue_type="whole brain"
/dev_stage="embryo 12.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_F00"
/notes="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according to

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Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is TGAGAGAGCC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BNAP). Gene Discovery in the Developing Mouse Nervous System, supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 78.2%; Score 17.2; DB 8; Length 603;
Best Local Similarity 86.4%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTCGGGGTGCTC 22
||||| ||||| ||||| ||||| |||||

Db 416 GAAGGCGCTTCGGGGTGCTC 437

RESULT 68

CA163213

LOCUS SCRLRZ3112F12.2 g23 Saccharum officinarum cDNA clone SCRLRZ3112F12
DEFINITION 5', mRNA sequence.

ACCESSION CA163213

VERSION CA163213.1 GI:35079390

KEYWORDS EST.

SOURCE Saccharum officinarum

ORGANISM Saccharum officinarum

REFERENCE

1 (bases 1 to 608)

Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.

The libraries that made SUCSEST

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: parruda@unicamp.br

Clone distribution: clone distribution information can be found

through the Brazilian Clone Collection Center (BCCC) at

http://www.bcccenter.fcav.unesp.br

Plate: 112 row: F column: 12

Seq primer: T7 Promoter Primer.

Location/Qualifiers

FEATURES

source

1..608

/organism="Saccharum officinarum"

/mol_type="mRNA"

/db_xref="taxon:4547"

/clone="SCRLRZ3112F12"

/lab_host="DH10B"

/clone_lib="RZ3"

/note="Organ: Shoot-root transition zone from adult plants; Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [Shoot-root transition zone from adult plants]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at

http://sucst.lad.ic.unicamp.br/public"

ORIGIN

Query Match 78.2%; Score 17.2; DB 4; Length 608;
Best Local Similarity 86.4%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTCGGGGTGCTC 22
||||| ||||| ||||| ||||| |||||

Db 571 GGAAGGCGCTTCGGGGGGGCTC 592

RESULT 69

CK975625

LOCUS 4106617 BARC 9BOV Bos taurus cDNA clone 9BOV33_C24 3', mRNA
DEFINITION sequence.

ACCESSION CK975625

VERSION CK975625.1 GI:45493599

KEYWORDS EST.

SOURCE Bos taurus (cattle)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

1 (bases 1 to 609)

Sonstegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harhay,

G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.

Production of EST from cDNA libraries derived from immunologically

activated bovine gut

Unpublished (2004)

Contact: Tad S. Sonstegard

Bovine Functional Genomics Laboratory

Animal and Natural Resources Institute

Bd19-200 Rm2A BARC-East, Beltsville, MD 20705, USA

Tel: 3015048416

Fax: 3015048414

Email: tads@anri.barc.usda.gov

Single pass sequencing. Bases called and trimmed with phred

0.00995 using options -trim alt - -trim fasta. Vector identified

by cross match using options -minmatch 12 -minscore 18

Plate: 33 row: C column: 24

Seq primer: AGCGGATAACAATTCACACAGG

High quality sequence stop: 609.

FEATURES

source

1..609

/organism="Bos taurus"

/mol_type="mRNA"

/strain="Holstein"

/db_xref="taxon:9913"

/clone="9BOV33_C24"

/sex="Male"

/tissue_type="Pooled"

/lab_host="DH10B T1 phage resistant"

/clone_lib="BARC 9BOV"

/note="Organ: Abomasum; Vector: pAGEN-1; Site 1: EcoRV;

Site 2: NotI; Equimolar amounts of mRNA extracted from

fundic and pyloric abomasums of 18 and 21 week old steers.

Exposure to Osteragia osteragi was initiated at 15 weeks

of age. fundic and pyloric abomasum"

ORIGIN

Query Match 78.2%; Score 17.2; DB 8; Length 609;
Best Local Similarity 86.4%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTCGGGGTGCTC 22
||||| ||||| ||||| ||||| |||||

Db 441 GAAGGACCTTCGGGGGATGCTC 462

RESULT 70

LBAP055F03/c

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LOCUS      LBAF055F03      614 bp      DNA      linear      GSS 20-JUN-2003
DEFINITION Leishmania braziliensis GSS, clone LBAF055F03, genomic survey
sequence.
ACCESSION   BX542565
VERSION     BX542565.1  GI:32137791
KEYWORDS    GSS; genomic survey sequence.
SOURCE      Leishmania braziliensis
ORGANISM    Leishmania braziliensis
            Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
            Leishmania; Leishmania braziliensis species complex.
REFERENCE   1
AUTHORS     Laurentino E.C., Ruiz J.C. and Cruz A.K.
TITLE       GSS analysis of the Leishmania braziliensis genome
JOURNAL     Unpublished
REFERENCE   2  (bases 1 to 614)
AUTHORS     Cruz A.K.
TITLE       Direct Submission
JOURNAL     Submitted (17-JUN-2003) Cruz A.K., University of Sao Paulo,
            Department of Molecular and Cell Biology, FMRP, Avenida
            Bandeirantes 3900, Ribeirao Preto, SP, 14049-900, BRAZIL
COMMENT     Clone requests: akcruz@fmrp.usp.br.
FEATURES    Location/Qualifiers
             1..614
             /organism="Leishmania braziliensis"
             /mol_type="genomic DNA"
             /strain="MHOM/BR/75/M2904"
             /db_xref="taxon:5660"
             /clone="LBAF055F03"
ORIGIN
Query Match      78.2%; Score 17.2; DB 14; Length 614;
Best Local Similarity 86.4%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  1  GAAAGGCGCTTCGGGGGTGCTC 22
      |||||
Db  27  GAAAGGCGCTTCGGGGGTGCTC 6

RESULT 71
CL864502
LOCUS      CL864502      622 bp      DNA      linear      GSS 19-AUG-2004
DEFINITION TM1-GSS000422r BAC and BIBAC libraries from upland cotton genetic
standard TM-1 Gossypium hirsutum genomic clone GH-TM1-CBV131B22 5',
genomic survey sequence.
ACCESSION   CL864502
VERSION     CL864502.1  GI:51321232
KEYWORDS    GSS.
SOURCE      Gossypium hirsutum (upland cotton)
ORGANISM    Gossypium hirsutum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
REFERENCE   1  (bases 1 to 622)
AUTHORS     Xu, Z., Kohel, R.J., Zhang, H.B., Dong, J., Covalada, L., Lee, M., Koo, P.
            and Yu, J.Z.
TITLE       Genome-Wide Synteny between Arabidopsis and Cotton
JOURNAL     Unpublished (2004)
COMMENT     Other GSSs: TM1-GSS000422f
            Contact: John Z. Yu
            Cotton Molecular Genetics Laboratory
            USDA-ARS Crop Germplasm Research Unit
            2765 F&B Road, Building 11, College Station, TX 77845. USA
            Tel: 979-260-9237
            Fax: 979-260-9333
            Email: zyu@qutun.tamu.edu
            for more detail, please see
            http://algonodon.tamu.edu/htdocs-cotton/cottondb.html
            Seq primer: sp030
            Class: BAC ends
            High quality sequence stop: 622.
FEATURES    Location/Qualifiers
             1..622

LOCUS      LBAF055F03      614 bp      DNA      linear      GSS 20-JUN-2003
DEFINITION Leishmania braziliensis GSS, clone LBAF055F03, genomic survey
sequence.
ACCESSION   BX542565
VERSION     BX542565.1  GI:32137791
KEYWORDS    GSS; genomic survey sequence.
SOURCE      Leishmania braziliensis
ORGANISM    Leishmania braziliensis
            Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
            Leishmania; Leishmania braziliensis species complex.
REFERENCE   1
AUTHORS     Laurentino E.C., Ruiz J.C. and Cruz A.K.
TITLE       GSS analysis of the Leishmania braziliensis genome
JOURNAL     Unpublished
REFERENCE   2  (bases 1 to 614)
AUTHORS     Cruz A.K.
TITLE       Direct Submission
JOURNAL     Submitted (17-JUN-2003) Cruz A.K., University of Sao Paulo,
            Department of Molecular and Cell Biology, FMRP, Avenida
            Bandeirantes 3900, Ribeirao Preto, SP, 14049-900, BRAZIL
COMMENT     Clone requests: akcruz@fmrp.usp.br.
FEATURES    Location/Qualifiers
             1..614
             /organism="Leishmania braziliensis"
             /mol_type="genomic DNA"
             /strain="MHOM/BR/75/M2904"
             /db_xref="taxon:5660"
             /clone="LBAF055F03"
ORIGIN
Query Match      78.2%; Score 17.2; DB 14; Length 614;
Best Local Similarity 86.4%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  1  GAAAGGCGCTTCGGGGGTGCTC 22
      |||||
Db  27  GAAAGGCGCTTCGGGGGTGCTC 6

RESULT 71
CL864502
LOCUS      CL864502      622 bp      DNA      linear      GSS 19-AUG-2004
DEFINITION TM1-GSS000422r BAC and BIBAC libraries from upland cotton genetic
standard TM-1 Gossypium hirsutum genomic clone GH-TM1-CBV131B22 5',
genomic survey sequence.
ACCESSION   CL864502
VERSION     CL864502.1  GI:51321232
KEYWORDS    GSS.
SOURCE      Gossypium hirsutum (upland cotton)
ORGANISM    Gossypium hirsutum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
REFERENCE   1  (bases 1 to 622)
AUTHORS     Xu, Z., Kohel, R.J., Zhang, H.B., Dong, J., Covalada, L., Lee, M., Koo, P.
            and Yu, J.Z.
TITLE       Genome-Wide Synteny between Arabidopsis and Cotton
JOURNAL     Unpublished (2004)
COMMENT     Other GSSs: TM1-GSS000422f
            Contact: John Z. Yu
            Cotton Molecular Genetics Laboratory
            USDA-ARS Crop Germplasm Research Unit
            2765 F&B Road, Building 11, College Station, TX 77845. USA
            Tel: 979-260-9237
            Fax: 979-260-9333
            Email: zyu@qutun.tamu.edu
            for more detail, please see
            http://algonodon.tamu.edu/htdocs-cotton/cottondb.html
            Seq primer: sp030
            Class: BAC ends
            High quality sequence stop: 622.
FEATURES    Location/Qualifiers
             1..622
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LOCUS      Gossypium hirsutum
DEFINITION Gossypium hirsutum
sequence.
ACCESSION   Gossypium hirsutum
VERSION     Gossypium hirsutum
KEYWORDS    GSS; genomic survey sequence.
SOURCE      Gossypium hirsutum
ORGANISM    Gossypium hirsutum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
REFERENCE   1  (bases 1 to 632)
AUTHORS     Kirchner, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
            Rusch, D.B., Deicher, A.L., Pop, M., Wang, W., Fraser, C.M. and
            Venter, J.C.
TITLE       The dog genome: survey sequencing and comparative analysis
JOURNAL     Science 301 (5641), 1898-1903 (2003)
COMMENT     Contact: Kirchner EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirchner@tigr.org
            Class: shotgun.
FEATURES    Location/Qualifiers
             1..632
             /organism="Gossypium hirsutum"
             /mol_type="genomic DNA"
             /strain="Standard Poodle"
             /db_xref="taxon:9615"
             /clone_lib="Dog Library"
             /notes="Site 1: BstXI; Libraries were prepared from
             peripheral blood"
ORIGIN
Query Match      78.2%; Score 17.2; DB 12; Length 632;
Best Local Similarity 86.4%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  1  GAAAGGCGCTTCGGGGGTGCTC 22
      |||||
Db  371  GAAAGGCGCTTCGGGGGTGCTC 392

RESULT 73
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CF902767 638 bp mRNA linear EST 04-NOV-2003
 LOCUS A0345F09-5 NIA Mouse Trophoblast Stem Cell cDNA Library (long 1)
 DEFINITION Mus musculus cDNA clone NIA:A0345F09 IMAGE:30737540 5', mRNA sequence.

ACCESSION CF902767
 VERSION CF902767.1 GI:38169816
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.
 1 (bases 1 to 638)
 AUTHORS Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
 TITLE Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification method

JOURNAL Genome Res. 11 (9), 1553-1558 (2001)
 PUBMED 11544199
 COMMENT Contact: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@igun.grc.nia.nih.gov
 Plate: A0345 row: F column: 09
 Seq primer: M13 Reverse
 High quality sequence stop: 638
 POLYA=No.

FEATURES

source Location/Qualifiers

1. .638
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="B5/EGFP transgenic ICR mice"
 /db_xref="tae: A0345F09-5"
 /db_xref="taxon:10090"
 /clone="NIA:A0345F09 IMAGE:30737540"
 /dev_stage="3.5-dpc"
 /lab_host="DH10B"
 /clone_lib="NIA Mouse Trophoblast Stem Cell cDNA Library (long 1)"
 /notes="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library [Ref.]. Total Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]. Total RNAs were obtained from Dr. Janet Rossant and Tilo Kunath (Samuel Lunenfeld Research Institute, Canada). Double-stranded cDNAs were synthesized with an Oligo (dT) primer (Invitrogen): 5'-pGACTAGTCTAGATCGGCGCGCCCTTTT-3' from 4 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.6 kb. The library was constructed by Yulan Piao."

ORIGIN

Query Match 78.2%; Score 17.2; DB 5; Length 638;
 Best Local Similarity 86.4%; Pred. No. 3e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 GAAAGCCCTTCGGGGTGCTC 22
 |||||

Db

516 GAAAGCCCTTCGGATGAGCTC 537

RESULT 74

BB614371

LOCUS

DEFINITION BB614371 RIKEN full-length enriched, adult male testis Mus musculus cDNA clone 4921535F14 5', mRNA sequence.

ACCESSION

BB614371

VERSION

BB614371.1 GI:16454813

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.
 1 (bases 1 to 638)

AUTHORS

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.

TITLE

RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

JOURNAL

Unpublished (2001)

COMMENT

Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yananaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

e mouse tissues.

Location/Qualifiers

1. .638
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="4921535F14"
 /sex="male"
 /tissue_type="testis"
 /dev_stage="adult"
 /lab_host="SOLR"

/clone_lib="RIKEN full-length enriched, adult male testis"
 /note="Site 1: XhoI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia

FEATURES

source

RESULT 77
CD406831/c
LOCUS
DEFINITION
Gm_cK3178 Soybean induced by Salicylic Acid Glycine max cDNA 3',
mRNA sequence.
CD406831
CD406831.1 GI:31464818
VERSION
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 652)
Tian,A.G., Wang,J., Cui,P., Han,Y.J., Xu,H., Cong,L.J., Huang,X.G.,
Wang,X.L., Jiao,Y.Z., Wang,B.J., Wang,Y.J., Zhang,J.S. and
Chen,S.Y.
TITLE
Characterization of soybean genomic features by analysis of its
expressed sequence tags
JOURNAL
PUBLISHED
Theor. Appl. Genet. 108 (5), 903-913 (2004)
14624337
COMMENT
Contact: Chen S-Y
Plant Biotechnology Laboratory
Institute of Genetics and Developmental Biology, CAS, China
Datun road, Beijing 100101, China
Tel: 86-10-64886859
Fax: 86-10-64873428
Email: sychen@genetics.ac.cn
Email: sychen@genetics.ac.cn
Seq primer: T7 primer
Location/Qualifiers
1. .652
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Kefeng 1"
/db_xref="taxon:3847"
/tissue_type="Seedlings"
/dev_stage="two-week seedlings"
/lab_host="XLI-Blue MRF" strain"
/clone_lib="Soybean induced by Salicylic Acid"
/notes="Vector: pBluescript SK+; Site 1: EcoR I; Site 2:
Xho I; The cDNA library was constructed by He, C-Y from
mRNA isolated from two-week seedlings (cultivar Kefeng 1)
treated by spraying 2.0mM salicylic acid for 24, 36, 48
and 72 h. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
XhoI restriction site. EcoRI adapters were ligated to the
blunt-ended cDNA fragments followed by XhoI digestion. The
cDNA fragments were directionally cloned into the
EcoRI-XhoI restriction site of the pBluescript vector. The
ligated cDNA fragments were transformed into XLI-Blue MRF
host cells (Stratagene)."

Query Match 78.2%; Score 17.2; DB 5; Length 652;
Best Local Similarity 86.4%; Pred. No. 3e+03; Mismatches 0; Gaps 0;
Matches 19; Conservative 0; Indels 3; Indels 0; Gaps 0;
QY 1 GAAAGGCGCTTCGGGGGTGCTC 22
|||||
Db 243 GAAAGGCGCTTCGGGGGTGCTC 222
|||||

RESULT 78
CK976084/c
LOCUS
DEFINITION
4107001 BARC 9BOV Bos taurus cDNA clone 9BOV33_C24 5', mRNA
sequence.
CK976084
CK976084.1 GI:45494058
VERSION

KEYWORDS
SOURCE
ORGANISM
Bos taurus (cattle)
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 659)
Sonstegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harhay,
G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
Production of EST from cDNA libraries derived from immunologically
activated bovine gut
Unpublished (2004)
Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
Tel: 3015048416
Fax: 3015048414
Email: tads@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alt "-trim_fasta. Vector identified
by cross_match using options -minmatch 12 -minscore 12
Plate: 33 row: C column: 24
Seq primer: CCGAGTCACGAGCTTGTAAAACG
High quality sequence stop: 659.
Location/Qualifiers
1. .659
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clone="9BOV33_C24"
/sex="Male"
/tissue_type="Pooled"
/dev_stage="Multiple"
/lab_host="DH10B T1 phage resistant"
/clone_lib="BARC 9BOV"
/note="Organ: Abomasum; Vector: pAGEN-1; Site 1: EcoRV;
Site 2: NotI; Equimolar amounts of mRNA extracted from
fundic and pyloric abomasums of 18 and 21 week old steers.
Exposure to Ostertagia osteragi was initiated at 15 weeks
of age. fundic and pyloric abomasum"
ORIGIN
Query Match 78.2%; Score 17.2; DB 8; Length 659;
Best Local Similarity 86.4%; Pred. No. 3e+03; Mismatches 0; Gaps 0;
Matches 19; Conservative 0; Indels 3; Indels 0; Gaps 0;
QY 1 GAAAGGCGCTTCGGGGGTGCTC 22
|||||
Db 334 GAAGGACCTTCGGGGATGCTC 313
|||||

RESULT 79
BB619260/c
LOCUS
DEFINITION
BB619260 RIKEN full-length enriched mouse cDNA library. C57BL/6J 8
days embryo Mus musculus cDNA clone 5730519C19 5', mRNA sequence.
BB619260
BB619260.1 GI:15396773
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 673)
The FANTOM Consortium and RIKEN Genome Exploration Research Group
and Genome Science Group (Genome Network Project Core Group).
The transcriptional landscape of the mammalian genome
Science 309 (5740), 1559-1563 (2005)
16141072
Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute.
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-resgsc.riken.jp, URL: <http://genome.gsc.riken.jp/>
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.jp/>.

FEATURES

source
1. .673
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="5730519C19"
/dev_stage="8 days embryo"
/clone_lib="RIKEN full-length enriched mouse cDNA library,
C57BL/6J 8 days embryo"

ORIGIN

Query Match 78.2%; Score 17.2; DB 7; Length 673;
Best Local Similarity 86.4%; Pred. No. 3e+03; 3; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCCCTTCGGGGTGCTC 22

|||||
Db 597 GAAAGGCCCTTCGGGGTGCTC 576

RESULT 80

CO426515
LOCUS
DEFINITION
UT-M-HU0-crg-i-05-0-UT.r1 NIH BMAP_HU0 Mus musculus cDNA clone
IMAGE:30682084 5', mRNA sequence.

ACCESSION
CO426515

VERSION
CO426515.1

KEYWORDS
EST.

SOURCE
Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.

1 (bases 1 to 673)

NTH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. James Lin University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

<http://genome.uiowa.edu/distribution/mousefl.html>

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

Seq primer: pyX-5.

Location/Qualifiers

1. .673

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="IMAGE:30682084"

/tissue_type="whole eye"

/dev_stage="newborn(1, 5, 15 days)"

/lab_host="DH10B (T1 phage resistant)"

FEATURES

source

/clone_lib="NIH BMAP_HU0"
/notes="Organ: Eye; Vector: pyX-Asc; Site: 1: EcoR I;
Site 2: Not I; The library was constructed according
BonaIco, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pyX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AATAATACG. This library was created for the University
of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."

ORIGIN

Query Match 78.2%; Score 17.2; DB 8; Length 673;
Best Local Similarity 86.4%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCCCTTCGGGGTGCTC 22

|||||
Db 237 GAAAGGCCCTTCGGATGAGCTC 258

RESULT 81

CI252013

LOCUS

DEFINITION

CI252013 Oryza sativa (japonica cultivar-group) Panicle mixture of
one, two, three weeks after flowering and supermix Oryza sativa
(japonica cultivar-group) cDNA clone 044-M012R-G09 3', mRNA
sequence.

ACCESSION
CI252013

VERSION
CI252013.1

KEYWORDS
EST.

SOURCE
Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 674)

Kikuchi, S.

Collection and mapping of over 30,000 transcription units by the

rice full-length cDNA project from japonica rice

Unpublished (2006)

Contact: Shoshi Kikuchi

Department of Molecular Genetics, Head of Laboratory of Gene

Expression

National Institute of Agrobiological Sciences

2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan

Tel: 81-29-838-7007

Fax: 81-29-838-7007

Email: skikuchi@nias.affrc.go.jp

This EST clone is one of 780k ESTs of Rice full length cDNA Project

URL: <http://cdna01.dna.affrc.go.jp/cDNA/>

NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K.,

Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,

Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,

Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T.,

Yamanoto, M. and Nakahama, Y.

FAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y.,

Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,

Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,

Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S.,

Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,

Yoshimura, A., Matsubara, K. and Murakami, K.

Genome Exploration Research Group in Riken Genomic Sciences Center

and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,

Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,

Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,

Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,

Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,

Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saichoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A., and Hayashizaki, Y.

Location/Qualifiers

1. .674

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nipponbare"

/db_xref="taxon:39947"

/clone="044-M012R-G09"

/tissue_type="Panicles mixture of one, two, three weeks after flowering and supermix"

/clone_lib="Oryza sativa (japonica cultivar-group) Panicles mixture of one, two, three weeks after flowering and supermix"

ORIGIN

Query Match 78.2%; Score 17.2; DB 5; Length 674;
Best Local Similarity 86.4%; Pred. No. 3e+03; 3; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

QY 1 GAAAGGCCTTCGGGGTGCTC 22
|||||

Db 503 GAAAGGCATCGGGGGTGCTC 524
|||||

RESULT 82
CJ093902
LOCUS
DEFINITION
CJ093902 RIKEN full-length enriched mouse cDNA library, C57BL/6J kidney 17 days embryo Mus musculus cDNA clone 1920142B03 5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

Contact: Yoshihide Hayaishizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/.

Location/Qualifiers

1. .674

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="1920142B03"

/tissue_type="kidney"

/dev_stage="17 days embryo"

/clone_lib="RIKEN full-length enriched mouse cDNA library, C57BL/6J kidney 17 days embryo"

ORIGIN

Query Match 78.2%; Score 17.2; DB 5; Length 674;
Best Local Similarity 86.4%; Pred. No. 3e+03; 3; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

QY 1 GAAAGGCCTTCGGGGTGCTC 22
|||||

Db 548 GAAAGGCCTTCGGATGAGCTC 569
|||||

RESULT 83
DR749476
LOCUS
DEFINITION
DR749476 674 bp mRNA linear EST 19-JUL-2005
taurus cDNA clone BP250026B10D12 3', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Bos taurus (cattle)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Contact: Lewin, H.A.
Department of Animal Sciences
University of Illinois at Urbana-Champaign
206 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Base Calling/Quality Scores using PHRED from Washington University Genome Center. Vector Trimming using Cross_match from Washington University Genome Center PHRAP suite. This sequence is vector-free and at least 200 bp in length.
PCR Primers
BACKWARD: TCACACAGGAACAGCTATGAC
Plate: BP250026B10 row: D column: 12
Seq primer: dt(18)N
High quality sequence stop: 674.

Location/Qualifiers

1. .674

/organism="Bos taurus"

/mol_type="mRNA"

/db_xref="taxon:9913"

/clone="BP250026B10D12"

/dev_stage="near-term"

/clone_lib="NG01 rearrayed Soares normalized bovine placenta"

/note="Organ: placenta"

ORIGIN

Query Match 78.2%; Score 17.2; DB 10; Length 674;
Best Local Similarity 86.4%; Pred. No. 3e+03; 3; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

QY 1 GAAAGGCCTTCGGGGTGCTC 22
|||||

Db 393 GAAAGGCCTTCGGGATGCTC 414
|||||

RESULT 84
BU654491/c
LOCUS

BU654491 682 bp mRNA linear EST 30-SEP-2002

```

DEFINITION 112113H11.Y1 C. reinhardtii CC-1690 (mt+), CC-1691 (mt-), Gamete
(sequence), Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA
ACCESSION BU654491
VERSION BU654491.1 GI:23366672
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii
ORGANISM Chlamydomonas reinhardtii
REFERENCE 1 (bases 1 to 682)
AUTHORS Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C.,
Lefebvre,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D.
TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants. Project: 1112
JOURNAL Unpublished (2002)
COMMENT Contact: Charles Hauser
DCMB Box 91000
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
FEATURES
    source
        Location/Qualifiers
            1..682
                /organism="Chlamydomonas reinhardtii"
                /mol_type="mRNA"
                /strain="21gr (CC-1690 wild type mt+) & 6145c (CC-1691
                wild type mt-)"
                /db_xref="taxon:3055"
                /clone_lib="C. reinhardtii CC-1690 (mt+), CC-1691 (mt-),
                Gamete (normalized), Lambda Zap II"
                /notes="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2:
                XhoI; Gamete library was constructed by Hui Zhao, Min Lu,
                Jeffrey McDermott, William J. Snell and John Davies.
                Strain 21gr cells (CC-1690; mating type plus) and strain
                6145c cells (CC-1691; mating type minus) that had been
                growing on a light-dark cycle (13:11 L/D) in R-medium
                (Sager and Granick) were separately transferred into
                nitrogen-free medium at 8 hours into the light period.
                PolyA mRNA was purified from each sample every 2 hours for
                the next 18 hours. The mRNA was pooled and used for cDNA
                synthesis. The cDNA was directionally cloned into lambda
                Zap II (Stratagene) in the EcoRI (5') and XhoI (3')
                sites. pBluescript II SK- plasmids were excised from the
                lambda Zap clones by superinfection with ExAssist
                (Stratagene) phage. The library was normalized using
                method 4 described in Bonaldo et al., (1996) Genome
                Research 6: 791-806."
ORIGIN
    Query Match 78.2%; Score 17.2; DB 3; Length 682;
    Best Local Similarity 86.4%; Pred. No. 3e+03;
    Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCCCTTCGGGGGTGCTC 22
|||||
DB 204 GAAAGGCCGTAGGGGATGCTC 183

RESULT 85
AM029523/c
LOCUS AM029523 692 bp mRNA linear EST 30-JUN-2005
DEFINITION Chlamydomonas reinhardtii CC-1690 (mt+) & 6145c (CC-1691
(sequence), Lambda Zap II Chlamydomonas reinhardtii cDNA clone
ACCESSION AM029523
VERSION AM029523
KEYWORDS EST.
SOURCE Bos indicus (Bos taurus indicus)
ORGANISM Bos indicus
REFERENCE 1 (bases 1 to 682)
AUTHORS Kirkness,E.F., Bafna V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
FEATURES
    source
        Location/Qualifiers
            1..692
                /organism="Canis familiaris"
                /mol_type="genomic DNA"
                /strain="Standard Poodle"
                /db_xref="taxon:9615"
                /clone_lib="Dog Library"
                /notes="Site 1: BstXI; Libraries were prepared from
                peripheral blood"
ORIGIN
    Query Match 78.2%; Score 17.2; DB 12; Length 692;
    Best Local Similarity 86.4%; Pred. No. 3e+03;
    Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

REFERENCE 1 (bases 1 to 692)
AUTHORS Anderson,S.I., Taylor,R., Talbot,R., Speed,D., Law,A.S.,
Humphray,S., Hanotte,O., Mwakaya,J. and Archibald,A.L.
TITLE Development of cDNA and EST resources for studying host responses
to trypanosome infection in cattle
JOURNAL Unpublished (2005)
COMMENT Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM.
FEATURES
    source
        Location/Qualifiers
            1..692
                /organism="Bos indicus"
                /mol_type="mRNA"
                /db_xref="taxon:9915"
                /clone="C0007396117"
                /tissue_type="lymph node"
                /clone_lib="KN-252-lymph, Bos indicus"
                /notes="breed: Boran"
ORIGIN
    Query Match 78.2%; Score 17.2; DB 1; Length 692;
    Best Local Similarity 86.4%; Pred. No. 3e+03;
    Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCCCTTCGGGGGTGCTC 22
|||||
DB 275 GAAAGGACCTTCGGGGATGCTC 254

RESULT 86
CE717742/c
LOCUS CE717742 692 bp DNA linear GSS 29-SEP-2003
DEFINITION tigr-gss-dog-17000314584495 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE717742
VERSION CE717742.1 GI:37037180
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
REFERENCE 1 (bases 1 to 692)
AUTHORS Kirkness,E.F., Bafna V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
FEATURES
    source
        Location/Qualifiers
            1..692
                /organism="Canis familiaris"
                /mol_type="genomic DNA"
                /strain="Standard Poodle"
                /db_xref="taxon:9615"
                /clone_lib="Dog Library"
                /notes="Site 1: BstXI; Libraries were prepared from
                peripheral blood"
ORIGIN
    Query Match 78.2%; Score 17.2; DB 12; Length 692;
    Best Local Similarity 86.4%; Pred. No. 3e+03;
    Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY	1 GAAAGGCGCTTCGGGGTGCTC 22																			
Db	128 GAAAGGCGCTTCGGGGTGCTC 107																			
RESULT 87	DT891101/c																			
LOCUS	1472214 MARC 7BOV Bos taurus cDNA 5', mRNA linear EST 19-SEP-2005																			
DEFINITION	DT891101																			
ACCESSION	DT891101.1 GI:75871508																			
VERSION	EST.																			
KEYWORDS	Bos taurus (cattle)																			
SOURCE	Bos taurus																			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.																			
REFERENCE	1 (bases 1 to 700)																			
AUTHORS	Smith, T.P.L., Roberts, A.J., Echterkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.																			
TITLE	A second set of bovine ESTs from pooled-tissue normalized libraries																			
JOURNAL	Unpublished (2003)																			
COMMENT	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross match v0.990329. Plates: QQP8030 row: B column: 10 Seq primer: GTAATAGCACTCACTATAGG.																			
FEATURES	Location/Qualifiers																			
source	1..700																			

```

Best Local Similarity 86.4%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCGCTTTCGGGGGTGCTC 22
||||| ||||| ||||| ||||| ||
Db 734 GAAAGGACTTTCGGGGGTGCTC 713

RESULT 90
DT889744
LOCUS DT889744 749 bp mRNA linear EST 19-SEP-2005
DEFINITION 1470678 MARC 7BOV Bos taurus cDNA 3', mRNA sequence.
ACCESSION DT889744
VERSION DT889744.1 GI:75870151
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 749)
AUTHORS Smith,T.P.L., Roberts,A.J., Echtenkamp,S.E., Chitko-McKown,C.G.,
Wray,J.E. and Keele,J.W.
TITLE A second set of bovine ESTs from pooled-tissue normalized libraries
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329.
Plate: QOP8030 row: B column: 10
Seq primer: TAGAAGCAGACATCGAGG.
Location/Qualifiers
1..749
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH108"
/clone_lib="MARC 7BOV"
/notes="Vector; pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including ovary, hindbrain, uterus, and day-30 whole
embryos."

ORIGIN
Query Match 78.2%; Score 17.2; DB 10; Length 749;
Best Local Similarity 86.4%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCGCTTTCGGGGGTGCTC 22
||||| ||||| ||||| ||||| ||
Db 386 GAAGGACCTTTCGGGGGTGCTC 407

RESULT 91
BP766344
LOCUS BP766344 756 bp mRNA linear EST 02-DEC-2004
DEFINITION BP766344 mouse (C57BL/6) pancreatic islet library with
recombination-based method Mus musculus cDNA clone mid10071 5',
mRNA sequence.
ACCESSION BP766344
VERSION BP766344.1 GI:50225042
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

```

```

REFERENCE 1 (bases 1 to 756)
AUTHORS Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
TITLE Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
JOURNAL DNA Res. 11 (5), 315-323 (2004)
PUBMED 15747579
COMMENT Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.
Location/Qualifiers
1..756
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="mid10071"
/sex="male"
/tissue_type="pancreatic islet"
/dev_stage="adult"
/clone_lib="mouse (C57BL/6) pancreatic islet library with
recombination-based method"

ORIGIN
Query Match 78.2%; Score 17.2; DB 3; Length 756;
Best Local Similarity 86.4%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCGCTTTCGGGGGTGCTC 22
||||| ||||| ||||| ||||| ||
Db 577 GAAAGGCGCTTTCGGATGAGCTC 598

RESULT 92
DN542745/c
LOCUS DN542745 773 bp mRNA linear EST 11-MAR-2005
DEFINITION 1391525 MARC 7BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION DN542745
VERSION DN542745.1 GI:61001051
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 773)
AUTHORS Smith,T.P.L., Roberts,A.J., Echtenkamp,S.E., Chitko-McKown,C.G.,
Wray,J.E. and Keele,J.W.
TITLE A second set of bovine ESTs from pooled-tissue normalized libraries
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329.
Plate: RLK8071 row: J column: 24
Seq primer: GTAATAGGACTCATTATAGG.
Location/Qualifiers
1..773
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH108"
/clone_lib="MARC 7BOV"

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Xenopus; Silurana.

REFERENCE
AUTHORS 1 (bases 1 to 785)
TITLE Richardson, P., Lucas, S., Rokhsar, D., Detter, J.C., Ng, D.C., Brokstein, P., and Lindquist, E.A.
JOURNAL DOE Joint Genome Institute Xenopus tropicalis EST project
COMMENT Unpublished (2004)
On Feb 4, 2005 this sequence version replaced gi:58626852.
Other ESTs: JGI CAAM1558.fwd
DOE Joint Genome Institute
Contact: Lindquist, E.A., Richardson, P.
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory, University of California, Berkeley)
http://tropicalis.berkeley.edu/home
cDNA Library Preparation: DOE Joint Genome Institute:
http://www.jgi.doe.gov
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Clone Distribution: I.M.A.G.E. Consortium/LLNL:
http://image.llnl.gov
Naming Conventions: EST name is generated by the concatenation of the JGI Clone id and the direction of sequencing. The suffix '.rev' indicates a reverse sequencing read of the insert. It does not necessarily reflect the orientation of the insert.
Plate: CAAM 0017 row: k column: 5
High quality sequence stop: 691
POLYA=Yes.

FEATURES

source
1. .785
Location/Qualifiers
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:7675903"
/sex="male"
/tissue_type="Testes"
/dev_stage="Adult"
/lab_host="Electromax DH10B"
/clone_lib="NIH_XGC_crypt3"
/notes="vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
This library was made from dt primed cDNA and cloned into Invitrogen pCMVSPORT6 vector. The work was done at DOE Joint Genome Institute. Poly A RNA were primed with 5' GACTAGTCTAGATCGGAG CGGCCGCCCTTTTCTTTT 3'. cDNA were ligated to SalI adapter (5' TCGACCCACGGTCCG and 5' CGGAGCGTGGG), digested with NotI, size fractionated in 1.1% agarose gel electrophoresis and ligated into NotI and SalI digested pCMVSPORT6 vector."

ORIGIN

Query Match 78.2%; Score 17.2; DB 9; Length 785;
Best Local Similarity 86.4%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAGGCGCTTCGGGGTGCTC 22
Db 493 GAAGGCGCTTCGGGGTGCTC 514

RESULT 96

DN524756
LOCUS DN524756 800 bp mRNA linear EST 11-MAR-2005
DEFINITION 1268443 MARC 7BOV Bos taurus cDNA 3', mRNA sequence.
ACCESSION DN524756
VERSION DN524756.1 GI:60969064
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

REFERENCE
AUTHORS 1 (bases 1 to 800)
TITLE Smith, T.P.L., Roberts, A.J., Echterkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.
JOURNAL A second set of bovine ESTs from pooled-tissue normalized libraries
COMMENT Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329.
Plate: RLK8048 row: A column: 22
Seq primer: TAGAAGGCACAGTCGAGG.

FEATURES

source
1. .800
Location/Qualifiers
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 7BOV"
/notes="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues including ovary, hindbrain, uterus, and day-30 whole embryos."

ORIGIN

Query Match 78.2%; Score 17.2; DB 9; Length 800;
Best Local Similarity 86.4%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCGCTTCGGGGTGCTC 22
Db 428 GAAGGACCTTCGGGGTGCTC 449

RESULT 97

CA315865
LOCUS CA315865 806 bp mRNA linear EST 09-JUL-2003
DEFINITION UI-M-FWO-cbo-e-01-0-UI-r1 NIH_BMAP_FWO Mus musculus cDNA clone
IMAGE:6812234 5', mRNA sequence.
ACCESSION CA315865
VERSION CA315865.1 GI:245333999
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

FEATURES

source
1. .806
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"

Seq primer: pYX-5.

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/strain="CS7BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6812234"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DHI0B (T1 phage resistant)"
/clone_lib="NIH_BMAP_FW0"
/notes="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bernaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN
Query Match 78.2%; Score 17.2; DB 4; Length 806;
Best Local Similarity 86.4%; Pred. No. 3e+03; 3; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGCTC 22
|||||
Db 138 GAAAGGCTTTCGGATGAGCTC 159

RESULT 98
BP434131/c
LOCUS
DEFINITION
BP434131 full-length enriched swine cDNA library, adult lung Sus
scrofa cDNA clone LNG010001B03 5', mRNA sequence.
ACCESSION
BP434131.1 GI:40424198
VERSION
EST.
KEYWORDS
Sus scrofa (pig)
SOURCE
Sus scrofa
ORGANISM
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 829)
Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H., Okumura,N., Hamasima,N. and Awata,T.
PEDE (Pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries
Nucleic Acids Res. 32 (1), D484-D488 (2004)
PUBMED
14681463
COMMENT
Contact: Hirohide Uenishi
Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Fax: +81-29-838-8627
Email: huenishi@affrc.go.jp
EST project with full-length enriched cDNA libraries carried out in Animal Genome Research Program (Japan) by National Institute of Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA library
Vector sequences were eliminated by RepeatMasker version 2002/07/13 and crossmatch version 0.990319
Low quality bases were trimmed based on the quality values.

FEATURES
Location/Qualifiers
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/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"

ORIGIN
Query Match 78.2%; Score 17.2; DB 3; Length 829;
Best Local Similarity 86.4%; Pred. No. 3e+03; 3; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGCTC 22
|||||
Db 304 GAAAGGCCATTTCAGGGTGCTC 283

RESULT 99
BZ654405/c
LOCUS
DEFINITION
BZ654405 848 bp DNA linear GSS 29-JAN-2003
genomic survey sequence.
ACCESSION
BZ654405
VERSION
BZ654405.1 GI:28123665
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 848)
White, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
COMMENT
Other GSSs: OGCGG58TM
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: methylation filtered.
Location/Qualifiers
1..848
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0139J19"
/clone_lib="ZM_0.7-1.5_KB"
/notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"

ORIGIN
Query Match 78.2%; Score 17.2; DB 12; Length 848;
Best Local Similarity 86.4%; Pred. No. 3e+03; 3; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGCTC 22
|||||
Db 210 GAGAGGCCGTTTCGGGGTGCTC 189

RESULT 100
CV069365/c
LOCUS
DEFINITION
CV069365 849 bp mRNA linear EST 24-AUG-2004
WPABHx1516F2_B01_430068T7_A1_001.ab1 Preamplified custom cDNA library in pCMVSPORT6.1 (ResGen, Invitrogen Inc.) Emiliania huxleyi cDNA, mRNA sequence.
ACCESSION
CV069365
VERSION
CV069365.1 GI:51532529

```

KEYWORDS EST.
SOURCE Emiliana huxleyi
ORGANISM Emiliana huxleyi
REFERENCE Eukaryota; Haptophyceae; Isochrysidales; Emiliana.
1 (bases 1 to 849)
AUTHORS Wahland, F.W., Zhang, X. and Read, B.A.
TITLE Expressed Sequence Tag Profiles from Calcifying and Non-Calcifying
Cultures of Emiliana huxleyi
JOURNAL Micropaleontology (2004) In press
COMMENT Contact: Betsy Read
Department of Biological Sciences
California State University San Marcos
333 S. Twin Oaks Valley Road, San Marcos, CA 92096-0001, USA
Tel: 760 750 4129
Email: bread@csusm.edu.

FEATURES
source
1..849
/organism="Emiliana huxleyi"
/mol_type="mRNA"
/strain="1516"
/db_xref="taxon:2903"
/dev_stage="Late log growth phase"
/clone_lib="Preamplified custom cDNA library in
pcwvspor6.1 (ResGen, Invitrogen Inc.)"
/notes="Emiliana huxleyi grown in Artificial Seawater
(Guillard's F/2 media)."

ORIGIN
Query Match 78.2%; Score 17.2; DB 8; Length 849;
Best Local Similarity 86.4%; Fred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GAAAGGCGCTTTTCGGGGGTGCTC 22
||| ||||| ||||| |||||
Db 609 GAATGGCGCTTTCGAGGGGGCTC 588

Search completed: May 19, 2006, 07:06:39
Job time : 1492.35 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 18, 2006, 23:59:38 ; Search time 67.3253 Seconds
(without alignments)
611.425 Million cell updates/sec

Title: US-10-665-708-25

Perfect score: 22

Sequence: 1 gaaagccttcgggggtgctc 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 93554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Issued Patents NA:*

- 1: /EMC Celerra_SIDS3/ptodata/2/ina/1 COMB.seq:*
- 2: /EMC Celerra_SIDS3/ptodata/2/ina/5 COMB.seq:*
- 3: /EMC Celerra_SIDS3/ptodata/2/ina/6A COMB.seq:*
- 4: /EMC Celerra_SIDS3/ptodata/2/ina/6B COMB.seq:*
- 5: /EMC Celerra_SIDS3/ptodata/2/ina/7 COMB.seq:*
- 6: /EMC Celerra_SIDS3/ptodata/2/ina/H COMB.seq:*
- 7: /EMC Celerra_SIDS3/ptodata/2/ina/PTUS COMB.seq:*
- 8: /EMC Celerra_SIDS3/ptodata/2/ina/PP COMB.seq:*
- 9: /EMC Celerra_SIDS3/ptodata/2/ina/RE COMB.seq:*
- 10: /EMC Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	3	US-09-738-274-25
2	22	100.0	25	3	US-09-738-274-26
C 3	17.8	80.9	513	3	US-09-270-767-8270
C 4	17.8	80.9	513	3	US-09-270-767-8270
C 5	17.4	79.1	4637	3	US-09-221-017B-818
C 6	16.8	76.4	276	3	US-09-252-991A-15626
C 7	16.2	73.6	601	3	US-09-949-016-194496
C 8	16.2	73.6	601	3	US-09-949-016-194497
C 9	16.2	73.6	601	3	US-09-949-016-195241
C 10	16.2	73.6	771	3	US-09-252-991A-1476
C 11	16.2	73.6	828	3	US-09-252-991A-1701
C 12	16.2	73.6	909	3	US-09-573-080A-342
C 13	16.2	73.6	909	5	US-09-854-867-342
C 14	16.2	73.6	1239	3	US-09-252-991A-1603
C 15	16.2	73.6	8412	3	US-09-976-594-560
C 16	16.2	73.6	8412	3	US-09-919-039-223
C 17	16.2	73.6	28378	3	US-09-949-016-17281
C 18	16.2	73.6	119032	3	US-09-949-016-12160
C 19	16.2	73.6	119032	3	US-09-949-016-17268
C 20	16.2	73.6	4403765	3	US-09-103-840A-2
C 21	16.2	73.6	4411529	3	US-09-103-840A-1
C 22	15.8	71.8	579	3	US-09-328-352-161
C 23	15.8	71.8	601	3	US-09-949-016-54878

C 24	15.8	71.8	17879	3	US-09-949-016-13325	Sequence 13325, A
C 25	15.6	70.9	479	3	US-09-471-276-779	Sequence 779, App
C 26	15.6	70.9	601	3	US-09-949-016-47594	Sequence 47594, A
C 27	15.6	70.9	601	3	US-09-949-016-83107	Sequence 83107, A
C 28	15.6	70.9	601	3	US-09-949-016-107747	Sequence 107747, A
C 29	15.6	70.9	601	3	US-09-949-016-107748	Sequence 107748, A
C 30	15.6	70.9	601	3	US-09-949-016-146881	Sequence 146881, A
C 31	15.6	70.9	601	3	US-09-949-016-166269	Sequence 166269, A
C 32	15.6	70.9	893	3	US-09-247-155-44	Sequence 44, Appl
C 33	15.6	70.9	893	3	US-09-903-190-44	Sequence 44, Appl
C 34	15.6	70.9	1098	3	US-09-748-264A-1	Sequence 1, Appli
C 35	15.6	70.9	1247	3	US-08-647-960-1	Sequence 1, Appli
C 36	15.6	70.9	1410	5	US-09-974-300-666	Sequence 666, App
C 37	15.6	70.9	1429	3	US-09-023-655-689	Sequence 689, App
C 38	15.6	70.9	1449	3	US-09-489-039A-2738	Sequence 2738, Ap
C 39	15.6	70.9	1746	3	US-09-422-936-58	Sequence 58, Appl
C 40	15.6	70.9	1862	3	US-10-104-047-900	Sequence 900, App
C 41	15.6	70.9	1990	3	US-09-016-434-1056	Sequence 1056, Ap
C 42	15.6	70.9	2297	4	US-10-094-749-421	Sequence 421, App
C 43	15.6	70.9	2895	3	US-09-422-936-52	Sequence 52, Appl
C 44	15.6	70.9	3995	3	US-09-917-254-18	Sequence 18, Appl
C 45	15.6	70.9	3995	3	US-09-919-497-9	Sequence 9, Appli
C 46	15.6	70.9	20076	3	US-09-949-016-13141	Sequence 13141, A
C 47	15.6	70.9	25973	3	US-09-949-016-14140	Sequence 14140, A
C 48	15.6	70.9	37059	3	US-09-949-016-15865	Sequence 15865, A
C 49	15.6	70.9	83516	3	US-09-949-016-15378	Sequence 15378, A
C 50	15.6	70.9	234884	3	US-09-949-016-16420	Sequence 16420, A
C 51	15.6	70.9	390890	3	US-09-949-016-14720	Sequence 14720, A
C 52	15.4	70.0	383	3	US-09-497-855A-43	Sequence 43, Appl
C 53	15.4	70.0	668	3	US-09-533-559-4582	Sequence 4582, Ap
C 54	15.4	70.0	14438	3	US-09-949-016-12300	Sequence 12300, A
C 55	15.4	70.0	60990	3	US-09-949-016-14080	Sequence 14080, A
C 56	15.4	70.0	60990	3	US-09-949-016-14080	Sequence 14080, A
C 57	15.2	69.1	600	3	US-09-370-838-264	Sequence 264, App
C 58	15.2	69.1	600	3	US-09-854-133-264	Sequence 264, App
C 59	15.2	69.1	601	3	US-09-949-016-76799	Sequence 76799, A
C 60	15.2	69.1	833	2	US-08-343-443B-97	Sequence 97, Appl
C 61	15.2	69.1	931	3	US-09-902-540-4292	Sequence 4292, Ap
C 62	15.2	69.1	1185	3	US-09-252-991A-7914	Sequence 7914, Ap
C 63	15.2	69.1	1320	3	US-09-248-796A-1866	Sequence 1866, Ap
C 64	15.2	69.1	1347	3	US-09-252-991A-7842	Sequence 7842, Ap
C 65	15.2	69.1	1738	4	US-10-056-790-15	Sequence 15, Appl
C 66	15.2	69.1	1738	4	US-10-056-790-35	Sequence 35, Appl
C 67	15.2	69.1	1794	3	US-08-920-270-1	Sequence 1, Appli
C 68	15.2	69.1	1794	5	US-10-229-346-12	Sequence 12, Appl
C 69	15.2	69.1	1797	5	US-10-229-346-20	Sequence 20, Appl
C 70	15.2	69.1	1801	5	US-10-229-346-6	Sequence 6, Appli
C 71	15.2	69.1	1803	5	US-10-229-346-3	Sequence 3, Appli
C 72	15.2	69.1	1807	5	US-10-229-346-8	Sequence 8, Appli
C 73	15.2	69.1	1813	5	US-10-229-346-16	Sequence 16, Appl
C 74	15.2	69.1	1816	5	US-10-229-346-14	Sequence 14, Appl
C 75	15.2	69.1	1818	5	US-10-229-346-10	Sequence 10, Appl
C 76	15.2	69.1	1819	5	US-10-229-346-18	Sequence 18, Appl
C 77	15.2	69.1	1830	4	US-10-094-749-1246	Sequence 1246, Ap
C 78	15.2	69.1	1957	2	US-08-295-060-3	Sequence 3, Appli
C 79	15.2	69.1	2198	3	US-09-774-528-10	Sequence 10, Appl
C 80	15.2	69.1	2198	3	US-10-120-988-10	Sequence 10, Appl
C 81	15.2	69.1	2229	3	US-09-252-991A-7718	Sequence 7718, Ap
C 82	15.2	69.1	2256	3	US-09-774-528-11	Sequence 11, Appl
C 83	15.2	69.1	2256	3	US-10-120-988-11	Sequence 11, Appl
C 84	15.2	69.1	2426	3	US-09-028-327-2	Sequence 2, Appli
C 85	15.2	69.1	2426	3	US-09-571-078A-2	Sequence 2, Appli
C 86	15.2	69.1	2453	3	US-09-949-016-2230	Sequence 2230, Ap
C 87	15.2	69.1	2511	3	US-09-489-039A-530	Sequence 444, App
C 88	15.2	69.1	2742	3	US-09-489-039A-444	Sequence 444, App
C 89	15.2	69.1	2770	3	US-09-008-697A-13	Sequence 13, Appl
C 90	15.2	69.1	3124	3	US-09-949-016-5461	Sequence 5461, Ap
C 91	15.2	69.1	3271	3	US-09-865-879-6	Sequence 6, Appli
C 92	15.2	69.1	4522	3	US-09-949-016-4008	Sequence 4008, Ap
C 93	15.2	69.1	6454	3	US-09-949-016-13972	Sequence 13972, A
C 94	15.2	69.1	7208	5	US-10-229-346-5	Sequence 5, Appli
C 95	15.2	69.1	12723	3	US-09-949-016-14771	Sequence 14771, A
C 96	15.2	69.1	13438	3	US-09-949-016-16808	Sequence 16808, A

C 97	15.2	69.1	16287	3	US-09-949-016-17203	Sequence 17203, A	170	14.6	66.4	251	4	US-09-297-648-351	Sequence 351, App
C 98	15.2	69.1	20250	3	US-09-902-540-1213	Sequence 1213, App	C 171	14.6	66.4	254	3	US-09-513-9990-30679	Sequence 30679, A
C 99	15.2	69.1	20444	3	US-09-949-016-15750	Sequence 15750, A	C 172	14.6	66.4	260	4	US-09-297-648-460	Sequence 460, App
C 100	15.2	69.1	21831	3	US-09-949-016-15330	Sequence 15330, A	C 173	14.6	66.4	270	3	US-09-313-294A-1466	Sequence 1466, App
C 101	15.2	69.1	30569	3	US-09-949-016-12592	Sequence 12592, A	C 174	14.6	66.4	565	5	US-09-974-300-6342	Sequence 6342, App
C 102	15.2	69.1	32594	3	US-09-949-016-12219	Sequence 12219, A	C 175	14.6	66.4	601	3	US-09-949-016-17981	Sequence 17981, A
C 103	15.2	69.1	32658	3	US-09-949-016-16242	Sequence 16242, A	C 176	14.6	66.4	601	3	US-09-949-016-40574	Sequence 40574, A
C 104	15.2	69.1	35784	3	US-09-949-016-16785	Sequence 16785, A	C 177	14.6	66.4	601	3	US-09-949-016-40575	Sequence 40575, A
C 105	15.2	69.1	35784	3	US-09-949-016-16786	Sequence 16786, A	C 178	14.6	66.4	601	3	US-09-949-016-40576	Sequence 40576, A
C 106	15.2	69.1	35881	3	US-08-311-731A-127	Sequence 127, App	C 179	14.6	66.4	601	3	US-09-949-016-40577	Sequence 40577, A
C 107	15.2	69.1	45587	3	US-09-949-016-15836	Sequence 15836, A	C 180	14.6	66.4	601	3	US-09-949-016-40578	Sequence 40578, A
C 108	15.2	69.1	51719	3	US-09-918-686-2	Sequence 2, Appli	C 181	14.6	66.4	601	3	US-09-949-016-55749	Sequence 55749, A
C 109	15.2	69.1	59076	3	US-09-949-016-15097	Sequence 15097, A	C 182	14.6	66.4	601	3	US-09-949-016-55749	Sequence 55749, A
C 110	15.2	69.1	79787	3	US-09-949-016-13637	Sequence 13637, A	C 183	14.6	66.4	601	3	US-09-949-016-95005	Sequence 95005, A
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C 115	15	68.2	601	3	US-09-949-016-67429	Sequence 67429, A	C 188	14.6	66.4	601	3	US-09-949-016-117440	Sequence 117440, A
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C 121	14.8	67.3	39725	3	US-09-949-016-39725	Sequence 39725, A	C 194	14.6	66.4	601	3	US-09-949-016-177762	Sequence 177762, A
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C 123	14.8	67.3	601	3	US-09-949-016-44241	Sequence 44241, A	C 196	14.6	66.4	601	3	US-09-949-016-181733	Sequence 181733, A
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C 125	14.8	67.3	601	3	US-09-949-016-70021	Sequence 70021, A	C 198	14.6	66.4	601	3	US-09-949-016-181852	Sequence 181852, A
C 126	14.8	67.3	601	3	US-09-949-016-70022	Sequence 70022, A	C 199	14.6	66.4	601	3	US-09-949-016-181970	Sequence 181970, A
C 127	14.8	67.3	601	3	US-09-949-016-177215	Sequence 177215, A	C 200	14.6	66.4	601	3	US-09-949-016-181971	Sequence 181971, A
C 128	14.8	67.3	636	4	US-09-605-703B-2657	Sequence 2657, App	C 201	14.6	66.4	601	3	US-09-949-016-194577	Sequence 194577, A
C 129	14.8	67.3	696	3	US-09-252-991A-13687	Sequence 13687, A	C 202	14.6	66.4	601	3	US-09-949-016-194578	Sequence 194578, A
C 130	14.8	67.3	804	3	US-09-773-748-2	Sequence 2, Appli	C 203	14.6	66.4	655	3	US-09-533-559-3387	Sequence 199356, A
C 131	14.8	67.3	804	3	US-10-327-726-2	Sequence 2, Appli	C 204	14.6	66.4	721	3	US-09-533-559-5117	Sequence 3387, App
C 132	14.8	67.3	950	3	US-09-484-970B-31	Sequence 31, Appl	C 205	14.6	66.4	759	3	US-09-543-681A-2176	Sequence 2176, App
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C 136	14.8	67.3	1976	4	US-10-094-749-1455	Sequence 1465, App	C 209	14.6	66.4	1075	3	US-09-276-531-95	Sequence 95, Appli
C 137	14.8	67.3	1980	3	US-09-252-991A-13782	Sequence 13782, A	C 210	14.6	66.4	1485	3	US-09-252-991A-15968	Sequence 15968, A
C 138	14.8	67.3	2242	3	US-09-620-312D-15	Sequence 15, Appl	C 211	14.6	66.4	1330	2	US-08-933-750C-80	Sequence 80, Appl
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C 141	14.8	67.3	5693	3	US-09-262-537-19	Sequence 19, Appl	C 214	14.6	66.4	1473	3	US-09-902-540-9684	Sequence 9684, App
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C 143	14.8	67.3	23673	3	US-09-773-816-1	Sequence 1, Appli	C 216	14.6	66.4	1558	3	US-09-311-021-79	Sequence 79, Appli
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C 147	14.8	67.3	71989	3	US-09-724-876-2	Sequence 2, Appli	C 220	14.6	66.4	1662	3	US-10-090-190-1	Sequence 1, Appli
C 148	14.8	67.3	81681	3	US-09-949-016-13274	Sequence 13274, A	C 221	14.6	66.4	1662	3	US-10-082-902-1	Sequence 1, Appli
C 149	14.8	67.3	98037	3	US-09-949-016-16623	Sequence 16623, A	C 222	14.6	66.4	1888	3	US-09-799-451-438	Sequence 438, App
C 150	14.8	67.3	102008	3	US-09-949-016-16623	Sequence 16617, A	C 223	14.6	66.4	1764	3	US-09-815-923-3	Sequence 3, Appli
C 151	14.8	67.3	126468	3	US-09-949-016-14418	Sequence 14418, A	C 224	14.6	66.4	1784	3	US-09-073-009-102	Sequence 102, App
C 152	14.8	67.3	131724	3	US-09-949-016-12893	Sequence 12893, A	C 225	14.6	66.4	1784	3	US-09-073-010-102	Sequence 102, App
C 153	14.8	67.3	134890	3	US-09-949-016-15602	Sequence 15602, A	C 226	14.6	66.4	1863	3	US-09-902-540-1919	Sequence 1919, App
C 154	14.8	67.3	136264	3	US-09-949-016-12756	Sequence 12756, A	C 227	14.6	66.4	1947	5	US-10-128-713A-1	Sequence 1, Appli
C 155	14.8	67.3	136285	3	US-09-949-016-13001	Sequence 13001, A	C 228	14.6	66.4	2121	3	US-09-303-518D-257	Sequence 257, App
C 156	14.8	67.3	168971	3	US-09-949-016-13807	Sequence 13807, A	C 229	14.6	66.4	2178	4	US-10-094-749-718	Sequence 718, App
C 157	14.8	67.3	194714	3	US-09-949-016-11869	Sequence 11869, A	C 230	14.6	66.4	2200	3	US-10-104-047-1287	Sequence 1287, App
C 158	14.8	67.3	196714	3	US-09-949-016-15474	Sequence 15474, A	C 231	14.6	66.4	2425	7	US-08-132-990A-3	Sequence 3, Appli
C 159	14.8	67.3	235033	5	US-08-852-495C-1	Sequence 1, Appli	C 232	14.6	66.4	2425	7	US-08-852-495C-3	Sequence 3, Appli
C 160	14.8	67.3	237326	5	US-08-852-495C-2	Sequence 2, Appli	C 233	14.6	66.4	2493	3	US-08-804-439A-11	Sequence 11, Appl
C 161	14.8	67.3	246240	2	US-08-724-394A-20	Sequence 20, Appl	C 234	14.6	66.4	2493	3	US-08-720-229-11	Sequence 11, Appl
C 162	14.8	67.3	246240	2	US-08-724-394A-21	Sequence 21, Appl	C 235	14.6	66.4	2944	3	US-10-104-047-976	Sequence 976, App
C 163	14.8	67.3	246240	2	US-08-724-394A-22	Sequence 22, Appl	C 236	14.6	66.4	3397	3	US-09-949-016-21888	Sequence 2188, App
C 164	14.8	67.3	385136	3	US-09-949-016-16073	Sequence 16073, A	C 237	14.6	66.4	4352	3	US-09-620-312D-555	Sequence 555, App
C 165	14.8	67.3	4403765	3	US-09-103-840A-1	Sequence 2, Appli	C 238	14.6	66.4	6291	3	US-09-976-594-1039	Sequence 1039, App
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C 168	14.6	66.4	239	4	US-09-297-648-1435	Sequence 1435, App	C 241	14.6	66.4	13533	3	US-09-949-016-17162	Sequence 17162, A
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US-09-949-016-110211

ALIGNMENTS

RESULT 1
US-09-738-274-25
; Sequence 25, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc

; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GPI07-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-25

Query Match 100.0%; Score 22; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.088;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTTCGGGGTGCTC 22

Db 1 GAAAGGCTTTTCGGGGTGCTC 22

RESULT 2

US-09-738-274-26
; Sequence 26, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GPI07-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-26

Query Match 100.0%; Score 22; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTTCGGGGTGCTC 22

Db 1 GAAAGGCTTTTCGGGGTGCTC 22

RESULT 3

US-09-270-767-8270/c
; Sequence 8270, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8270
; LENGTH: 513
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-8270

Query Match 80.9%; Score 17.8; DB 3; Length 513;
Best Local Similarity 90.5%; Pred. No. 19;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 383 ACAGGCCTTTCGGGTGGTCTC 363

RESULT 4
US-09-270-767-23552/c
; Sequence 23552, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23552
; LENGTH: 513
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-23552

Query Match 80.9%; Score 17.8; DB 3; Length 513;
Best Local Similarity 90.5%; Pred. No. 19;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTCGGGGTGCTC 22
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Db 383 ACAGGCCTTTCGGGTGGTCTC 363

RESULT 5
US-09-221-017B-818/c
; Sequence 818, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Ross, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221,017B
; FILING DATE: 23-DEC-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: Pp1182
; FILING DATE: 31-DEC-1997
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: Pp1546
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA: Pp2911
; APPLICATION NUMBER: Pp2911
; FILING DATE: 09-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU98/01023
; FILING DATE: 10-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Monroy, Gladys H
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 27340-20021.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141

; INFORMATION FOR SEQ ID NO: 818:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4637 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: UNKNOWN
; ORIGINAL SOURCE:
; ORGANISM: PORYPHYROMONAS GINGIVALIS
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1...4637
US-09-221-017B-818

Query Match 79.1%; Score 17.4; DB 3; Length 4637;
Best Local Similarity 94.7%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTCGGGGGTG 19
| | | | | | | | | | | | | | | | | | | | | |
Db 4588 GAAAGGCCTTTCGGGGGTG 4570

RESULT 6
US-09-252-991A-15626/c
; Sequence 15626, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15626
; LENGTH: 276
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15626

Query Match 76.4%; Score 16.8; DB 3; Length 276;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTCGGGGTGCT 21
| | | | | | | | | | | | | | | | | | | | | |
Db 87 AAAGGCCTTTCGTAGTGCT 68

RESULT 7

; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190

;
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1701
; LENGTH: 828
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1701

Query Match 73.6%; Score 16.2; DB 3; Length 828;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTCGGGGTGCT 21
||| ||||| ||||| ||||| |||||
DB 226 GAAGGGCTTTCGGCGTGCT 246

RESULT 12

US-09-573-080A-342
; Sequence 342, Application US/09573080A
; Patent No. 6828097
; GENERAL INFORMATION:
; APPLICANT: JOAN, KNOLL
; APPLICANT: ROGAN, PETER
; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
; FILE REFERENCE: 30307
; CURRENT APPLICATION NUMBER: US/09/573,080A
; CURRENT FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 342
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Homo sapiens

;
; FEATURE:
; NAME/KEY: repeat region
; LOCATION: (1)..(909)
; OTHER INFORMATION: l1me3a

;
; NAME/KEY: misc feature
; OTHER INFORMATION: n is a, c, g or t

;
; PUBLICATION INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A

;
; TITLE: Prototypic sequences for human repetitive DNA
; JOURNAL: Journal of Molecular Evolution
; VOLUME: 35

;
; ISSUE: 4
; PAGES: 286-291
; DATE: 1992-10-

;
; DATABASE ACCESSION NUMBER: Database of repetitive elements (repbase)
; DATABASE ENTRY DATE:
; DATABASE ENTRY DATE: 1996-01-26

US-09-573-080A-342

Query Match 73.6%; Score 16.2; DB 3; Length 909;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTCGGGGTGCT 21
||| ||||| ||||| ||||| |||||
DB 762 GAGAGGGCTTTCGGCGTGCT 782

RESULT 13

US-09-854-867-342
; Sequence 342, Application US/09854867
; Patent No. 7014997
; GENERAL INFORMATION:
; APPLICANT: JOAN, KNOLL H
; APPLICANT: ROGAN, PETER K
; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
; FILE REFERENCE: 30307
; CURRENT APPLICATION NUMBER: US/09/854,867

;
; CURRENT FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 613
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 342
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Homo sapiens

;
; FEATURE:
; NAME/KEY: repeat region
; LOCATION: (1)..(909)
; OTHER INFORMATION: l1me3a

;
; NAME/KEY: misc feature
; LOCATION: (647)..(647)
; OTHER INFORMATION: n is a, c, g or t

;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (657)..(658)
; OTHER INFORMATION: n is a, c, g or t

;
; NAME/KEY: misc feature
; LOCATION: (705)..(705)
; OTHER INFORMATION: n is a, c, g or t

US-09-854-867-342

Query Match 73.6%; Score 16.2; DB 5; Length 909;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTCGGGGTGCT 21
||| ||||| ||||| ||||| |||||
DB 762 GAGAGGGCTTTCGGGGTGCT 782

RESULT 14

US-09-252-991A-1603
; Sequence 1603, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1603
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1603

RESULT 15

US-09-976-594-560
; Sequence 560, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

```
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 560
; LENGTH: 8411
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1327024.5
; NAME/KEY: unsure
; LOCATION: 8361, 8372, 8381, 8388, 8398, 8405-8406
; OTHER INFORMATION: a, t, c, g, or other
US-09-976-594-560
```

```
Query Match 73.6%; Score 16.2; DB 3; Length 8411;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 2 AAAGGCTTTTCGGGGTGCTC 22
||| ||||| ||| |||||
Db 4595 AAATGCCTTTGGGGAGTGCTC 4615
```

```
RESULT 16
US-09-919-039-223
; Sequence 223, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 223
; LENGTH: 8412
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 380283.1
; NAME/KEY: unsure
; LOCATION: 4053-4099, 8362, 8373, 8382, 8389, 8406-8407
; OTHER INFORMATION: a, t, c, g, or other
US-09-919-039-223
```

```
Query Match 73.6%; Score 16.2; DB 3; Length 8412;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 2 AAAGGCTTTTCGGGGTGCTC 22
||| ||||| ||| |||||
Db 4595 AAATGCCTTTGGGGAGTGCTC 4615
```

```
RESULT 17
US-09-949-016-17281
; Sequence 17281, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
```

```
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17281
; LENGTH: 28378
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-17281
```

```
Query Match 73.6%; Score 16.2; DB 3; Length 28378;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 GAAAGGCTTTTCGGGGTGCT 21
||| ||||| ||| |||||
Db 18269 GGAAGGCTTTCTGGGGAGCT 18289
```

```
RESULT 18
US-09-949-016-12160
; Sequence 12160, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12160
; LENGTH: 119032
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(119032)
; OTHER INFORMATION: n = A, T, C or G
US-09-949-016-12160
```

```
Query Match 73.6%; Score 16.2; DB 3; Length 119032;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 2 AAAGGCTTTTCGGGGTGCTC 22
||| ||||| ||| |||||
Db 29218 ACAGGCTTTCTGGGGTGCTC 29238
```

```
RESULT 19
US-09-949-016-17268
; Sequence 17268, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
```



```
Query Match      71.8%; Score 15.8; DB 3; Length 601;
Best Local Similarity 89.5%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGGTG 19
    ||||| ||||| ||||| |||||
Db 158 GAAAGGCATTTCGGGGGTG 140

RESULT 24
US-09-949-016-13325/c
; Sequence 13325 Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13325
; LENGTH: 17879
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13325

Query Match      71.8%; Score 15.8; DB 3; Length 17879;
Best Local Similarity 89.5%; Pred. No. 3.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGGTG 19
    ||||| ||||| ||||| |||||
Db 5076 GAAAGGCATTTCGGGGGTG 5058

RESULT 25
US-09-471-276-779/c
; Sequence 779 Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
; FILE REFERENCE: GENSET.025CP1
; CURRENT APPLICATION NUMBER: US/09/471,276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 779
; LENGTH: 479
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 73...429
; NAME/KEY: sig_peptide
```

```
; LOCATION: 73..231
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 5.8000019073486
; OTHER INFORMATION: seq ILSQLVLLTTVTS/TV
US-09-471-276-779

Query Match      70.9%; Score 15.6; DB 3; Length 479;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGGTGCTC 22
    ||||| ||||| ||||| |||||
Db 175 GAAAGGCCATTTCGGATGTGCAC 154

RESULT 26
US-09-949-016-47594/c
; Sequence 47594 Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 47594
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-47594

Query Match      70.9%; Score 15.6; DB 3; Length 601;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGGTGCTC 22
    ||||| ||||| ||||| |||||
Db 170 GCAAGGGCATTTCGGGGGTGCGC 149

RESULT 27
US-09-949-016-83107/c
; Sequence 83107 Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 83107
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-83107
```


RESULT 32
US-09-247-155-44/c
; Sequence 44, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET.021A
; CURRENT APPLICATION NUMBER: US/09/247,155A
; PRIOR FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,121
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/081,563
; EARLIER FILING DATE: 1998-04-13
; EARLIER APPLICATION NUMBER: 60/096,116
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/099,273
; EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm
; SEQ ID NO 44
; LENGTH: 893
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 42..755
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 42..200
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 5.8
; OTHER INFORMATION: seq ILSLQVLLTTVTS/TV
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 860..865
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 878..893
US-09-247-155-44

Query Match 70.9%; Score 15.6; DB 3; Length 893;
Best Local Similarity 81.8%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 GAAAGGCTTTCGGGGTGCTC 22
Db 144 GAAAGGCCATTCGGATGTGCAC 123

RESULT 33
US-09-903-190-44/c
; Sequence 44, Application US/09903190
; Patent No. 6936692
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET.021A
; CURRENT APPLICATION NUMBER: US/09/903,190
; PRIOR FILING DATE: 2001-07-11
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/099,273

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm
; SEQ ID NO 44
; LENGTH: 893
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 42..755
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 42..200
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 5.8
; OTHER INFORMATION: seq ILSLQVLLTTVTS/TV
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 860..865
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 878..893
US-09-903-190-44

Query Match 70.9%; Score 15.6; DB 3; Length 893;
Best Local Similarity 81.8%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTCGGGGTGCTC 22
Db 144 GAAAGGCCATTCGGATGTGCAC 123

RESULT 34
US-09-748-264A-1/c
; Sequence 1, Application US/09748264A
; Patent No. 6642439
; GENERAL INFORMATION:
; APPLICANT: SECRETARY OF AGENCY OF INDUSTRIAL SCIENCE AND TECHNOLOGY
; APPLICANT: Yosuke IIMURA
; TITLE OF INVENTION: A BASIDIOMYCETE PEROXIDASE GENE-TRANSFERRED PLANT AND A METHOD FOR
; FILE REFERENCE: 04853.0050
; CURRENT APPLICATION NUMBER: US/09/748,264A
; CURRENT FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: JP 2000-223653
; PRIOR FILING DATE: 2000-07-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1098
; TYPE: DNA
; ORGANISM: Corioliolus versicolor
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ..(1095)
US-09-748-264A-1

Query Match 70.9%; Score 15.6; DB 3; Length 1098;
Best Local Similarity 81.8%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 GAAAGGCTTTCGGGGTGCTC 22
Db 660 GAAAGGGGTTCCGGGATGTGCTC 639

RESULT 35
US-08-647-960-1/c
; Sequence 1, Application US/08647960
; Patent No. 5908761
; GENERAL INFORMATION:
; APPLICANT: ZICK, Yehiel

```

; TITLE OF INVENTION: GALECTIN-8 AND GALECTIN-8-LIKE PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/647,960
; FILING DATE: 30-MAY-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107880
; FILING DATE: 05-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: ZICK=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3527
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1247 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 121..1068
; US-08-647-960-1

```

```

Query Match      70.9%; Score 15.6; DB 2; Length 1247;
Best Local Similarity 81.8%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY      1 GAAAGGCCTTTCGGGGTGCTC 22
Db      408 GAAAGGCATGTCGTGGTGATC 387

```

```

RESULT 36
US-09-974-300-666
; Sequence 666, Application US/09974300
; Patent No. 7018794
; GENERAL INFORMATION:
; APPLICANT: Berk, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 666
; LENGTH: 1410
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
; US-09-974-300-666

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```

Query Match      70.9%; Score 15.6; DB 5; Length 1410;
Best Local Similarity 81.8%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY      1 GAAAGGCCTTTCGGGGTGCTC 22
Db      390 GAAAGCCTTTCGGGCATGATC 411

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RESULT 37
US-09-023-655-689
; Sequence 689, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 689:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1429 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: TLYMNOT02
; CLONE: 450088
; US-09-023-655-689

```

```

Query Match      70.9%; Score 15.6; DB 3; Length 1429;
Best Local Similarity 81.8%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      1 GAAAGGCCTTTCGGGGTGCTC 22
Db      181 GAAAGCCTTTCGATGGGCTC 202

```

```

RESULT 38
US-09-489-039A-2738
; Sequence 2738, Application US/09489039A
; Patent No. 6610936
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al

```

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 2738

; LENGTH: 1449
; TYPE: DNA

; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-2738

Query Match 70.9%; Score 15.6; DB 3; Length 1449;
Best Local Similarity 81.8%; Pred. No. 3e+02;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTTCGGGGGTGCTC 22

Db 147 GAAAGGCTGCGCGGGTGCTC 168

RESULT 39

US-09-422-936-58
; Sequence 58, Application US/09422936

; Patent No. 6465213
; GENERAL INFORMATION:

; APPLICANT: Ekstrand, Jonas
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES

; FILE REFERENCE: 06275-165002
; CURRENT APPLICATION NUMBER: US/09/422,936

; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US 09/242,608

; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: PCT/SE98/01947

; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9703914-2

; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9800864-2

; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: SWEDEN 9802575-2

; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 85

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58

; LENGTH: 1746
; TYPE: DNA

; ORGANISM: Canis familiaris
; FEATURE:

; NAME/KEY: CDS
; LOCATION: (1)...(1743)

US-09-422-936-58

Query Match 70.9%; Score 15.6; DB 3; Length 1746;
Best Local Similarity 81.8%; Pred. No. 3.1e+02;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTTCGGGGGTGCTC 22

Db 1470 GAGCGCCGTTTCGGGGGTGCGC 1491

RESULT 40

US-10-104-047-900/c

; Sequence 900, Application US/10104047

; Patent No. 6943241
; GENERAL INFORMATION:

; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA

; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047

; CURRENT FILING DATE: 2002-03-25

; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:

; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 900
; LENGTH: 1862

; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-104-047-900

Query Match 70.9%; Score 15.6; DB 3; Length 1862;
Best Local Similarity 81.8%; Pred. No. 3.1e+02;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTTCGGGGGTGCTC 22

Db 793 GAAAGGCTGCGCGGGTTGCGC 772

RESULT 41

US-09-016-434-1056

; Sequence 1056, Application US/09016434

; Patent No. 6500938
; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO
; STATE: CALIFORNIA

; COUNTRY: USA
; ZIP: 94304

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith

; CLASSIFICATION:
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:
; FILING DATE:

; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071

; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166

; INFORMATION FOR SEQ ID NO: 1056:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 1990 base pairs
; TYPE: nucleic acid

; STRANDEDNESS: single
; TOPOLOGY: linear

; IMMEDIATE SOURCE:
; LIBRARY: GENBANK

; CLONE: g1041044
US-09-016-434-1056

Query Match 70.9%; Score 15.6; DB 3; Length 1990;
Best Local Similarity 81.8%; Pred. No. 3.1e+02;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTTCGGGGGTGCTC 22

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```
Db      1197 GAAAGGCCTTTGGGACCTGCTC 1218

RESULT 42
US-10-094-749-421
; Sequence 421, Application US/10094749
; Patent No. 6979557
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 421
; LENGTH: 2297
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-094-749-421

Query Match      70.9%; Score 15.6; DB 4; Length 2297;
Best Local Similarity 81.8%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GAAAGGCCTTTGGGGGTGCTC 22
Db      1277 GAAAGGCCTTTAGAGTGAGCTC 1298

RESULT 43
US-09-422-936-52
; Sequence 52, Application US/09422936
; Patent No. 6465213
; GENERAL INFORMATION:
; APPLICANT: Ekstrand, Jonas
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 06275-165002
; CURRENT APPLICATION NUMBER: US/09/422,936
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US 09/242,608
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: PCT/SE98/01947
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9703914-2
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9800864-2
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: SWEDEN 9802575-2
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0

Db      1197 GAAAGGCCTTTGGGACCTGCTC 1218

Query Match      70.9%; Score 15.6; DB 3; Length 2895;
Best Local Similarity 81.8%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GAAAGGCCTTTGGGGGTGCTC 22
Db      1470 GAGCGGCGGTCGCGGGTGGC 1491

RESULT 44
US-09-917-254-18/c
; Sequence 18, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Baak, Jan
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224(JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 3995
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-917-254-18

Query Match      70.9%; Score 15.6; DB 3; Length 3995;
Best Local Similarity 81.8%; Pred. No. 3.5e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GAAAGGCCTTTGGGGGTGCTC 22
Db      2281 GAAACCCCTTTGGGGTTCCTC 2260

RESULT 45
US-09-919-497-9/c
; Sequence 9, Application US/09919497
; Patent No. 6773883
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 3995
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-497-9

Query Match      70.9%; Score 15.6; DB 3; Length 3995;
Best Local Similarity 81.8%; Pred. No. 3.5e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GAAAGGCCTTTGGGGGTGCTC 22
```

Db 2281 GAAACCCCTTTGGGTGCTC 2260
||||| ||||| ||||| ||||| |||||

RESULT 46

US-09-949-016-13141/c
; Sequence 13141, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13141
; LENGTH: 20076
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13141

Query Match 70.9%; Score 15.6; DB 3; Length 20076;
Best Local Similarity 81.8%; Pred. No. 4.5e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTTCGGGGTGCTC 22
Db 14656 GCAAGGCGATTCGGGGTGCGC 14635
||||| ||||| ||||| ||||| |||||

RESULT 47

US-09-949-016-14140/c
; Sequence 14140, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14140
; LENGTH: 25973
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14140

Query Match 70.9%; Score 15.6; DB 3; Length 25973;
Best Local Similarity 81.8%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTTCGGGGTGCTC 22
Db 20553 GCAAGGCGATTCGGGGTGCGC 20532
||||| ||||| ||||| ||||| |||||

RESULT 48

US-09-949-016-15865
; Sequence 15865, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15865
; LENGTH: 37059
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/Key: misc_feature
; LOCATION: (1)...(37059)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15865

Query Match 70.9%; Score 15.6; DB 3; Length 37059;
Best Local Similarity 81.8%; Pred. No. 5e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTTCGGGGTGCTC 22
Db 10641 GAAAGGCCTTTCGTGCTC 10662
||||| ||||| ||||| ||||| |||||

RESULT 49

US-09-949-016-15378
; Sequence 15378, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15378
; LENGTH: 83516
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15378

Query Match 70.9%; Score 15.6; DB 3; Length 83516;
Best Local Similarity 81.8%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTTCGGGGTGCTC 22
Db 49986 GAAAGCCTTTCGGGTGCTC 50007
||||| ||||| ||||| ||||| |||||

RESULT 50

US-09-949-016-16420


```
; Sequence 16420, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16420
; LENGTH: 234884
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(234884)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16420

Query Match          70.9%; Score 15.6; DB 3; Length 234884;
Best Local Similarity 81.8%; Pred. No. 6.4e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1  GAAAGGCTTTTCGGGGGTGCTC 22
      ||||| ||||| ||||| ||||| |||||
Db      226956  GAATGGGTTTTCGGGGGTGCTC 226977

RESULT 51
US-09-949-016-14720/c
; Sequence 14720, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14720
; LENGTH: 390890
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(390890)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14720

Query Match          70.9%; Score 15.6; DB 3; Length 390890;
Best Local Similarity 81.8%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1  GAAAGGCTTTTCGGGGGTGCTC 22
      ||||| ||||| ||||| ||||| |||||
Db      101368  GAAAGGTTTTCGGGGGTGCC 101347
```

```
RESULT 52
US-09-497-855A-43/c
; Sequence 43, Application US/09497855A
; Patent No. 6605432
; GENERAL INFORMATION:
; APPLICANT: Huang, Tim
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
; FILE REFERENCE: UMO1523
; CURRENT APPLICATION NUMBER: US/09/497,855A
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/120,592
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/118,760
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 383
; TYPE: DNA
; ORGANISM: Homo sapiens;
US-09-497-855A-43

Query Match          70.0%; Score 15.4; DB 3; Length 383;
Best Local Similarity 94.1%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6  GCCTTTCGGGGGTGCTC 22
      ||||| ||||| ||||| |||||
Db      234  GCCTTTAGGGGTGCTC 218

RESULT 53
US-09-533-559-4582
; Sequence 4582, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 5849,200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4582
; LENGTH: 668
; TYPE: DNA
; ORGANISM: Aspergillus oryzae
US-09-533-559-4582

Query Match          70.0%; Score 15.4; DB 3; Length 668;
Best Local Similarity 94.1%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6  GCCTTTCGGGGGTGCTC 22
      ||||| ||||| ||||| |||||
Db      422  GCCTTTCGGGTGCTC 438

RESULT 54
US-09-949-016-12300
; Sequence 12300, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
```

```

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12300
; LENGTH: 14438
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(14438)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12300

Query Match          70.0%; Score 15.4; DB 3; Length 14438;
Best Local Similarity 94.1%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 GCCTTTCGGGGTGCTC 22
Db      5389 GCCTTTCGGGGTGCTC 5405

RESULT 55
US-09-949-016-14080
; Sequence 14080, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14080
; LENGTH: 60990
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (32)
; OTHER INFORMATION: n=A,T,C or G
US-09-949-016-14080

Query Match          70.0%; Score 15.4; DB 3; Length 60990;
Best Local Similarity 94.1%; Pred. No. 6.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GAAAGGCCTTTCGGGGG 17
Db      34457 GAAAGGCCTTTCGGGG 34473

RESULT 56
US-09-949-016-14080/c
; Sequence 14080, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

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; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14080
; LENGTH: 60990
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (32)
; OTHER INFORMATION: n=A,T,C or G
US-09-949-016-14080

Query Match          70.0%; Score 15.4; DB 3; Length 60990;
Best Local Similarity 94.1%; Pred. No. 6.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GAAAGGCCTTTCGGGGG 17
Db      34468 GAAAGGCCTTTCAGGGG 34452

RESULT 57
US-09-370-838-264
; Sequence 264, Application US/09370838
; Patent No. 644425
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raedoh
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
; FILE REFERENCE: 210121.475C1
; CURRENT APPLICATION NUMBER: US/09/370,838
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/285,323
; EARLIER FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 264
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (32)
; OTHER INFORMATION: n=A,T,C or G
US-09-370-838-264

Query Match          69.1%; Score 15.2; DB 3; Length 600;
Best Local Similarity 85.0%; Pred. No. 4.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GAAAGGCCTTTCGGGGTGC 20
Db      120 GAAAGGCCTCTCGAGCTGC 139

RESULT 58
US-09-854-133-264
; Sequence 264, Application US/09854133
; Patent No. 6759508
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raedoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.

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; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 264
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (32)_feature
; OTHER INFORMATION: n=A,T,C or G
US-09-854-133-264

Query Match          69.1%; Score 15.2; DB 3; Length 600;
Best Local Similarity 85.0%; Pred. No. 4.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GAAAGGCCTTCGGGGTGC 20
DB      120 GAAAGGCCTTCGGAGTGC 139

RESULT 59
US-09-949-016-76799
; Sequence 76799, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76799
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-76799

Query Match          69.1%; Score 15.2; DB 3; Length 601;
Best Local Similarity 85.0%; Pred. No. 4.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 AAAGGCCTTCGGGGTGCT 21
DB      209 AAATGCCTTCGAAGTCT 228

RESULT 60
US-08-343-443B-97/C
; Sequence 97, Application US/08343443B
; Patent No. 5968734
; GENERAL INFORMATION:
; APPLICANT: Aurias, Alain
; APPLICANT: Delattre, Olivier
; APPLICANT: Desmaze, Chantal
; APPLICANT: Melot, Thomas
; APPLICANT: Peter, Martine
; APPLICANT: Ploougastel, Beatrice
; APPLICANT: Thomas, Gilles

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; APPLICANT: Zucman, Jessica
; TITLE OF INVENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF
; FILE REFERENCE: CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL
; TITLE OF INVENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS
; TITLE OF INVENTION: TUMORS, AND NUCLEIC ACIDS OF FUSION RESULTING FROM SAID
; NUMBER OF SEQUENCES: 129
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weiser & Associates
; STREET: 230 South Fifteenth Street
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: AEDIT 1.0 DOS text editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/343,443B
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR93/00494
; FILING DATE: 19-MAY-1993
; PRIOR APPLICATION DATA: FR 92/06123
; FILING DATE: 20-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 989.6121P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8393
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 833 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-343-443B-97

Query Match          69.1%; Score 15.2; DB 2; Length 833;
Best Local Similarity 85.0%; Pred. No. 4.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GAAAGGCCTTCGGGGTGC 20
DB      37 GACCGGCCTTCGGGGTGC 18

RESULT 61
US-09-902-540-4292
; Sequence 4292, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 4292
; LENGTH: 931
; TYPE: DNA
; ORGANISM: Myxococcus xanthus

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US-09-902-540-4292

Query Match 69.1%; Score 15.2; DB 3; Length 931;
Best Local Similarity 85.0%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGGCCTTTCGGGGTGCT 21
|||||
Db 664 AAGGCCTTCGGGTGATGCT 683

RESULT 62

US-09-252-991A-7914
; Sequence 7914, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7914
; LENGTH: 1185
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7914

Query Match 69.1%; Score 15.2; DB 3; Length 1185;
Best Local Similarity 85.0%; Pred. No. 4.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGCCTTTCGGGGTGCT 22
|||||
Db 1058 AAGCCTTCGGGTGCTC 1077

RESULT 63

US-09-248-796A-1866
; Sequence 1866, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248.796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR FILING DATE: 1998-02-13
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 1866
; LENGTH: 1320
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-1866

Query Match 69.1%; Score 15.2; DB 3; Length 1320;
Best Local Similarity 85.0%; Pred. No. 4.7e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGCCTTTCGGGGTGCT 22
|||||
Db 500 ATGCCCTTCGGGTGCTC 519

RESULT 64

US-09-252-991A-7642/c
; Sequence 7642, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7642
; LENGTH: 1347
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7642

Query Match 69.1%; Score 15.2; DB 3; Length 1347;
Best Local Similarity 85.0%; Pred. No. 4.7e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGCCTTTCGGGGTGCTC 22
|||||
Db 185 AAGCCTTCGGGTGCTC 166

RESULT 65

US-10-056-790-15
; Sequence 15, Application US/10056790
; Patent No. 6972179
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: RRP SEQUENCES AND KNOCKOUT MICE AND USES THEREOF
; FILE REFERENCE: RRP2002
; CURRENT APPLICATION NUMBER: US/10/056.790
; CURRENT FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: US 09/908,419
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/219,289
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US 60/277,487
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/277,471
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/304,863
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/305,017
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/328,491
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 1738
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-056-790-15

Query Match 69.1%; Score 15.2; DB 4; Length 1738;
Best Local Similarity 85.0%; Pred. No. 4.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGCCTTTCGGGGTGCT 20
|||

Db 144 GACCGGCTTTCGGGGTTC 163

RESULT 66

US-10-056-790-35

; Sequence 35, Application US/10056790

; Patent No. 6972179

; GENERAL INFORMATION:

; APPLICANT: EXELIXIS, INC.

; TITLE OF INVENTION: RRP SEQUENCES AND KNOCKOUT MICE AND USES THEREOF

; FILE REFERENCE: RRPICP2002

; CURRENT APPLICATION NUMBER: US/10/056,790

; CURRENT FILING DATE: 2002-01-23

; PRIOR APPLICATION NUMBER: US 09/908,419

; PRIOR FILING DATE: 2001-07-18

; PRIOR APPLICATION NUMBER: US 60/219,289

; PRIOR FILING DATE: 2000-07-19

; PRIOR APPLICATION NUMBER: US 60/277,487

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: US 60/277,471

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: US 60/304,863

; PRIOR FILING DATE: 2001-07-12

; PRIOR APPLICATION NUMBER: US 60/296,076

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: US 60/305,017

; PRIOR FILING DATE: 2001-07-12

; PRIOR APPLICATION NUMBER: US 60/328,605

; PRIOR FILING DATE: 2001-10-10

; PRIOR APPLICATION NUMBER: US 60/328,491

; PRIOR FILING DATE: 2001-10-10

; NUMBER OF SEQ ID NOS: 70

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 35

; LENGTH: 1738

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-056-790-35

Query Match 69.1%; Score 15.2; DB 4; Length 1738;

Best Local Similarity 85.0%; Pred. No. 4.9e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGC 20

Db 144 GACCGGCTTTCGGGGTTC 163

RESULT 67

US-08-920-270-1/c

; Sequence 1, Application US/08920270A

; Patent No. 6072105

; GENERAL INFORMATION:

; APPLICANT: Jelenkovic, Gojko

; APPLICANT: Billings, Sharon

; TITLE OF INVENTION: Insect-Resistant Transgenic Eggplant and

; TITLE OF INVENTION: Method of Making

; FILE REFERENCE: RUC.96-0630-1

; CURRENT APPLICATION NUMBER: US/08/920,270A

; CURRENT FILING DATE: 1998-08-22

; EARLIER APPLICATION NUMBER: US 60/024,544

; EARLIER FILING DATE: 1997-08-23

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 1794

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: /note = synthetic construct

US-08-920-270-1

Query Match 69.1%; Score 15.2; DB 3; Length 1794;

Best Local Similarity 85.0%; Pred. No. 4.9e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGGCCTTTCGGGGTGCTC 22

Db 185 AAGGCCTTCAGGGGTCTC 166

RESULT 68

US-10-229-346-12/c

; Sequence 12, Application US/10229346

; Patent No. 7030295

; GENERAL INFORMATION:

; APPLICANT: Chen, Eric

; APPLICANT: Stacy, Cheryl

; TITLE OF INVENTION: Modified Cry3A Toxins

; FILE REFERENCE: 60065A

; CURRENT APPLICATION NUMBER: US/10/229,346

; CURRENT FILING DATE: 2002-08-27

; PRIOR APPLICATION NUMBER: 60/316,421

; PRIOR FILING DATE: 2001-08-31

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 12

; LENGTH: 1794

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(1794)

; OTHER INFORMATION: Maize optimized modified cry3A082 coding sequence.

; NAME/KEY: misc feature

; LOCATION: (1609)..(1620)

; OTHER INFORMATION: Cathepsin G recognition site coding sequence

US-10-229-346-12

Query Match 69.1%; Score 15.2; DB 5; Length 1794;

Best Local Similarity 85.0%; Pred. No. 4.9e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGGCCTTTCGGGGTGCTC 22

Db 185 AAGGCCTTCAGGGGTCTC 166

RESULT 69

US-10-229-346-20/c

; Sequence 20, Application US/10229346

; Patent No. 7030295

; GENERAL INFORMATION:

; APPLICANT: Chen, Eric

; APPLICANT: Stacy, Cheryl

; TITLE OF INVENTION: Modified Cry3A Toxins

; FILE REFERENCE: 60065A

; CURRENT APPLICATION NUMBER: US/10/229,346

; CURRENT FILING DATE: 2002-08-27

; PRIOR APPLICATION NUMBER: 60/316,421

; PRIOR FILING DATE: 2001-08-31

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 20

; LENGTH: 1797

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(1791)

; OTHER INFORMATION: Maize optimized modified cry3A083 coding sequence.

; NAME/KEY: misc feature

; LOCATION: (322)..(333)

; OTHER INFORMATION: Cathepsin G recognition site coding sequence.

```
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1612)..(1623)
; OTHER INFORMATION: cathepsin G recognition site coding sequence
US-10-229-346-20

Query Match          69.1%; Score 15.2; DB 5; Length 1797;
Best Local Similarity 85.0%; Pred. No. 4.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGGCCTTTCGGGGTGCTC 22
    |||||  |||||  |||||  |||||
Db 185 AAGCCTTCCAGGGTGCTC 166

RESULT 70
US-10-229-346-6/c
; Sequence 6, Application US/10229346
; Patent No. 7030295
; GENERAL INFORMATION:
; APPLICANT: Chen, Eric
; TITLE OF INVENTION: Modified Cry3A Toxins
; FILE REFERENCE: 60065A
; CURRENT APPLICATION NUMBER: US/10/229,346
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/316,421
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1791)
; OTHER INFORMATION: Maize optimized modified cry3A054 coding sequence.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (322)..(333)
; OTHER INFORMATION: cathepsin G recognition site coding sequence
US-10-229-346-6

Query Match          69.1%; Score 15.2; DB 5; Length 1801;
Best Local Similarity 85.0%; Pred. No. 4.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGGCCTTTCGGGGTGCTC 22
    |||||  |||||  |||||  |||||
Db 185 AAGCCTTCCAGGGTGCTC 166

RESULT 71
US-10-229-346-3/c
; Sequence 3, Application US/10229346
; Patent No. 7030295
; GENERAL INFORMATION:
; APPLICANT: Chen, Eric
; TITLE OF INVENTION: Modified Cry3A Toxins
; FILE REFERENCE: 60065A
; CURRENT APPLICATION NUMBER: US/10/229,346
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/316,421
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1803
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; NAME/KEY: CDS
; LOCATION: (1)..(1794)
; OTHER INFORMATION: Maize optimized cry3A coding sequence
US-10-229-346-3

Query Match          69.1%; Score 15.2; DB 5; Length 1803;
Best Local Similarity 85.0%; Pred. No. 4.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGGCCTTTCGGGGTGCTC 22
    |||||  |||||  |||||  |||||
Db 185 AAGCCTTCCAGGGTGCTC 166

RESULT 72
US-10-229-346-8/c
; Sequence 8, Application US/10229346
; Patent No. 7030295
; GENERAL INFORMATION:
; APPLICANT: Chen, Eric
; TITLE OF INVENTION: Modified Cry3A Toxins
; FILE REFERENCE: 60065A
; CURRENT APPLICATION NUMBER: US/10/229,346
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/316,421
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 1807
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1806)
; OTHER INFORMATION: Maize optimized modified cry3A055 coding sequence.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (322)..(333)
; OTHER INFORMATION: Cathepsin G recognition site coding sequence.
US-10-229-346-8

Query Match          69.1%; Score 15.2; DB 5; Length 1807;
Best Local Similarity 85.0%; Pred. No. 4.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGGCCTTTCGGGGTGCTC 22
    |||||  |||||  |||||  |||||
Db 185 AAGCCTTCCAGGGTGCTC 166

RESULT 73
US-10-229-346-16/c
; Sequence 16, Application US/10229346
; Patent No. 7030295
; GENERAL INFORMATION:
; APPLICANT: Chen, Eric
; TITLE OF INVENTION: Modified Cry3A Toxins
; FILE REFERENCE: 60065A
; CURRENT APPLICATION NUMBER: US/10/229,346
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/316,421
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 1813
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
```

```
; LOCATION: (1)..(1812)
; OTHER INFORMATION: Maize optimized modified cry3A057 coding sequence.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (322)..(333)
; OTHER INFORMATION: Cathepsin G recognition site coding sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1618)..(1629)
; OTHER INFORMATION: Cathepsin G recognition site coding sequence
US-10-229-346-16

Query Match          69.1%; Score 15.2; DB 5; Length 1813;
Best Local Similarity 85.0%; Pred. No. 4.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGGCCTTTCGGGGTGCTC 22
Db 185 AAGGCCTTCACGGGGTCTC 166

RESULT 74
US-10-229-346-14/c
; Sequence 14, Application US/10229346
; Patent No. 7030295
; GENERAL INFORMATION:
; APPLICANT: Chen, Eric
; APPLICANT: Stacy, Cheryl
; TITLE OF INVENTION: Modified Cry3A Toxins
; FILE REFERENCE: 60065A
; CURRENT APPLICATION NUMBER: US/10/229,346
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/316,421
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 1816
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1812)
; OTHER INFORMATION: Maize optimized modified cry3A058 coding sequence.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1621)..(1632)
; OTHER INFORMATION: Cathepsin G recognition site coding sequence
US-10-229-346-14

Query Match          69.1%; Score 15.2; DB 5; Length 1816;
Best Local Similarity 85.0%; Pred. No. 4.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGGCCTTTCGGGGTGCTC 22
Db 185 AAGGCCTTCACGGGGTCTC 166

RESULT 75
US-10-229-346-10/c
; Sequence 10, Application US/10229346
; Patent No. 7030295
; GENERAL INFORMATION:
; APPLICANT: Chen, Eric
; APPLICANT: Stacy, Cheryl
; TITLE OF INVENTION: Modified Cry3A Toxins
; FILE REFERENCE: 60065A
; CURRENT APPLICATION NUMBER: US/10/229,346
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/316,421
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 38
```

```
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 1818
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1818)
; OTHER INFORMATION: Maize optimized modified cry3A085 coding sequence.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (346)..(357)
; OTHER INFORMATION: Cathepsin G recognition site coding sequence.
US-10-229-346-10

Query Match          69.1%; Score 15.2; DB 5; Length 1818;
Best Local Similarity 85.0%; Pred. No. 4.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGGCCTTTCGGGGTGCTC 22
Db 209 AAGGCCTTCACGGGGTCTC 190

RESULT 76
US-10-229-346-18/c
; Sequence 18, Application US/10229346
; Patent No. 7030295
; GENERAL INFORMATION:
; APPLICANT: Chen, Eric
; APPLICANT: Stacy, Cheryl
; TITLE OF INVENTION: Modified Cry3A Toxins
; FILE REFERENCE: 60065A
; CURRENT APPLICATION NUMBER: US/10/229,346
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/316,421
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 1819
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1818)
; OTHER INFORMATION: Maize optimized modified cry3A056 coding sequence.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (322)..(333)
; OTHER INFORMATION: Cathepsin G recognition site coding sequence.
; NAME/KEY: misc feature
; LOCATION: (1624)..(1635)
; OTHER INFORMATION: Cathepsin G recognition site coding sequence.
US-10-229-346-18

Query Match          69.1%; Score 15.2; DB 5; Length 1819;
Best Local Similarity 85.0%; Pred. No. 4.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGGCCTTTCGGGGTGCTC 22
Db 185 AAGGCCTTCACGGGGTCTC 166

RESULT 77
US-10-094-749-1246
; Sequence 1246, Application US/10094749
; Patent No. 6979557
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
```

```
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1246
; LENGTH: 1830
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-094-749-1246

Query Match          69.1%; Score 15.2; DB 4; Length 1830;
Best Local Similarity 85.0%; Pred. No. 4.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGGCCTTTCGGGGTGCTC 22
| 3 ||||| ||||| |||||
Db 1041 ATGGCCTTTCGTGTGCTC 1060

RESULT 78
US-08-295-060-3/c
; Sequence 3, Application US/08295060
; Patent No. 5659123
; GENERAL INFORMATION:
; APPLICANT: VAN RIE, Jeroen
; APPLICANT: JANSENS, Stefan
; APPLICANT: PERFEROEN, Mathix
; TITLE OF INVENTION: NEW DIABROTICA TOXINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,060
; FILING DATE: 26-AUG-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-052
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
```

```
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1957 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 13..1947
US-08-295-060-3

Query Match          69.1%; Score 15.2; DB 2; Length 1957;
Best Local Similarity 85.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGGCCTTTCGGGGTGCTC 22
| 3 ||||| ||||| |||||
Db 341 AAGGCCTTTCAGGGTGCTC 322

RESULT 79
US-09-774-528-10
; Sequence 10, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: NO. 6743619el Nucleic Acids and
; FILE REFERENCE: 802
; CURRENT APPLICATION NUMBER: US/09/774,528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 10
; LENGTH: 2198
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (124)..(891)
US-09-774-528-10

Query Match          69.1%; Score 15.2; DB 3; Length 2198;
Best Local Similarity 85.0%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGGCCTTTCGGGGTGCTC 22
| 3 ||||| ||||| |||||
Db 1398 ATGGCCTTTCGTGTGCTC 1417

RESULT 80
US-10-120-988-10
; Sequence 10, Application US/10120988
; Patent No. 6919193
; GENERAL INFORMATION:
```



```
; APPLICANT: Tang, Y. Tom
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Ren, Feiyan
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 802CON
; CURRENT APPLICATION NUMBER: US/10/120,988
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/774,528
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 10
; LENGTH: 2198
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (124)..(891)
US-10-120-988-10
```

```
Query Match 69.1%; Score 15.2; DB 3; Length 2198;
Best Local Similarity 85.0%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 3 AAGGCCTTTCGGGGTGCTC 22
| | | | | | | | | |
Db 1398 ATGGCCTTCTGTGGTGCTC 1417
```

```
RESULT 81
US-09-252-991A-7718/c
; Sequence 7718, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7718
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7718
```

```
Query Match 69.1%; Score 15.2; DB 3; Length 2229;
Best Local Similarity 85.0%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 3 AAGGCCTTTCGGGGTGCTC 22
| | | | | | | | | |
Db 2119 AAGGCCTGGCGGTGGTGCTC 2100
```

```
RESULT 82
US-09-774-528-11
; Sequence 11, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
```

```
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; FILE REFERENCE: 802
; CURRENT APPLICATION NUMBER: US/09/774,528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 11
; LENGTH: 2256
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)..(947)
US-09-774-528-11
```

```
Query Match 69.1%; Score 15.2; DB 3; Length 2256;
Best Local Similarity 85.0%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 3 AAGGCCTTTCGGGGTGCTC 22
| | | | | | | | | |
Db 1454 ATGGCCTTCTGTGGTGCTC 1473
```

```
RESULT 83
US-10-120-988-11
; Sequence 11, Application US/10120988
; Patent No. 6919193
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Ren, Feiyan
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6919193el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; FILE REFERENCE: 802CON
; CURRENT APPLICATION NUMBER: US/10/120,988
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/774,528
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 11
; LENGTH: 2256
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)..(947)
US-10-120-988-11
```

```
Query Match 69.1%; Score 15.2; DB 3; Length 2256;
Best Local Similarity 85.0%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 3 AAGGCCTTTCGGGGTGCTC 22
| | | | | | | | | |
Db 1454 ATGGCCTTCTGTGGTGCTC 1473
```

RESULT 84
US-09-028-327-2/c
; Sequence 2, Application US/09028327
; Patent No. 6130064
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; TITLE OF INVENTION: HUMAN SMN-LIKE PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/028,327
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0482 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2426 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRSTNOT24
; CLONE: 3769729
US-09-028-327-2

Query Match 69.1%; Score 15.2; DB 3; Length 2426;
Best Local Similarity 85.0%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGCGCTTTCGGGGTGC 20
| | | | | | | | | | | | | | | | | | | | | |
Db 257 GGAAGCGCTTTCGGGGTGC 238

RESULT 85
US-09-571-078A-2/c
; Sequence 2, Application US/09571078A
; Patent No. 6620783
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; TITLE OF INVENTION: HUMAN SMN-LIKE PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/571,078A
FILING DATE: 15-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0482 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2426 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRSTNOT24
CLONE: 3769729
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-571-078A-2

Query Match 69.1%; Score 15.2; DB 3; Length 2426;
Best Local Similarity 85.0%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGCGCTTTCGGGGTGC 20
| | | | | | | | | | | | | | | | | | | | | |
Db 257 GGAAGCGCTTTCGGGGTGC 238

RESULT 86
US-09-949-016-2230/c
; Sequence 2230, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2230
; LENGTH: 2453
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2230

Query Match 69.1%; Score 15.2; DB 3; Length 2453;
Best Local Similarity 85.0%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGCGCTTTCGGGGTGC 21
| | | | | | | | | | | | | | | | | | | | | |

Db 394 AAATGCCTTTTCGGAAGTGCT 375

RESULT 87

US-09-489-039A-530
; Sequence 530, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 530
; LENGTH: 2511
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-530

Query Match 69.1%; Score 15.2; DB 3; Length 2511;
Best Local Similarity 85.0%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGCCCTTTTCGGGGTGCTC 22

Db 169 AACGCCTTTCGGGGTGCTC 188

RESULT 88

US-09-489-039A-444
; Sequence 444, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 444
; LENGTH: 2742
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-444

Query Match 69.1%; Score 15.2; DB 3; Length 2742;
Best Local Similarity 85.0%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGCCCTTTTCGGGGTGCTC 22

Db 2588 AACGCCTTTCGGGGTGCTC 2607

RESULT 89

US-09-008-697A-13/c
; Sequence 13, Application US/09008697A
; Patent No. 6197504
; GENERAL INFORMATION:
; APPLICANT: Chow, King Lau
; TITLE OF INVENTION: USES OF MAB-21
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York

; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,697A
; FILING DATE: January 19, 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Chan, Albert Wai-Kit
; REGISTRATION NUMBER: 36,479
; REFERENCE/DOCKET NUMBER: 50752-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2770 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-008-697A-13

Query Match 69.1%; Score 15.2; DB 3; Length 2770;
Best Local Similarity 85.0%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGCCTTTTCGGGGTGCT 21

Db 695 AAATGCCTTTCGGAAGTGCT 676

RESULT 90

US-09-949-016-5461/c
; Sequence 5461, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5461
; LENGTH: 3124
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5461

Query Match 69.1%; Score 15.2; DB 3; Length 3124;
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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGCCCTTTTCGGGGTGCTC 22

Db 2546 AGGCATTTTCGGAGGTGCTC 2527

RESULT 91

US-09-865-879-6/c

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; Sequence 6, Application US/09865879
; Patent No. 6767705
; GENERAL INFORMATION:
; APPLICANT: Roninson, Igor
; APPLICANT: Dokmanovic, Milos
; APPLICANT: Chang, Bey-Dih
; TITLE OF INVENTION: REAGENTS AND METHODS FOR IDENTIFYING AND MODULATING EXPRESSION OF
; FILE REFERENCE: 99,216-H
; CURRENT APPLICATION NUMBER: US/09/865,879
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/207,535
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 3271
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Mac-2 BP promoter NCBI acc. number U91729.1
US-09-865-879-6

Query Match      69.1%; Score 15.2; DB 3; Length 3271;
Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAGGCTTCGGGGTGTC 20
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RESULT 92
US-09-949-016-4008/c
; Sequence 4008, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4008
; LENGTH: 4522
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4008

Query Match      69.1%; Score 15.2; DB 3; Length 4522;
Best Local Similarity 85.0%; Pred. No. 5.7e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGGCTTCGGGGTGCTC 22
Db 567 AGGCGCTTCGGGCTGCTC 548

RESULT 93
US-09-949-016-13972/c
; Sequence 13972, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
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; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13972
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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13972

Query Match      69.1%; Score 15.2; DB 3; Length 6454;
Best Local Similarity 85.0%; Pred. No. 6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCTTCGGGGTGCT 21
Db 2394 AAATGCCCTTCGGAAGTGCT 2375

RESULT 94
US-10-229-346-5/c
; Sequence 5, Application US/10229346
; Patent No. 7030295
; GENERAL INFORMATION:
; APPLICANT: Chen, Eric
; APPLICANT: Stacy, Cheryl
; TITLE OF INVENTION: Modified Cry3A Toxins
; FILE REFERENCE: 60065A
; CURRENT APPLICATION NUMBER: US/10/229,346
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/316,421
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 7208
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: pCIB6850
US-10-229-346-5

Query Match      69.1%; Score 15.2; DB 5; Length 7208;
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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGGCTTCGGGGTGCTC 22
Db 193 AAGGCTTCAGGGGTCTC 174

RESULT 95
US-09-949-016-14771/c
; Sequence 14771, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14771

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Best Local Similarity 85.0%; Pred. No. 6.7e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTCGGGGTGTC 20
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RESULT 96
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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16808
; LENGTH: 13438
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16808

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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 97
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; Sequence 17203, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
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; NUMBER OF SEQ ID NOS: 207012
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US-09-949-016-17203

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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGGCCTTTCGGGGTGCTC 22
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RESULT 98
US-09-902-540-1213
; Sequence 1213, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
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; LENGTH: 20250
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1213

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Best Local Similarity 85.0%; Pred. No. 7.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 19983 AAAGCCTCTCGGTGATGCT 20002

RESULT 99
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; Sequence 15750, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
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; LOCATION: (1)...(20444)
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US-09-949-016-15750

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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 AAGCCTTCGGGGTGCTC 22
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RESULT 100
US-09-949-016-15130/c
; Sequence 15130, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15130
; LENGTH: 21831
; TYPE: DNA
; ORGANISM: Human
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; LOCATION: (1)...(21831)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15130

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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 AAGCCTTCGGGGTGCTC 22
Db      1469 AACGCTTCGGGGAGCCC 1450

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SUMMARIES

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4	22	100.0	25	10	US-10-665-708-26
5	18.8	85.5	493	8	US-10-424-599-34282
6	17.8	80.9	487	10	US-10-506-454-1690
7	17.8	80.9	688	4	US-09-925-065A-944213
8	17.8	80.9	688	5	US-09-925-065A-944213
9	17.8	80.9	3175	6	US-10-027-632-116247
10	17.8	80.9	3175	7	US-10-027-632-116247
11	17.8	80.9	40491	6	US-10-087-192-1426
12	17.8	80.9	25	13	US-11-036-317-122359
13	17.4	79.1	549	6	US-10-027-632-133700
14	17.4	79.1	549	7	US-10-027-632-133700
15	17.4	79.1	4637	6	US-10-194-163-818
16	17.4	79.1	374849	6	US-10-087-192-1627
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9	US-10-719-900-152165	25	78.2	17.2	Sequence 152165,
3	US-09-864-761-6845	569	78.2	17.2	Sequence 6845, Ap
3	US-10-424-599-34279	682	78.2	17.2	Sequence 34279, A
21	US-10-282-122A-23975	1440	78.2	17.2	Sequence 23975, A
22	US-10-052-482-46	58822	78.2	17.2	Sequence 46, Appl
6	US-10-087-192-466	63686	78.2	17.2	Sequence 466, App
195	US-10-425-115-69008	195	76.4	16.8	Sequence 69008, A
518	US-10-425-115-118256	518	76.4	16.8	Sequence 118256,
551	US-10-437-963-78913	551	76.4	16.8	Sequence 78913, A
601	US-10-021-323-8399	601	76.4	16.8	Sequence 8399, Ap
2107	US-10-282-122A-19508	2107	76.4	16.8	Sequence 19508, A
8	US-10-322-281-115	8	76.4	16.8	Sequence 115, App
6	US-10-106-698-3878	309	74.5	16.4	Sequence 3878, Ap
31	US-10-021-323-2667	521	74.5	16.4	Sequence 2667, Ap
47804	US-10-017-161-717	47804	74.5	16.4	Sequence 717, App
7	US-10-292-798-629	47804	74.5	16.4	Sequence 629, App
82	US-10-990-355-32	82	73.6	16.2	Sequence 32, Appl
314	US-10-425-115-176343	314	73.6	16.2	Sequence 176343,
353	US-10-425-115-106353	353	73.6	16.2	Sequence 106353,
426	US-10-137-113-21	426	73.6	16.2	Sequence 21, Appl
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506	US-10-301-480-890292	506	73.6	16.2	Sequence 890292,
506	US-09-925-065A-186776	506	73.6	16.2	Sequence 186776,
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561	US-09-925-065A-301027	561	73.6	16.2	Sequence 301027,
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592	US-09-925-065A-821134	592	73.6	16.2	Sequence 821134,
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633	US-10-027-632-268485	633	73.6	16.2	Sequence 884151,
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636	US-09-925-065A-818614	636	73.6	16.2	Sequence 818614,
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642	US-09-925-065A-674788	642	73.6	16.2	Sequence 674788,
642	US-09-925-065A-674788	642	73.6	16.2	Sequence 674788,
825	US-10-750-185-32645	825	73.6	16.2	Sequence 32645, A
825	US-10-750-623-32645	825	73.6	16.2	Sequence 32645, A
909	US-09-854-867-342	909	73.6	16.2	Sequence 342, App
909	US-10-786-970A-342	909	73.6	16.2	Sequence 342, App
935	US-10-027-632-163064	935	73.6	16.2	Sequence 163064,
935	US-10-027-632-163064	935	73.6	16.2	Sequence 163064,
1014	US-09-864-761-20761	1014	73.6	16.2	Sequence 20761, A
1218	US-09-864-761-20761	1218	73.6	16.2	Sequence 20761, A
1377	US-10-282-122A-26246	1377	73.6	16.2	Sequence 26246, A
1380	US-10-282-122A-28592	1380	73.6	16.2	Sequence 28592, A
1704	US-10-240-965-33	1704	73.6	16.2	Sequence 33, Appl
1740	US-09-349-015-30	1740	73.6	16.2	Sequence 224, App
1740	US-10-219-664-22	1740	73.6	16.2	Sequence 23, Appl
1954	US-09-864-761-4001	1954	73.6	16.2	Sequence 9, Appli
2772	US-10-264-049-815	2772	73.6	16.2	Sequence 116, App
3135	US-10-175-523-151	3135	73.6	16.2	Sequence 136, App
3135	US-11-099-266-151	3135	73.6	16.2	Sequence 136, App
4258	US-10-287-436A-1061	4258	73.6	16.2	Sequence 122, App
4315	US-09-925-013-224	4315	73.6	16.2	Sequence 1893, Ap
4315	US-10-137-113-23	4315	73.6	16.2	Sequence 1800, Ap
4758	US-09-842-777-9	4758	73.6	16.2	Sequence 1341, Ap
4831	US-10-334-143-116	4831	73.6	16.2	Sequence 82, Appl
5994	US-10-205-219-136	5994	73.6	16.2	Sequence 116, App
5994	US-10-173-999-122	5994	73.6	16.2	Sequence 136, App
5994	US-10-723-860-1893	5994	73.6	16.2	Sequence 1893, Ap
5994	US-10-756-149-1800	5994	73.6	16.2	Sequence 1800, Ap
6332	US-10-276-774-1341	6332	73.6	16.2	Sequence 1341, Ap
6332	US-10-960-414-82	6332	73.6	16.2	Sequence 82, Appl

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92	16.2	73.6	8682	7	US-10-062-674-1976	Sequence 1976, Ap	c 165	15.6	70.9	479	10	US-10-926-683-779	Sequence 779, App
93	16.2	73.6	25759	7	US-10-388-934-556	Sequence 556, App	c 166	15.6	70.9	481	4	US-09-925-065A-603436	Sequence 603436, A
94	16.2	73.6	25759	16	US-11-224-663-556	Sequence 556, App	c 167	15.6	70.9	481	4	US-09-925-065A-603437	Sequence 603437, A
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97	16.2	73.6	106664	6	US-10-175-523-97	Sequence 97, Appl	c 170	15.6	70.9	487	3	US-09-864-761-2696	Sequence 2696, Ap
98	16.2	73.6	106664	13	US-11-099-266-97	Sequence 97, Appl	c 171	15.6	70.9	496	8	US-10-240-425-15	Sequence 15, Appl
99	16	72.7	297	7	US-10-012-697-422	Sequence 422, App	c 172	15.6	70.9	502	8	US-10-276-774-451	Sequence 451, App
100	16	72.7	297	10	US-10-779-543-22422	Sequence 22422, A	c 173	15.6	70.9	516	7	US-10-029-386-10386	Sequence 10386, A
101	15.8	71.8	132	3	US-09-560-863-447	Sequence 447, App	c 174	15.6	70.9	537	4	US-09-925-065A-463860	Sequence 463860, A
102	15.8	71.8	201	16	US-11-124-367A-27450	Sequence 27450, A	c 175	15.6	70.9	537	4	US-09-925-065A-463861	Sequence 463861, A
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109	15.8	71.8	515	4	US-09-925-065A-635951	Sequence 635951, A	c 182	15.6	70.9	554	12	US-10-301-480-520274	Sequence 520274, A
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117	15.8	71.8	645	4	US-09-925-065A-862116	Sequence 862116, A	c 190	15.6	70.9	600	10	US-10-972-079-56715	Sequence 56715, A
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132	15.8	71.8	9661	13	US-11-097-143-11329	Sequence 11497, A	c 205	15.6	70.9	631	12	US-10-424-599-134792	Sequence 134792, A
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155	15.6	70.9	407	3	US-09-764-891-2357	Sequence 2357, Ap	c 228	15.6	70.9	967	7	US-10-024-212-97	Sequence 97, Appl
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C 253	15.6	70.9	1552	8	US-10-437-963-18968	Sequence 18968, A
C 254	15.6	70.9	1746	8	US-10-235-463-58	Sequence 58, Appl
C 255	15.6	70.9	1761	8	US-10-282-122A-1449	Sequence 1449, A
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C 257	15.6	70.9	1862	7	US-10-104-047-900	Sequence 900, App
C 258	15.6	70.9	1862	16	US-11-072-512-900	Sequence 900, App
C 259	15.6	70.9	1898	10	US-10-750-185-46119	Sequence 46119, A
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C 261	15.6	70.9	1920	8	US-10-437-963-44355	Sequence 44355, A
C 262	15.6	70.9	1923	11	US-10-932-182A-75858	Sequence 75858, A
C 263	15.6	70.9	1935	8	US-10-437-963-85597	Sequence 85597, A
C 264	15.6	70.9	1990	7	US-10-305-720-1056	Sequence 1056, Ap
C 265	15.6	70.9	1998	8	US-10-437-963-37469	Sequence 37469, A
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C 267	15.6	70.9	2129	10	US-10-486-977-38	Sequence 38, Appl
C 268	15.6	70.9	2172	8	US-10-437-963-85975	Sequence 85975, A
C 269	15.6	70.9	2297	7	US-10-094-749-421	Sequence 421, Appl
C 270	15.6	70.9	2304	10	US-10-826-478-5	Sequence 5, Appl
C 271	15.6	70.9	2370	8	US-10-437-963-85896	Sequence 85896, A
C 272	15.6	70.9	2544	8	US-10-424-599-53236	Sequence 53236, A
C 273	15.6	70.9	2667	8	US-10-437-963-85931	Sequence 85931, A
C 274	15.6	70.9	2708	13	US-11-097-143-16156	Sequence 16156, A
C 275	15.6	70.9	2796	8	US-10-437-963-86274	Sequence 86274, A
C 276	15.6	70.9	2835	8	US-10-437-963-44350	Sequence 44350, A
C 277	15.6	70.9	2895	8	US-10-235-463-52	Sequence 52, Appl
C 278	15.6	70.9	2922	8	US-10-437-963-85997	Sequence 85997, A
C 279	15.6	70.9	2970	8	US-10-437-963-85652	Sequence 85652, A
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C 282	15.6	70.9	3581	4	US-09-925-065A-676738	Sequence 676738, A
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C 290	15.6	70.9	3995	7	US-10-170-385-300	Sequence 300, App
C 291	15.6	70.9	4149	9	US-10-425-115-163575	Sequence 163575, A
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C 294	15.6	70.9	4857	6	US-10-208-948-1	Sequence 1, Appl
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C 298	15.6	70.9	6065	3	US-09-764-891-9652	Sequence 9652, Ap
C 299	15.6	70.9	7110	6	US-10-208-948-23	Sequence 23, Appl
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ALIGNMENTS

RESULT 1
US-09-738-274-25
; Sequence 25, Application US/09738274
; Publication No. US20030165824A1

; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
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; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-25

Query Match 100.0%; Score 22; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GAAAGCCCTTCGGGGTGCTC 22

RESULT 2

US-10-665-708-25
; Sequence 25, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-10-665-708-25

Query Match 100.0%; Score 22; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

US-09-738-274-26
; Sequence 26, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAI, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 26
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide

Query Match 100.0%; Score 22; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAAGGCCTTCGGGGTGCTC 22
|||||
Db 1 GAAAGGCCTTCGGGGTGCTC 22

RESULT 4
US-10-665-708-26
; Sequence 26, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAI, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 26
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide

Query Match 100.0%; Score 22; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAAGGCCTTCGGGGTGCTC 22
|||||
Db 1 GAAAGGCCTTCGGGGTGCTC 22

RESULT 5
US-10-424-599-34282
; Sequence 34282, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Chao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 34282
; LENGTH: 493
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_130960C.1
US-10-424-599-34282

Query Match 85.5%; Score 18.8; DB 8; Length 493;
Best Local Similarity 90.9%; Pred. No. 56;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GAAAGGCCTTCGGGGTGCTC 22
|||||
Db 321 GAAAGGCCTTCGGGGTGCTC 342

RESULT 6
US-10-506-454-1690/c
; Sequence 1690, Application US/10506454
; Publication No. US20060068386A1
; GENERAL INFORMATION:
; APPLICANT: Slesarev, Alexi I
; APPLICANT: Mezhevaya, Katja V
; APPLICANT: Polushin, Nikolai N
; APPLICANT: Shcherbinina, Olga V
; APPLICANT: Shakhova, Vera V
; APPLICANT: Malykh, Andrei G
; APPLICANT: Kozyavkin, Sergei A
; TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophile
; TITLE OF INVENTION: Methanopyrus Kandleri AV19 and Monophyly of Archaeal Methanogens
; FILE REFERENCE: FID001
; CURRENT APPLICATION NUMBER: US/10/506,454
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/US03/06664
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/361,742
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 1722
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1690
; LENGTH: 1694969
; TYPE: DNA
; ORGANISM: Methanopyrus kandleri
US-10-506-454-1690

Query Match 85.5%; Score 18.8; DB 12; Length 1694969;
Best Local Similarity 90.9%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GAAAGGCCTTCGGGGTGCTC 22
|||||
Db 54678 GAAAGGCCTTCGGGGTGATC 54657

```
RESULT 7
US-10-287-436A-794
; Sequence 794, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; PRIOR FILING DATE: 2002-10-31
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 794
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-287-436A-794

Query Match      80.9%; Score 17.8; DB 10; Length 487;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTTCGGGGTGCT 21
Db 79 GACAGGCTTTTCGGGGTGCT 99

RESULT 8
US-09-925-065A-944213
; Sequence 944213, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 944213
; LENGTH: 688
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-944213

Query Match      80.9%; Score 17.8; DB 4; Length 688;
Best Local Similarity 90.5%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTTCGGGGTGCT 21
Db 76 GACAGGCTTTTCGGGGTGCT 96

RESULT 9
US-09-925-065A-944213
; Sequence 944213, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 944213
; LENGTH: 688
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-944213

Query Match      80.9%; Score 17.8; DB 4; Length 688;
Best Local Similarity 90.5%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTTCGGGGTGCT 21
Db 76 GACAGGCTTTTCGGGGTGCT 96
```

```
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 944213
; LENGTH: 688
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-944213

Query Match      80.9%; Score 17.8; DB 5; Length 688;
Best Local Similarity 90.5%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTTCGGGGTGCT 21
Db 76 GACAGGCTTTTCGGGGTGCT 96

RESULT 10
US-10-027-632-116247
; Sequence 116247, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-04-20
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-09-28
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 116247
; LENGTH: 3175
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-116247

Query Match      80.9%; Score 17.8; DB 6; Length 3175;
Best Local Similarity 90.5%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTTCGGGGTGCT 21
Db 1073 GACAGGCTTTTCGGGGTGCT 1093
```


Db 100 GAAAGCCTTCCTGGGGTGCT 120

RESULT 15

US-10-027-632-133700

; Sequence 133700, Application US/10027632

; Publication No. US20030204075A9

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; TITLE OF INVENTION: Polymorphisms in the Human Genome

; FILE REFERENCE: 108927.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 133700

; LENGTH: 549

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-133700

Query Match 79.1%; Score 17.4; DB 7; Length 549;

Best Local Similarity 85.7%; Pred. No. 2.5e+02;

Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGCCTTCCTGGGGTGCT 120

Db 100 GAAAGCCTTCCTGGGGTGCT 120

RESULT 16

US-10-194-163-818/c

; Sequence 818, Application US/10194163

; Publication No. US20020172976A1

; GENERAL INFORMATION:

; APPLICANT: Ross, Bruce Carter

; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS POLYNUCLEOTIDES

; AND USES THEREOF

; NUMBER OF SEQUENCES: 1120

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 755 PAGE MILL ROAD

; CITY: PALO ALTO

; STATE: CA

; COUNTRY: USA

; ZIP: 94304-1018

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows

; SOFTWARE: FastSeq for Windows Version 2.0b

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/194,163

; FILING DATE: 04-Nov-2002

; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Baeu, Shantanu

; REGISTRATION NUMBER: 43,318

REFERENCE/DOCKET NUMBER: 529282000101

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-813-5995

TELEFAX: 650-494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 818

SEQUENCE CHARACTERISTICS:

LENGTH: 4637 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHEICAL: NO

ANTI-SENSE: UNKNOWN

ORGANISM: PORPHYROMONAS GINGIVALIS

FEATURE:

NAME/KEY: misc feature

LOCATION: 1...4637

SEQUENCE DESCRIPTION: SEQ ID NO: 818

US-10-194-163-818

Query Match 79.1%; Score 17.4; DB 6; Length 4637;

Best Local Similarity 94.7%; Pred. No. 2.1e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAAGCCTTCCTGGGGTGCT 19

Db 4588 GAAAGCCTTCCTGGGGTGCT 4570

RESULT 17

US-10-087-192-1627

; Sequence 1627, Application US/10087192

; Publication No. US20020182586A1

; GENERAL INFORMATION:

; APPLICANT: Morris, David W.

; APPLICANT: Engelhard, Eric K.

; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR

; TITL OF INVENTION: CANCER

; FILE REFERENCE: 529452000122

; CURRENT APPLICATION NUMBER: US/10/087,192

; CURRENT FILING DATE: 2002-03-01

; PRIOR APPLICATION NUMBER: US 09/747,377

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: US 09/798,586

; PRIOR FILING DATE: 2001-03-02

; NUMBER OF SEQ ID NOS: 2059

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1627

; LENGTH: 374849

; TYPE: DNA

; ORGANISM: Mus musculus

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(374849)

; OTHER INFORMATION: n = A,T,C or G

US-10-087-192-1627

Query Match 79.1%; Score 17.4; DB 6; Length 374849;

Best Local Similarity 94.7%; Pred. No. 1.4e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AAGGCCTTCCTGGGGTGCT 21

Db 353594 AAGGCCTTCCTGGGGTGCT 353612

RESULT 18

US-10-719-900-152165/c

; Sequence 152165, Application US/10719900

; Publication No. US20050026164A1

; GENERAL INFORMATION:


```
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23975
; LENGTH: 1440
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-10-282-122A-23975

Query Match      78.2%; Score 17.2; DB 8; Length 1440;
Best Local Similarity 86.4%; Pred. No. 2.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1  GAAAGGCGCTTCGGGGGTGCTC 22
Db      141  GAAAGGCGTGGCCGGGTGCTC 162

RESULT 22
US-10-052-482-46
; Sequence 46, Application US/10052482
; Publication No. US2004007226A1
; GENERAL INFORMATION:
; APPLICANT: Engelhard, Eric
; APPLICANT: Morris, David
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71087/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/052,482
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 58822
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4679) ..(5145)
```

```
; OTHER INFORMATION: "n" at positions 4679 to 5145 can be any base
US-10-052-482-46

Query Match      78.2%; Score 17.2; DB 8; Length 58822;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1  GAAAGGCGCTTCGGGGGTGCTC 22
Db      26859  GACAGGCGCTTTGGGGGTCTC 26880

RESULT 23
US-10-087-192-466
; Sequence 466, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 466
; LENGTH: 63686
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-087-192-466

Query Match      78.2%; Score 17.2; DB 6; Length 63686;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1  GAAAGGCGCTTCGGGGGTGCTC 22
Db      45915  GAAAGGCGCTCTCAGGGGTGCTC 45936

RESULT 24
US-10-425-115-69008/c
; Sequence 69008, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 69008
; LENGTH: 195
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) ..(195)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_162929C.1
US-10-425-115-69008

Query Match      76.4%; Score 16.8; DB 9; Length 195;
```


Best Local Similarity 90.0%; Pred. No. 5.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 AAAGGCCTTCGGGGGTGCT 21
 Db 63 AAAGGCCTTCGGGGGGGCT 44

RESULT 25
 US-10-425-115-118256/c
 ; Sequence 118256, Application US/10425115
 ; Publication No. US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE OF INVENTION: Plants
 ; FILE REFERENCE: 38-21(53222)B
 ; CURRENT APPLICATION NUMBER: US/10/425,115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 118256
 ; LENGTH: 518
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(518)
 ; OTHER INFORMATION: unsure at all n locations
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MRT4577_39339C.1
 US-10-425-115-118256

Query Match 76.4%; Score 16.8; DB 9; Length 518;
 Best Local Similarity 90.0%; Pred. No. 4.9e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GAAAGGCCTTCGGGGGTGC 20
 Db 311 GAAAGGCCATTCGGGGGGC 292

RESULT 26
 US-10-437-963-78913
 ; Sequence 78913, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazov, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 78913
 ; LENGTH: 551
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_78674C.1
 US-10-437-963-78913

Query Match 76.4%; Score 16.8; DB 8; Length 551;
 Best Local Similarity 90.0%; Pred. No. 4.9e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GAAAGGCCTTCGGGGGTGC 20
 Db 176 GAAAGGCCTTCGGGGGTTC 195

RESULT 27
 US-10-021-323-8399/c
 ; Sequence 8399, Application US/10021323
 ; Publication No. US20040123340A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Deikman, Jill
 ; APPLICANT: Peng, Paul C.C.
 ; APPLICANT: Fincher, Karen L.
 ; APPLICANT: Ziegler, Todd E.
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE OF INVENTION: Plants
 ; FILE REFERENCE: 38-21(52274)B
 ; CURRENT APPLICATION NUMBER: US/10/021,323
 ; CURRENT FILING DATE: 2001-12-12
 ; PRIOR APPLICATION NUMBER: US 60/255, 619
 ; PRIOR FILING DATE: 2000-12-14
 ; NUMBER OF SEQ ID NOS: 17880
 ; SEQ ID NO 8399
 ; LENGTH: 601
 ; TYPE: DNA
 ; ORGANISM: Gossypium hirsutum
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: L1B3828-009-Q1-K6-G5
 US-10-021-323-8399

Query Match 76.4%; Score 16.8; DB 8; Length 601;
 Best Local Similarity 90.0%; Pred. No. 4.9e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GAAAGGCCTTCGGGGGTGC 20
 Db 525 GAAAGGCCTTCGGGGGGC 506

RESULT 28
 US-10-282-122A-19508
 ; Sequence 19508, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA.034A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242,578

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; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19508
; LENGTH: 2107
; TYPE: DNA
; ORGANISM: Enterobacter cloacae
US-10-282-122A-19508

Query Match          76.4%; Score 16.8; DB 8; Length 2107;
Best Local Similarity 90.0%; Pred. No. 4.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AAGCGCTTTCGGGGTGCTC 22
Db 113 AAGCGGTTCGGGGTGCTC 132

RESULT 29
US-10-322-281-115
; Sequence 115, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 115
; LENGTH: 289190
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(289190)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-281-115

Query Match          76.4%; Score 16.8; DB 8; Length 289190;
Best Local Similarity 90.0%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAGCGCTTTCGGGGTGCT 21
Db 116861 AAGCGCTTTCGGGTGTGCT 116880

RESULT 30
US-10-106-698-3878
; Sequence 3878, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
```

```
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 3878
; LENGTH: 309
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28)...(28)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (98)...(98)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (128)...(128)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (139)...(139)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (153)...(153)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (159)...(160)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (207)...(207)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (219)...(219)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (240)...(240)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (250)...(250)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (263)...(263)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (265)...(265)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-106-698-3878

Query Match          74.5%; Score 16.4; DB 6; Length 309;
Best Local Similarity 94.4%; Pred. No. 8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AAGCGCTTTCGGGGGTG 19
Db 74 AAGCGCTTTCGGGGGTG 91

RESULT 31
US-10-021-323-2667
; Sequence 2667, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Peng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
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/ SEQ ID NO 2667
/ LENGTH: 521
/ TYPE: DNA
/ ORGANISM: Gossypium hirsutum
/ FEATURE:
/ OTHER INFORMATION: Clone ID: LIB3825-016-Q1-N6-D3
US-10-021-323-2667

Query Match          74.5%; Score 16.4; DB 8; Length 521;
Best Local Similarity 94.4%; Pred. No. 7.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 AAAGGCTTCGGGGGTG 19
      |||||
Db      232 AAAGGCTTCGGGGGAG 249

RESULT 32
US-10-017-161-717/c
/ Sequence 717, Application US/10017161
/ Publication No. US2003014368A1
/ GENERAL INFORMATION:
/ APPLICANT: SUWA, MAKIKO
/ APPLICANT: ASAI, KIYOSHI
/ APPLICANT: AKIYAMA, YUTAKA
/ APPLICANT: ABURATANI, HIROYUKI
/ TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
/ FILE REFERENCE: 084335/0152
/ CURRENT APPLICATION NUMBER: US/10/017,161
/ CURRENT FILING DATE: 2002-12-18
/ PRIOR APPLICATION NUMBER: JP 2001/246789
/ PRIOR FILING DATE: 2001-06-18
/ NUMBER OF SEQ ID NOS: 2430
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 717
/ LENGTH: 47804
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: source
/ LOCATION: (1)..(47804)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (201)..(1022)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1093)..(1208)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1871)..(2040)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (3227)..(3386)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (3492)..(3698)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (5159)..(5424)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (5651)..(6504)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (18486)..(18612)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (19045)..(19140)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (25901)..(26126)
/ FEATURE:
/ NAME/KEY: CDS
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/ LOCATION: (26658)..(26848)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (30445)..(30482)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (37501)..(37634)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (38681)..(38889)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (46474)..(46682)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (46867)..(47604)
/ FEATURE:
/ NAME/KEY: modified base
/ LOCATION: (7478)..(7577)
/ OTHER INFORMATION: a, t, c, g, unknown or other
/ FEATURE:
/ NAME/KEY: modified base
/ LOCATION: (17033)..(17132)
/ OTHER INFORMATION: a, t, c, g, unknown or other
/ FEATURE:
/ NAME/KEY: modified base
/ LOCATION: (24561)..(24660)
/ OTHER INFORMATION: a, t, c, g, unknown or other
/ FEATURE:
/ NAME/KEY: modified base
/ LOCATION: (33542)..(33641)
/ OTHER INFORMATION: a, t, c, g, unknown or other
/ FEATURE:
/ NAME/KEY: modified base
/ LOCATION: (41424)..(41523)
/ OTHER INFORMATION: a, t, c, g, unknown or other
US-10-017-161-717

Query Match          74.5%; Score 16.4; DB 7; Length 47804;
Best Local Similarity 94.4%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 GGCTTTTCGGGGTGCTC 22
      |||||
Db      47345 GGCTTTTCGGGGTTCTC 47328

RESULT 33
US-10-292-798-629/c
/ Sequence 629, Application US/10292798
/ Publication No. US2003023583A1
/ GENERAL INFORMATION:
/ APPLICANT: SUWA, MAKIKO
/ APPLICANT: ASAI, KIYOSHI
/ APPLICANT: AKIYAMA, YUTAKA
/ APPLICANT: ABURATANI, HIROYUKI
/ TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
/ FILE REFERENCE: 084335/166
/ CURRENT APPLICATION NUMBER: US/10/292,798
/ CURRENT FILING DATE: 2002-11-13
/ PRIOR APPLICATION NUMBER: 10/017,161
/ PRIOR FILING DATE: 2001-12-18
/ PRIOR APPLICATION NUMBER: JP 2001-246789
/ PRIOR FILING DATE: 2001-06-18
/ NUMBER OF SEQ ID NOS: 2070
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 629
/ LENGTH: 47804
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ LOCATION: source
/ FEATURE:
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; LOCATION: (1)..(47804)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1022)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1093)..(1208)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1871)..(2040)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3227)..(3386)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3492)..(3698)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (5159)..(5424)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (5651)..(6504)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18486)..(18612)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19045)..(19140)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25901)..(26126)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (26658)..(26848)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (30445)..(30482)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (37501)..(37634)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (38681)..(38889)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (46474)..(466682)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (46867)..(47604)
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (7478)..(7577)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (17033)..(17132)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (24561)..(24660)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (33542)..(33641)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (41424)..(41523)
; OTHER INFORMATION: a, t, c, g, unknown or other
US-10-292-798-629

```

Query Match 74.5%; Score 16.4; DB 7; Length 47804;
 Best Local Similarity 94.4%; Pred. No. 5.1e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGCCTTTCGGGGTGTCT 22
 |||||
 Db 47345 GGCCTTTCGGGGTGTCT 47328

RESULT 34
 US-10-990-355-32
 ; Sequence 32, Application US/10990355
 ; Publication No. US20050158741A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mulligan, Richard
 ; APPLICANT: Yen, Laising
 ; TITLE OF INVENTION: SELF-CLEAVING RIBOZYMES AND USES THEREOF
 ; FILE REFERENCE: CHME-P01-001
 ; CURRENT APPLICATION NUMBER: US/10/990,355
 ; CURRENT FILING DATE: 2004-11-15
 ; PRIOR APPLICATION NUMBER: US 60/519,941
 ; PRIOR FILING DATE: 2003-11-14
 ; NUMBER OF SEQ ID NOS: 71
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 32
 ; LENGTH: 82
 ; TYPE: RNA
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: modified schistosome ribozyme partial sequence
 US-10-990-355-32

Query Match 73.6%; Score 16.2; DB 10; Length 82;
 Best Local Similarity 61.9%; Pred. No. 1.1e+03;
 Matches 13; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCCTTTCGGGGTGTCT 21
 |||||
 Db 43 GAAAGCCUUUCGGGGUCCU 63

RESULT 35

US-10-425-115-176343/c
 ; Sequence 176343, Application US/10425115
 ; Publication No. US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(53222)B
 ; CURRENT APPLICATION NUMBER: US/10/425,115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 176343
 ; LENGTH: 314
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MRT4577_92418C.1
 US-10-425-115-176343

Query Match 73.6%; Score 16.2; DB 9; Length 314;
 Best Local Similarity 85.7%; Pred. No. 1e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCCTTTCGGGGTGTCT 21
 |||||
 Db 105 GAAAGCCTTACGGTTGTCT 85

RESULT 36
 US-10-425-115-106353/c

; Sequence 106353, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 106353
; LENGTH: 353
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_28496C.1
US-10-425-115-106353

Query Match 73.6%; Score 16.2; DB 9; Length 353;
Best Local Similarity 85.7%; Pred. No. 9.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCCTTCGGGGGTGCTC 22
Db 152 AAAGGCCTTCGGGGGTGCTC 132

RESULT 37
US-10-137-113-21
; Sequence 21, Application US/10137113
; Publication No. US20030175725A1
; GENERAL INFORMATION:
; APPLICANT: Kepur, Vivek
; APPLICANT: Bannantine, John P.
; TITLE OF INVENTION: Mycobacterial Diagnostics
; FILE REFERENCE: 09531-112001
; CURRENT APPLICATION NUMBER: US/10/137,113
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/362,396
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Mycobacterium paratuberculosis
US-10-137-113-21

Query Match 73.6%; Score 16.2; DB 7; Length 426;
Best Local Similarity 85.7%; Pred. No. 9.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCCTTCGGGGGTGCTC 22
Db 77 AAAGACCTGTCGGGGGTGCC 97

RESULT 38
US-10-437-963-2250/c
; Sequence 2250, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 2250
; LENGTH: 483
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_102039C.1
US-10-437-963-2250

Query Match 73.6%; Score 16.2; DB 8; Length 483;
Best Local Similarity 85.7%; Pred. No. 9.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTCGGGGGTGCT 21
Db 435 GAAAGGCCTTCCTGGGTGCT 415

RESULT 39
US-10-301-480-276883
; Sequence 276883, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 276883
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-276883

Query Match 73.6%; Score 16.2; DB 12; Length 505;
Best Local Similarity 85.7%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTCGGGGGTGCT 21
Db 360 GTAAGGCCTTCCTGGGTGCT 380

RESULT 40
US-10-301-480-890292
; Sequence 890292, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 890292

```
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480-890292

Query Match      73.6%; Score 16.2; DB 12; Length 505;
Best Local Similarity 85.7%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTCGGGGTGCT 21
   ||||| ||||| ||||| |||||
Db 360 GTAAGGCCCTTCTGGGATGCT 380

RESULT 41
US-09-925-065A-186776
; Sequence 186776, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; NUCLEOTIDE POLYMORPHISMS IN THE HUMAN GENOME
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 186776
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-186776

Query Match      73.6%; Score 16.2; DB 4; Length 506;
Best Local Similarity 85.7%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTCGGGGTGCT 21
   ||||| ||||| ||||| |||||
Db 361 GTAAGGCCCTTCTGGGATGCT 381

RESULT 42
US-09-925-065A-186776
; Sequence 186776, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; NUCLEOTIDE POLYMORPHISMS IN THE HUMAN GENOME
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
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; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 186776
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-186776

Query Match      73.6%; Score 16.2; DB 5; Length 506;
Best Local Similarity 85.7%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTCGGGGTGCT 21
   ||||| ||||| ||||| |||||
Db 361 GTAAGGCCCTTCTGGGATGCT 381

RESULT 43
US-10-029-386-9545
; Sequence 9545, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: ABOMICA-X-2
; EXPRESSION ANALYSIS TWO
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 9545
; LENGTH: 511
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CH1.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.8
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.8
; OTHER INFORMATION: SWISSPROT HIT: Q01956, EVALUATE 1.60e+00
; OTHER INFORMATION: NT HIT: G16679159, EVALUATE 9.00e-49
; OTHER INFORMATION: EST_HUMAN HIT: AW752727.1, EVALUATE 4.00e-36
US-10-029-386-9545

Query Match      73.6%; Score 16.2; DB 7; Length 511;
Best Local Similarity 85.7%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTCGGGGTGCT 21
   ||||| ||||| ||||| |||||
Db 187 GTAAGGCCCTTCTGGGATGCT 207

RESULT 44
US-10-437-963-84361
; Sequence 84361, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
```

```
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 84361
; LENGTH: 528
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_83604C.1
US-10-437-963-84361

Query Match      73.6%; Score 16.2; DB 8; Length 528;
Best Local Similarity 85.7%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTTCGGGGGTGCTC 22
Db 279 AAGGGACTTTGGGGGGTCTC 299

RESULT 45
US-09-925-065A-301027
; Sequence 301027, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 301027
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-301027

Query Match      73.6%; Score 16.2; DB 4; Length 561;
Best Local Similarity 85.7%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTTCGGGGGTGCTC 22
Db 238 AAAGGCTTTTCGGTGGTCTC 258

RESULT 46
US-09-925-065A-301027
; Sequence 301027, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 301027
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-301027

Query Match      73.6%; Score 16.2; DB 4; Length 567;
Best Local Similarity 85.7%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTTCGGGGGTGCTC 22
Db 238 AAAGGCTTTTCGGTGGTCTC 258

RESULT 47
US-09-925-065A-301026
; Sequence 301026, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 301026
; LENGTH: 567
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-301026

Query Match      73.6%; Score 16.2; DB 4; Length 567;
Best Local Similarity 85.7%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTTCGGGGGTGCTC 22
Db 146 AAAGGCTTTTCGGTGGTCTC 166

RESULT 48
US-09-925-065A-301026
; Sequence 301026, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 301026
; LENGTH: 567
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-301026
```

```
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 301026
; LENGTH: 567
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-301026

Query Match      73.6%; Score 16.2; DB 5; Length 567;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAAGGCTTCGGGGGTGCTC 22
Db      146 AAAGTCTTCGGTGGTCTC 166

RESULT 49
US-09-925-065A-821134/c
; Sequence 821134, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 821134
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-821134

Query Match      73.6%; Score 16.2; DB 4; Length 592;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GAAAGGCTTCGGGGGTGCTC 21
Db      65 GAAAGGCTTCCTGGGGTCTC 45

RESULT 50
US-09-925-065A-821134/c
; Sequence 821134, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
```

```
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 821134
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-821134

Query Match      73.6%; Score 16.2; DB 5; Length 592;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GAAAGGCTTCGGGGGTGCTC 21
Db      65 GAAAGGCTTCCTGGGGTCTC 45

RESULT 51
US-10-750-185-19831/c
; Sequence 19831, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19831
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Bovine
MMBT00837
US-10-750-185-19831

Query Match      73.6%; Score 16.2; DB 10; Length 600;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAAGGCTTCGGGGGTGCTC 22
Db      159 AATGGCTTCCTGGGGGAATC 139

RESULT 52
US-10-750-623-19831/c
; Sequence 19831, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
```



```
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 19831
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Bovine NMBT00837
US-10-750-623-19831
```

```
Query Match 73.6%; Score 16.2; DB 10; Length 600;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 AAAGGCGCTTTCGGGGTGCTC 22
Db 159 AATGGCGCTTTCGGGGGAATC 139
```

```
RESULT 53
US-09-925-065A-884151
; Sequence 884151, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
```

```
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 884151
; LENGTH: 607
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-884151
```

```
Query Match 73.6%; Score 16.2; DB 4; Length 607;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 GAAAGCGCTTTCGGGGTGCT 21
Db 197 GAAAGCGCTTTCGGGAGTGAT 217
```

```
RESULT 54
US-09-925-065A-884151
; Sequence 884151, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
```

```
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
```

```
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 884151
; LENGTH: 607
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-884151
```

```
Query Match 73.6%; Score 16.2; DB 5; Length 607;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 GAAAGCGCTTTCGGGGTGCT 21
Db 197 GAAAGCGCTTTCGGGAGTGAT 217
```

```
RESULT 55
US-10-027-632-268485
; Sequence 268485, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 268485
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-268485
```

```
Query Match 73.6%; Score 16.2; DB 6; Length 623;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 AAAGCGCTTTCGGGGTGCTC 22
Db 517 AAAGCGCTTTCGTGAGCTC 537
```

```
RESULT 56
US-10-027-632-268485
```

```
; Sequence 268485, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 268485
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-268485

Query Match      73.6%; Score 16.2; DB 7; Length 623;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAAGGCGCTTTTCGGGGTGCTC 22
Db      517 AAAGGCGCTTTTCGGTGAGCTC 537

RESULT 57
US-09-925-065A-818614/c
; Sequence 818614, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 818614
; LENGTH: 626
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-818614

Query Match      73.6%; Score 16.2; DB 4; Length 626;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 GAAAGGCGCTTTTCGGGGTGCT 21
Db      568 GGAAGGCGCTTTTCGGGGTGTT 548

RESULT 58
US-09-925-065A-818614/c
; Sequence 818614, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 818614
; LENGTH: 626
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-818614

Query Match      73.6%; Score 16.2; DB 5; Length 626;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GAAAGGCGCTTTTCGGGGTGCT 21
Db      568 GGAAGGCGCTTTTCGGGGTGTT 548

RESULT 59
US-09-925-065A-848383/c
; Sequence 848383, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 848383
; LENGTH: 631
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-848383

Query Match      73.6%; Score 16.2; DB 4; Length 631;
```

```
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGCT 21
Db 568 GGAAGGCCCTTTGGGGGTGT 548

RESULT 60
US-09-925-065A-848383/c
; Sequence 848383, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 848383
; LENGTH: 631
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-848383

Query Match 73.6%; Score 16.2; DB 5; Length 631;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGCT 21
Db 568 GGAAGGCCCTTTGGGGGTGT 548

RESULT 61
US-09-925-065A-674788
; Sequence 674788, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 674788
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-674788

Query Match 73.6%; Score 16.2; DB 5; Length 642;
Best Local Similarity 85.7%; Pred. No. 9.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCCCTTTCGGGGTGCT 21
Db 349 GAAAGGCCCTTTCGGGGTGCT 369

RESULT 62
US-09-925-065A-674788
; Sequence 674788, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 674788
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-674788

Query Match 73.6%; Score 16.2; DB 5; Length 642;
Best Local Similarity 85.7%; Pred. No. 9.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCCCTTTCGGGGTGCT 21
Db 349 GAAAGGCCCTTTCGGGGTGCT 369

RESULT 63
US-10-750-185-32645/c
; Sequence 32645, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32645
; LENGTH: 825
; TYPE: DNA
; ORGANISM: Bovine 19866880690787
```

US-10-750-185-32645

Query Match 73.6%; Score 16.2; DB 10; Length 825;
Best Local Similarity 85.7%; Pred. No. 9.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGCCTTTTCGGGGTGCTC 22
Db 306 AATGGCCTTTTCGGGGGAAC 286

RESULT 64

US-10-750-623-32645/c
; Sequence 32645, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64322
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 32645
; LENGTH: 825
; TYPE: DNA
; ORGANISM: Bovine 19866880690787
US-10-750-623-32645

Query Match 73.6%; Score 16.2; DB 10; Length 825;
Best Local Similarity 85.7%; Pred. No. 9.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGCCTTTTCGGGGTGCTC 22
Db 306 AATGGCCTTTTCGGGGGAAC 286

RESULT 65

US-09-854-867-342
; Sequence 342, Application US/09854867
; Publication No. US20030224356A1
; GENERAL INFORMATION:
; APPLICANT: JOAN, KNOLL H
; APPLICANT: ROGAN, PETER K
; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
; FILE REFERENCE: 30307
; CURRENT APPLICATION NUMBER: US/09/854,867
; CURRENT FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 613
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 342
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: (1)..(909)
; OTHER INFORMATION: l1me3a
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (647)..(647)
; OTHER INFORMATION: n is a, c, g or t
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION: (657)..(658)
; OTHER INFORMATION: n is a, c, g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (705)..(705)
; OTHER INFORMATION: n is a, c, g or t
US-09-854-867-342

Query Match 73.6%; Score 16.2; DB 3; Length 909;
Best Local Similarity 85.7%; Pred. No. 9.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGCCTTTTCGGGGTGCT 21
Db 762 GAGAGGCCTTTCTGGGGTGCT 782

RESULT 66

US-10-786-970A-342
; Sequence 342, Application US/10786970A
; Publication No. US2005006449A1
; GENERAL INFORMATION:
; APPLICANT: JOAN, KNOLL
; APPLICANT: ROGAN, PETER
; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
; FILE REFERENCE: 30307
; CURRENT APPLICATION NUMBER: US/10/786,970A
; CURRENT FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: US/09/573,080
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 342
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: (1)..(909)
; OTHER INFORMATION: l1me3a
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: n is a, c, g or t
; PUBLICATION INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A
; TITLE: Prototypic sequences for human repetitive DNA
; JOURNAL: Journal of Molecular Evolution
; VOLUME: 35
; ISSUE: 4
; PAGES: 286-291
; DATE: 1992-10-
; DATABASE ACCESSION NUMBER: Database of repetitive elements (repbase)
; DATABASE ENTRY DATE: 1996-01-26
; DATABASE ENTRY DATE: 1996-01-26
US-10-786-970A-342

Query Match 73.6%; Score 16.2; DB 10; Length 909;
Best Local Similarity 85.7%; Pred. No. 9.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGCCTTTTCGGGGTGCT 21
Db 762 GAGAGGCCTTTCTGGGGTGCT 782

RESULT 67

US-10-027-632-163064
; Sequence 163064, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 163064
; LENGTH: 935
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-163064

Query Match 73.6%; Score 16.2; DB 6; Length 935;
Best Local Similarity 85.7%; Pred. No. 9e+02; 3; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 3;

QY 2 AAAGGCCTTTCGGGGTGCTC 22
|||||
Db 519 AAAGGCCTTTCGGTGAGCTC 539

RESULT 68
US-10-027-632-163064
; Sequence 163064, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 163064
; LENGTH: 935
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-163064

Query Match 73.6%; Score 16.2; DB 7; Length 935;
Best Local Similarity 85.7%; Pred. No. 9e+02; 3; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 3;

.QY 2 AAAGGCCTTTCGGGGTGCTC 22

Db 519 AAAGGCCTTTCGGTGAGCTC 539
|||||

RESULT 69
US-10-437-963-29828/c
; Sequence 29828, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 29828
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1014)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_34292C.1
US-10-437-963-29828

Query Match 73.6%; Score 16.2; DB 8; Length 1014;
Best Local Similarity 85.7%; Pred. No. 9e+02; 3; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 3;

QY 1 GAAAGGCCTTTCGGGGTGCT 21
|||||
Db 944 GAAGGCCCATTCGGGGGGCT 924

RESULT 70
US-09-864-761-20761/c
; Sequence 20761, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 20761
; LENGTH: 1218
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006115.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.5
; OTHER INFORMATION: NT HIT: AF208980.1, EVALUE 0.00e+00
; OTHER INFORMATION: EST HUMAN HIT: AU137741.1, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: P52742, EVALUE 2.00e-17

US-09-864-761-20761

Query Match 73.6%; Score 16.2; DB 3; Length 1218;
Best Local Similarity 85.7%; Pred. No. 8.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGGCTTTTCGGGGTGCTC 22
||| ||||| ||| |||||
Db 139 AAATGCCTTTGGGGAGTGCTC 119

RESULT 71

US-10-282-122A-26246
; Sequence 26246, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26246
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Mycobacterium bovis
; US-10-282-122A-26246

Query Match 73.6%; Score 16.2; DB 8; Length 1377;
Best Local Similarity 85.7%; Pred. No. 8.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGGCTTTTCGGGGTGCTC 22
||| ||||| ||| |||||
Db 538 AAAGGCGGTCGCGGGTGCTC 558

RESULT 72

US-10-282-122A-28592
; Sequence 28592, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625

```
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28592
; LENGTH: 1380
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-282-122A-28592

Query Match          73.6%; Score 16.2; DB 8; Length 1380;
Best Local Similarity 85.7%; Pred. No. 8.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCTTTTCGGGGTGCTC 22
Db 538 AAAGGCGGTTCGGGGTGCTC 558

RESULT 73
US-10-240-965-33/c
; Sequence 33, Application US/10240965
; Publication No. US20030165924A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: SHIFFMAN, Dov
; APPLICANT: SOMOGYI, Roland
; APPLICANT: LAWN, Richard M.
; APPLICANT: SEILHAMER, Jeffrey J.
; APPLICANT: PORTER, Gordon J.
; APPLICANT: MIKITA, Thomas
; APPLICANT: TAI, Julie
; TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION
; FILE REFERENCE: PA-0025 PCT
; CURRENT APPLICATION NUMBER: US/10/240,965
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 60/195,106
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 1704
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030165924A1 978788.1
; LOCATION: 216-390, 846-889, 1593
; OTHER INFORMATION: a, t, c, g, or other
US-10-240-965-33

Query Match          73.6%; Score 16.2; DB 7; Length 1704;
Best Local Similarity 85.7%; Pred. No. 8.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGTGCT 21
Db 41 GAAAGGCTTTTCGAGATGCT 21

RESULT 74
US-09-349-015-30/c
; Sequence 30, Application US/09349015A
; Patent No. US20020015950A1
; GENERAL INFORMATION:
; APPLICANT: HANZEL, David K.
```

```
; APPLICANT: Jones, Karen Anne
; APPLICANT: Volkmut, Wayne
; APPLICANT: Walker, Michael
; TITLE OF INVENTION: ATHEROSCLEROSIS-ASSOCIATED GENES
; FILE REFERENCE: PB-0013 US
; CURRENT APPLICATION NUMBER: US/09/349,015A
; CURRENT FILING DATE: 1999-07-07
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; FEATURE:
; LOCATION: 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227,
; OTHER INFORMATION: a or g or c or t, unknown, or other
US-09-349-015-30

Query Match          73.6%; Score 16.2; DB 3; Length 1740;
Best Local Similarity 85.7%; Pred. No. 8.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGTGCT 21
Db 41 GAAAGGCTTTTCGAGATGCT 21

RESULT 75
US-10-219-664-22/c
; Sequence 22, Application US/10219664
; Publication No. US20030129176A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen Anne
; APPLICANT: Volkmut, Wayne
; APPLICANT: Walker, Michael G.
; APPLICANT: Murty, Lynn E.
; TITLE OF INVENTION: ATHEROSCLEROSIS-ASSOCIATED GENES
; FILE REFERENCE: PB-0013-1 CIP
; CURRENT APPLICATION NUMBER: US/10/219,664
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 09/349,015
; PRIOR FILING DATE: 1999-07-07
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PERL Program
; SEQ ID NO 22
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 216-390, 846-889
; OTHER INFORMATION: a, t, c, g, or other
US-10-219-664-22

Query Match          73.6%; Score 16.2; DB 7; Length 1740;
Best Local Similarity 85.7%; Pred. No. 8.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGTGCT 21
Db 41 GAAAGGCTTTTCGAGATGCT 21

RESULT 76
US-09-864-761-4001/c
; Sequence 4001, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
```

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; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US 09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 4001
; LENGTH: 1954
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006115.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.9
US-09-864-761-4001

```

```

; Sequence 815, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133p1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 815
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1253)..(1253)
; OTHER INFORMATION: n equals a,t,g, or c
; US-10-264-049--815

Query Match 73.6%; Score 16.2; DB 7; Length 2772;
Best Local Similarity 85.7%; Pred. No. 8.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGGCCTTTCGGGGTGCTC 22
Db 1526 AAATGCCTTTGGGGAGTGCTC 1546

RESULT 78
US-10-175-523-151
; Sequence 151, Application US/10175523
; Publication No. US20030096264A1
; GENERAL INFORMATION:
; APPLICANT: Brockman, Jeffrey
; APPLICANT: Evans, David
; APPLICANT: Hook, Derek
; APPLICANT: Klimczak, Leszek
; APPLICANT: Laeng, Pascal
; APPLICANT: Palfreyman, Michael
; APPLICANT: Rajan, Prithi
; TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
; FILE REFERENCE: 3235/1J795-US3
; CURRENT APPLICATION NUMBER: US/10/175,523
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/299,151
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/317,828
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/325,150
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/333,047
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 60/349,936
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/361,834
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 151
; LENGTH: 3135
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-175-523-151

```

```

50      334  AGGAGGCTTGGGAGGAGGAGGAGC 374
      Query Match      73.6%; Score 16.2; DB 6; Length 3135;
      Best Local Similarity 85.7%; Pred. NO. 8.1e+02;
      Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
RESULT 77
US-10-264-049-815

```



```
QY      2 AAAGGCCTTTCGGGGGTGCTC 22
      ||| ||||| ||| |||||
Db      1689 AAATGCCTTTGGGAGTGCTC 1709

RESULT 79
US-11-099-266-151
; Sequence 151, Application US/11099266
; Publication No. US20050181433A1
; GENERAL INFORMATION:
; APPLICANT: Brockman, Jeffrey
; APPLICANT: Evans, David
; APPLICANT: Hook, Derek
; APPLICANT: Klimczak, Leszek
; APPLICANT: Laeng, Pascal
; APPLICANT: Palfreyman, Michael
; APPLICANT: Rajan, Prithi
; TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
; FILE REFERENCE: 03235/100J795-US4
; CURRENT APPLICATION NUMBER: US/11/099,266
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 10/175,523
; PRIOR FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/299,151
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/317,828
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/325,150
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/333,047
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 60/349,936
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/361,834
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 151
; LENGTH: 3135
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-099-266-151

Query Match      73.6%; Score 16.2; DB 13; Length 3135;
Best Local Similarity 85.7%; Pred. No. 8.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 AAAGGCCTTTCGGGGGTGCTC 22
      ||| ||||| ||| |||||
Db      1689 AAATGCCTTTGGGAGTGCTC 1709

RESULT 80
US-10-287-436A-1061
; Sequence 1061, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1061
; LENGTH: 4258
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-287-436A-1061

Query Match      73.6%; Score 16.2; DB 13; Length 3135;
Best Local Similarity 85.7%; Pred. No. 8.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 AAAGGCCTTTCGGGGGTGCTC 22
      ||| ||||| ||| |||||
Db      1689 AAATGCCTTTGGGAGTGCTC 1709

RESULT 81
US-09-925-301-224
; Sequence 224, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 224
; LENGTH: 4395
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (325)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (4382)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (4391)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-224

Query Match      73.6%; Score 16.2; DB 3; Length 4395;
Best Local Similarity 85.7%; Pred. No. 7.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 AAAGGCCTTTCGGGGGTGCTC 22
      ||| ||||| ||| |||||
Db      603 AAATGCCTTTGGGAGTGCTC 623

RESULT 82
US-10-137-113-23/c
; Sequence 23, Application US/10137113
; Publication No. US20030175725A1
; GENERAL INFORMATION:
; APPLICANT: Kepur, Vivek
; APPLICANT: Rannantine, John P.
; TITLE OF INVENTION: Mycobacterial Diagnostics
; FILE REFERENCE: 09531-112001
; CURRENT APPLICATION NUMBER: US/10/137,113
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/362,396
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 4415
; TYPE: DNA
; ORGANISM: Mycobacterium paratuberculosis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 44
; OTHER INFORMATION: n = A,T,C or G
```

US-10-137-113-23

Query Match 73.6%; Score 16.2; DB 7; Length 4415;
Best Local Similarity 85.7%; Pred. No. 7.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGGCCTTCGGGGGTGCTC 22
Db 625 AAAGACCTGTCGGGGGTGCC 605

RESULT 83

US-09-842-777-9
; Sequence 9, Application US/09842777
; Publication No. US20020182669A1
; GENERAL INFORMATION:
; APPLICANT: Surani, Azim
; TITLE OF INVENTION: Human PEG3 Gene and Uses Thereof
; FILE REFERENCE: 41657
; CURRENT APPLICATION NUMBER: US/09/842,777
; CURRENT FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-842-777-9

Query Match 73.6%; Score 16.2; DB 3; Length 4758;
Best Local Similarity 85.7%; Pred. No. 7.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGGCCTTCGGGGGTGCTC 22
Db 4599 AAATGCCTTTGGGAGTGCTC 4619

RESULT 84

US-10-334-143-116
; Sequence 116, Application US/10334143
; Publication No. US20040009549A1
; GENERAL INFORMATION:
; APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH
; TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
; TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD
; FILE REFERENCE: 038602/1543
; CURRENT APPLICATION NUMBER: US/10/334,143
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: 60/343,169
; PRIOR FILING DATE: 2001-12-31
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 116
; LENGTH: 4831
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-334-143-116

Query Match 73.6%; Score 16.2; DB 7; Length 4831;
Best Local Similarity 85.7%; Pred. No. 7.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGGCCTTCGGGGGTGCTC 22
Db 4672 AAATGCCTTTGGGAGTGCTC 4692

RESULT 85

US-10-205-219-136
; Sequence 136, Application US/10205219

Publication No. US20030138803A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pincock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018200
; CURRENT APPLICATION NUMBER: US/10/205,219
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 136
; LENGTH: 5994
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: KIAA0287
US-10-205-219-136

Query Match 73.6%; Score 16.2; DB 7; Length 5994;
Best Local Similarity 85.7%; Pred. No. 7.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGGCCTTCGGGGGTGCTC 22
Db 4591 AAATGCCTTTGGGAGTGCTC 4611

RESULT 86

US-10-173-999-122
; Sequence 122, Application US/10173999
; Publication No. US20040005583A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Ovarian
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-0024200S
; CURRENT APPLICATION NUMBER: US/10/173,999
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: US 60/299,234
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/315,287
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 122
; LENGTH: 5994
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-173-999-122

Query Match 73.6%; Score 16.2; DB 7; Length 5994;
Best Local Similarity 85.7%; Pred. No. 7.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGGCCTTCGGGGGTGCTC 22
Db 4591 AAATGCCTTTGGGAGTGCTC 4611

RESULT 87

US-10-723-860-1893

```
; Sequence 1893, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1893
; LENGTH: 5994
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-1893

Query Match      73.6%; Score 16.2; DB 9; Length 5994;
Best Local Similarity 85.7%; Pred. No. 7.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 AAAGGCTTTTCGGGGTGCTC 22
Db      4591 AAATGCTTTGGGAGTGCTC 4611

RESULT 88
US-10-756-149-1800
; Sequence 1800, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1800
; LENGTH: 5994
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-756-149-1800

Query Match      73.6%; Score 16.2; DB 10; Length 5994;
Best Local Similarity 85.7%; Pred. No. 7.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 AAAGGCTTTTCGGGGTGCTC 22
Db      4591 AAATGCTTTGGGAGTGCTC 4611

RESULT 89
US-10-276-774-1341
; Sequence 1341, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1e1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
```

```
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 1341
; LENGTH: 6332
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-1341

Query Match      73.6%; Score 16.2; DB 8; Length 6332;
Best Local Similarity 85.7%; Pred. No. 7.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 AAAGGCTTTTCGGGGTGCTC 22
Db      4899 AAATGCTTTGGGAGTGCTC 4919

RESULT 90
US-10-960-414-82
; Sequence 82, Application US/10960414
; Publication No. US200600074565A1
; GENERAL INFORMATION:
; APPLICANT: MILLER, LANCE D.
; APPLICANT: GEORGE, JOSHY
; APPLICANT: VEGA, VINSENSIUS B.
; TITLE OF INVENTION: METHODS, SYSTEMS, AND COMPOSITIONS FOR CLASSIFICATION,
; FILE REFERENCE: 38271-76067
; CURRENT APPLICATION NUMBER: US/10/960,414
; CURRENT FILING DATE: 2004-10-06
; NUMBER OF SEQ ID NOS: 500
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82
; LENGTH: 6371
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-960-414-82

Query Match      73.6%; Score 16.2; DB 12; Length 6371;
Best Local Similarity 85.7%; Pred. No. 7.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 AAAGGCTTTTCGGGGTGCTC 22
Db      4972 AAATGCTTTGGGAGTGCTC 4992

RESULT 91
US-09-919-039-223
; Sequence 223, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 223
; LENGTH: 8412
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 380283.1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 4053-4099, 8362, 8373, 8382, 8389, 8399, 8406-8407
; OTHER INFORMATION: a, t, c, g, or other
```

US-09-919-039-223

Query Match 73.6%; Score 16.2; DB 3; Length 8412;
Best Local Similarity 85.7%; Pred. No. 7.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGCCTTCGGGGTGCTC 22
||| ||||| ||| |||||
Db 4595 AAATGCCTTTGGGGAGTGCTC 4615

RESULT 92

US-10-062-674-1976
; Sequence 1976, Application US/10062674
; Publication No. US2004000559A1
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.
; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
; FILE REFERENCE: PA-0026-1 CIP
; CURRENT APPLICATION NUMBER: US/10/062,674
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: US 09/625,102
; PRIOR FILING DATE: 2000-07-24
; NUMBER OF SEQ ID NOS: 2217
; SOFTWARE: PERL Program
; SEQ ID NO 1976
; LENGTH: 8682
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US2004000559A1 380283.5
; FEATURE:
; LOCATION: (1)... (8682)
; OTHER INFORMATION: a, t, c, g, or other
US-10-062-674-1976

Query Match 73.6%; Score 16.2; DB 7; Length 8682;
Best Local Similarity 85.7%; Pred. No. 7.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGCCTTCGGGGTGCTC 22
||| ||||| ||| |||||
Db 4771 AAATGCCTTTGGGGAGTGCTC 4791

RESULT 93

US-10-388-934-556
; Sequence 556, Application US/10388934
; Publication No. US20040005547A1
; GENERAL INFORMATION:
; APPLICANT: Boess, Franziska
; APPLICANT: Suter-Dick, Laura
; TITLE OF INVENTION: Biomarkers and Expression Profiles for Toxicology
; FILE REFERENCE: 21199
; CURRENT APPLICATION NUMBER: US/10/388,934
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 02005336.9
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 02015657.6
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 862
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 556
; LENGTH: 25759
; TYPE: DNA
; ORGANISM: Rattus norvegicus (No. US20040005547A1way rat)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)... (7)
; OTHER INFORMATION: n

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8)... (8)
; OTHER INFORMATION: n
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)... (9)
; OTHER INFORMATION: n
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)... (10)
; OTHER INFORMATION: n
US-10-388-934-556

Query Match 73.6%; Score 16.2; DB 7; Length 25759;
Best Local Similarity 85.7%; Pred. No. 6.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGCCTTCGGGGTGCT 21
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Db 21445 GAAAGCATTAGTGGTGCT 21465

RESULT 94

US-11-224-663-556
; Sequence 556, Application US/11224663
; Publication No. US20060078921A1
; GENERAL INFORMATION:
; APPLICANT: BOESS, FRANZISKA
; APPLICANT: SUTER-DICK, LAURA
; TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
; FILE REFERENCE: 21199 US2
; CURRENT APPLICATION NUMBER: US/11/224,663
; CURRENT FILING DATE: 2005-09-12
; PRIOR APPLICATION NUMBER: 10/388,934
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: EP 02005336.9
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: EP 02015657.6
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 862
; SOFTWARE: PatentIn version 3.1
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; LENGTH: 25759
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7)... (10)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-11-224-663-556

Query Match 73.6%; Score 16.2; DB 16; Length 25759;
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Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGCCTTCGGGGTGCT 21
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Db 21445 GAAAGCATTAGTGGTGCT 21465

RESULT 95

US-11-224-525-556
; Sequence 556, Application US/11224525
; Publication No. US20060084096A1
; GENERAL INFORMATION:
; APPLICANT: BOESS, FRANZISKA
; APPLICANT: SUTER-DICK, LAURA
; TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
; FILE REFERENCE: 21199 US1
; CURRENT APPLICATION NUMBER: US/11/224,525

CURRENT APPLICATION NUMBER: US/10/175,523

Db 37462 GATATGCCCTTTCCGGGTGCT 37442
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RESULT 99
US-10-012-697-422/c
; Sequence 422, Application US/10012697
; Publication No. US20030215803A1
; GENERAL INFORMATION:
; APPLICANT: Escobedo, Jaime
; APPLICANT: Garcia, Pablo Dominguez
; APPLICANT: Kassam, Altaf
; APPLICANT: Lamson, George
; APPLICANT: Scott, Beth
; APPLICANT: Drmanac, Radoje
; APPLICANT: Crkvenjakov, Radomir
; APPLICANT: Dickson, Mark
; APPLICANT: Drmanac, Snezana
; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Kita, David
; APPLICANT: Garcia, Veronica
; APPLICANT: Jones, Lee William
; APPLICANT: Stache-Crain, Birgit
; TITLE OF INVENTION: HUMAN GENES AND GENE EXPRESSION PRODUCTS
; FILE REFERENCE: 2300-16252
; CURRENT APPLICATION NUMBER: US/10/012,697
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 60/254,648
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/275,668
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 1568
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 422
; LENGTH: 297
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
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; LOCATION: 243, 250, 252, 260, 278, 281, 285, 286, 297
; OTHER INFORMATION: n = A,T,C or G
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; NAME/KEY: misc feature
; LOCATION: 124, 150, 151, 180, 193, 218, 221, 229, 236, 237, 239, 241,
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; NAME/KEY: misc feature
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; LOCATION: 243, 250, 252, 260, 278, 281, 285, 286, 297
; OTHER INFORMATION: n = A,T,C or G
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; OTHER INFORMATION: n = A,T,C or G
US-10-012-697-422

Query Match 72.7%; Score 16; DB 7; Length 297;
Best Local Similarity 100.0%; Pred.No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 74 GAAAGGCCTTTCCGGG 59

RESULT 100
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; Sequence 22422, Application US/10779543
; Publication No. US20050227917A1
; GENERAL INFORMATION:
; APPLICANT: Williams et al
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; FILE REFERENCE: 2300-21302
; CURRENT APPLICATION NUMBER: US/10/779,543
; PRIOR FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 10/076,555
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 09/217,471
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/068,755
; PRIOR FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: 60/080,664
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/105,234
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 09/297,648
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: PCT/US99/01619
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: 60/072,910
; PRIOR FILING DATE: 1998-01-28
; PRIOR APPLICATION NUMBER: 60/075,954
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/080,114
; PRIOR FILING DATE: 1998-03-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 23767
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22422
; LENGTH: 297
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 124, 150, 151, 180, 193, 218, 221, 229, 236, 237, 239, 241,
; LOCATION: 243, 250, 252, 260, 278, 281, 285, 286, 297
; OTHER INFORMATION: n = A,T,C or G
US-10-779-543-22422

Query Match 72.7%; Score 16; DB 10; Length 297;
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Qy 1 GAAAGGCCTTTCCGGG 16
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Db 74 GAAAGGCCTTTCCGGG 59

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Job time : 891.518 secs

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 03:57:04 ; Search time 13.6506 Seconds
(without alignments)
113.711 Million cell updates/sec

Title: US-10-665-708-25

Perfect score: 22

Sequence: 1 gaaagccttcgggggtgctc 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 224314 seqs, 35277956 residues

Total number of hits satisfying chosen parameters: 448628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications NA New.*

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- 2: /EMC_Celerra_SID33/ptodata/2/pubnpna/US06_NEW_PUB.seq.*
- 3: /EMC_Celerra_SID33/ptodata/2/pubnpna/US07_NEW_PUB.seq.*
- 4: /EMC_Celerra_SID33/ptodata/2/pubnpna/US08_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	15.6	70.9	1923	7	US-11-217-529-75858
2	14.8	67.3	51	7	US-11-143-642-1563
3	14.6	66.4	352	6	US-10-488-619-487
4	14.6	66.4	4896	7	US-11-258-767-61
5	14.6	66.4	394191	6	US-10-506-549-3
6	14.2	64.5	415	6	US-10-473-173-344
7	14.2	64.5	597	6	US-10-488-619-2783
8	14.2	64.5	1869	7	US-11-217-529-76833
9	14.2	64.5	2063	6	US-10-196-749-329
10	14.2	64.5	2063	7	US-11-101-316-111
11	14.2	64.5	2104	7	US-11-145-307A-34
12	14	63.6	963	7	US-11-217-529-80486
13	14	63.6	1122	7	US-11-217-529-81650
14	14	63.6	1938	7	US-11-217-529-82499
15	14	63.6	2384	7	US-11-145-307A-259
16	14	63.6	3401	6	US-10-505-928-717
17	14	63.6	4277	6	US-10-196-749-439
18	14	63.6	4933	6	US-10-505-928-15
19	14	63.6	4933	6	US-10-505-928-88
20	14	63.6	135090	6	US-10-505-928-607
21	13.8	62.7	76	7	US-11-267-871-477
22	13.8	62.7	76	7	US-11-267-871-477
23	13.8	62.7	76	7	US-11-267-871-478
24	13.8	62.7	76	7	US-11-267-871-478
25	13.8	62.7	76	7	US-11-267-871-479

Sequence 479, App	7	US-11-267-871-479	76	62.7	13.8	c	26
Sequence 577, App	6	US-10-505-928-577	3432	62.7	13.8	c	27
GENERAL INFORMATI	6	US-10-489-730-10	138941	62.7	13.8	c	28
Sequence 2651, Ap	6	US-10-511-937-2651	50	61.8	13.6	c	29
Sequence 480, App	7	US-11-267-871-480	76	61.8	13.6	c	30
Sequence 480, App	7	US-11-267-871-480	76	61.8	13.6	c	31
Sequence 2876, Ap	7	US-11-217-529-2876	282	61.8	13.6	c	32
Sequence 1040, Ap	6	US-10-488-619-1040	393	61.8	13.6	c	33
Sequence 167012,	7	US-11-217-529-167012	420	61.8	13.6	c	34
Sequence 76, Appl	6	US-10-541-993-76	1170	61.8	13.6	c	35
Sequence 598, App	6	US-10-511-937-598	1458	61.8	13.6	c	36
Sequence 398, App	7	US-10-511-937-398	1631	61.8	13.6	c	37
Sequence 77050, A	7	US-11-217-529-77050	1950	61.8	13.6	c	38
Sequence 462, App	6	US-10-511-937-462	2615	61.8	13.6	c	39
Sequence 2820, Ap	6	US-10-511-937-2820	3003	61.8	13.6	c	40
Sequence 989, App	7	US-11-217-529-989	3435	61.8	13.6	c	41
Sequence 319, App	6	US-10-488-619-319	462	60.9	13.4	c	42
Sequence 1868, Ap	6	US-10-511-937-1868	20	60.0	13.2	c	43
Sequence 185666,	7	US-11-217-529-185666	25	60.0	13.2	c	44
Sequence 397, App	7	US-11-267-871-397	64	60.0	13.2	c	45
Sequence 397, App	7	US-11-267-871-397	64	60.0	13.2	c	46
Sequence 300, App	7	US-11-301-554-300	185	60.0	13.2	c	47
Sequence 1087, Ap	6	US-10-488-619-1087	253	60.0	13.2	c	48
Sequence 81832, A	7	US-11-217-529-81832	330	60.0	13.2	c	49
Sequence 13, Appl	7	US-11-301-554-373	467	60.0	13.2	c	50
Sequence 79160, A	6	US-10-514-738-19	574	60.0	13.2	c	51
Sequence 1381, Ap	6	US-11-217-529-79160	723	60.0	13.2	c	52
Sequence 417, App	7	US-11-217-529-417	894	60.0	13.2	c	53
Sequence 1664, Ap	7	US-10-511-937-1664	999	60.0	13.2	c	54
Sequence 613, App	6	US-10-511-937-613	1263	60.0	13.2	c	55
Sequence 2366, Ap	7	US-11-217-529-2366	1284	60.0	13.2	c	56
Sequence 3591, Ap	6	US-11-217-529-3591	1902	60.0	13.2	c	57
Sequence 605, App	6	US-10-511-937-605	2338	60.0	13.2	c	58
Sequence 95, Appl	6	US-11-217-529-1652	2436	60.0	13.2	c	59
Sequence 80783, A	6	US-10-196-749-95	2579	60.0	13.2	c	60
Sequence 836, App	7	US-11-217-529-80783	2760	60.0	13.2	c	61
Sequence 346, App	6	US-10-505-928-346	3269	60.0	13.2	c	62
Sequence 255, App	6	US-10-505-928-346	3396	60.0	13.2	c	63
Sequence 59, Appl	7	US-11-145-307A-255	3487	60.0	13.2	c	64
Sequence 3, Appl	6	US-11-312-958-59	3650	60.0	13.2	c	65
Sequence 629, App	6	US-10-505-928-629	3711	60.0	13.2	c	66
Sequence 3, Appl	6	US-10-473-173-18	3806	60.0	13.2	c	67
Sequence 2852, Ap	6	US-10-511-937-2852	4122	60.0	13.2	c	68
Sequence 37, Appl	6	US-10-511-937-37	7391	60.0	13.2	c	69
Sequence 48200, A	6	US-10-519-335-37	7603	60.0	13.2	c	70
Sequence 95163, A	6	US-11-217-529-48200	151830	60.0	13.2	c	71
Sequence 110861,	7	US-11-217-529-95163	25	59.1	13	c	72
Sequence 193133,	7	US-11-217-529-110861	25	59.1	13	c	73
Sequence 422, App	7	US-11-217-529-193133	25	59.1	13	c	74
Sequence 3817, Ap	6	US-10-473-173-422	455	59.1	13	c	75
Sequence 2860, Ap	6	US-11-217-529-3817	519	59.1	13	c	76
Sequence 2302, Ap	6	US-10-488-619-772	524	59.1	13	c	77
Sequence 190988,	6	US-10-488-619-2302	570	59.1	13	c	78
Sequence 7851, A	7	US-11-217-529-190988	595	59.1	13	c	79
Sequence 591, App	7	US-11-217-529-75649	838	59.1	13	c	80
Sequence 1664, Ap	7	US-11-217-529-75649	840	59.1	13	c	81
Sequence 77610, A	7	US-11-217-529-77610	924	59.1	13	c	82
Sequence 3014, Ap	7	US-11-217-529-77610	966	59.1	13	c	83
Sequence 76451, A	7	US-11-217-529-77610	975	59.1	13	c	84
Sequence 2, Appl	7	US-11-217-529-77610	999	59.1	13	c	85
Sequence 77917, A	7	US-11-301-554-1664	1299	59.1	13	c	86
Sequence 10, Appl	7	US-11-217-529-3014	1329	59.1	13	c	87
Sequence 7917, A	7	US-11-217-529-76451	1431	59.1	13	c	88
Sequence 76600, A	6	US-10-508-063A-2	1695	59.1	13	c	89
Sequence 384, App	7	US-11-217-529-77917	1731	59.1	13	c	90
Sequence 105, App	7	US-11-242-505A-10	1821	59.1	13	c	91
	7	US-11-217-529-76600	2007	59.1	13	c	92
	6	US-10-511-937-384	2106	59.1	13	c	93
	7	US-11-217-529-105	2610	59.1	13	c	94

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C 101	13	59.1	3360	7	US-11-217-529-82548	Sequence 82548, A	C 174	12.4	56.4	468	7	US-11-217-529-6074	Sequence 6074, Ap
C 102	13	59.1	3394	7	US-11-217-529-195593	Sequence 195593, A	C 175	12.4	56.4	585	7	US-11-217-529-3697	Sequence 3697, Ap
C 103	13	59.1	3394	7	US-11-217-529-195594	Sequence 195594, A	C 176	12.4	56.4	601	6	US-10-519-335-42	Sequence 42, Appl
C 104	13	59.1	3394	7	US-11-217-529-195595	Sequence 195595, A	C 177	12.4	56.4	609	6	US-10-488-619-1845	Sequence 1845, Ap
C 105	13	59.1	3394	7	US-11-217-529-195596	Sequence 195596, A	C 178	12.4	56.4	660	6	US-10-196-749-467	Sequence 467, App
C 106	13	59.1	3394	7	US-11-217-529-195597	Sequence 195597, A	C 179	12.4	56.4	720	7	US-11-217-529-1971	Sequence 1971, Ap
C 107	13	59.1	3714	6	US-10-505-928-390	Sequence 390, App	C 180	12.4	56.4	735	7	US-11-301-554-1387	Sequence 1387, Ap
C 108	13	59.1	128361	6	US-10-505-928-151	Sequence 151, App	C 181	12.4	56.4	882	7	US-11-217-529-79142	Sequence 79142, A
C 109	13	59.1	138941	6	US-10-489-730-10	GENERAL INFORMATI	C 182	12.4	56.4	1065	7	US-11-217-529-1893	Sequence 1893, Ap
C 110	12.8	58.2	25	7	US-11-217-529-53847	Sequence 53847, A	C 183	12.4	56.4	1113	7	US-11-217-529-2143	Sequence 2143, Ap
C 111	12.8	58.2	25	7	US-11-217-529-91576	Sequence 91576, A	C 184	12.4	56.4	1323	7	US-11-217-529-190822	Sequence 190822, A
C 112	12.8	58.2	417	7	US-11-217-529-4313	Sequence 4313, Ap	C 185	12.4	56.4	1376	7	US-11-219-635-17	Sequence 17, Appl
C 113	12.8	58.2	855	7	US-11-217-529-77669	Sequence 77669, A	C 186	12.4	56.4	1443	7	US-11-217-529-77791	Sequence 77791, A
C 114	12.8	58.2	1290	7	US-11-302-678-54	Sequence 54, Appl	C 187	12.4	56.4	1458	6	US-10-196-749-129	Sequence 129, App
C 115	12.8	58.2	1500	7	US-11-445-3078-260	Sequence 260, App	C 188	12.4	56.4	1508	7	US-11-101-316-19	Sequence 19, Appl
C 116	12.8	58.2	1557	7	US-11-302-678-52	Sequence 52, Appl	C 189	12.4	56.4	1611	7	US-11-217-529-1511	Sequence 1511, Ap
C 117	12.8	58.2	1593	7	US-11-217-529-1097	Sequence 1097, Ap	C 190	12.4	56.4	1905	7	US-11-217-529-82032	Sequence 82032, A
C 118	12.8	58.2	1984	6	US-10-523-290-20	Sequence 20, Appl	C 191	12.4	56.4	1948	1	US-09-949-925-71	Sequence 71, Appl
C 119	12.8	58.2	2853	7	US-11-217-529-76130	Sequence 76130, A	C 192	12.4	56.4	2052	7	US-11-217-529-634	Sequence 634, App
C 120	12.6	57.3	25	7	US-11-217-529-56074	Sequence 56074, A	C 193	12.4	56.4	2313	7	US-11-217-529-77342	Sequence 77342, A
C 121	12.6	57.3	25	7	US-11-217-529-188944	Sequence 188944, A	C 194	12.4	56.4	2339	6	US-10-196-749-327	Sequence 327, App
C 122	12.6	57.3	51	7	US-11-143-642-201	Sequence 201, App	C 195	12.4	56.4	2339	7	US-11-101-316-109	Sequence 109, App
C 123	12.6	57.3	462	6	US-10-488-619-2972	Sequence 319, App	C 196	12.4	56.4	2413	7	US-11-219-635-25	Sequence 25, Appl
C 124	12.6	57.3	478	6	US-10-488-619-379	Sequence 379, App	C 197	12.4	56.4	2829	7	US-11-217-529-3101	Sequence 3101, Ap
C 125	12.6	57.3	489	6	US-10-488-619-174434	Sequence 174434, A	C 198	12.4	56.4	2853	7	US-11-145-307A-175	Sequence 175, App
C 126	12.6	57.3	555	7	US-11-217-529-81230	Sequence 81230, A	C 199	12.4	56.4	3003	6	US-10-196-749-51	Sequence 51, Appl
C 127	12.6	57.3	573	7	US-11-217-529-81230	Sequence 81230, A	C 200	12.4	56.4	3054	7	US-11-217-529-2509	Sequence 2509, Ap
C 128	12.6	57.3	581	6	US-10-488-619-2947	Sequence 2947, Ap	C 201	12.4	56.4	3075	7	US-11-226-605-51	Sequence 51, Appl
C 129	12.6	57.3	584	6	US-10-488-619-2019	Sequence 2019, Ap	C 202	12.4	56.4	3157	6	US-10-468-193-29	Sequence 29, Appl
C 130	12.6	57.3	606	7	US-11-217-529-174334	Sequence 174334, A	C 203	12.4	56.4	3296	6	US-10-370-959-92	Sequence 92, Appl
C 131	12.6	57.3	618	6	US-10-511-937-526	Sequence 526, App	C 204	12.4	56.4	3417	7	US-11-131-901-7	Sequence 7, Appli
C 132	12.6	57.3	678	7	US-11-217-529-3208	Sequence 3208, App	C 205	12.4	56.4	3426	6	US-10-511-937-438	Sequence 438, App
C 133	12.6	57.3	711	7	US-11-217-529-78447	Sequence 78447, A	C 206	12.4	56.4	3484	7	US-11-181-115-34	Sequence 34, Appl
C 134	12.6	57.3	720	6	US-10-505-928-68	Sequence 68, Appl	C 207	12.4	56.4	3486	7	US-11-217-529-1392	Sequence 1392, Ap
C 135	12.6	57.3	744	7	US-11-217-529-4512	Sequence 4512, Ap	C 208	12.4	56.4	3494	6	US-10-505-928-796	Sequence 796, App
C 136	12.6	57.3	912	7	US-11-217-529-49	Sequence 49, Appl	C 209	12.4	56.4	3877	6	US-10-196-749-263	Sequence 263, Appl
C 137	12.6	57.3	924	7	US-11-217-529-6110	Sequence 6110, Ap	C 210	12.4	56.4	3877	7	US-11-101-316-71	Sequence 41, Appl
C 138	12.6	57.3	930	7	US-11-217-529-4685	Sequence 4685, Ap	C 211	12.4	56.4	3952	7	US-11-223-945-41	Sequence 41, Appl
C 139	12.6	57.3	981	7	US-11-217-529-80486	Sequence 80486, A	C 212	12.4	56.4	4010	6	US-10-511-937-359	Sequence 359, App
C 140	12.6	57.3	983	7	US-11-106-014-95	Sequence 95, Appl	C 213	12.4	56.4	4804	7	US-11-181-115-42	Sequence 42, Appl
C 141	12.6	57.3	1236	7	US-11-217-529-78751	Sequence 78751, A	C 214	12.4	56.4	4816	6	US-10-511-937-555	Sequence 555, App
C 142	12.6	57.3	1284	7	US-11-217-529-76846	Sequence 76846, A	C 215	12.4	56.4	4828	6	US-10-511-937-555	Sequence 555, App
C 143	12.6	57.3	1293	7	US-11-217-529-4748	Sequence 4748, Ap	C 216	12.4	56.4	4987	6	US-10-505-928-433	Sequence 433, App
C 144	12.6	57.3	1493	6	US-10-511-937-447	Sequence 447, App	C 217	12.4	56.4	4987	7	US-11-251-465-4	Sequence 4, Appli
C 145	12.6	57.3	1500	6	US-10-505-928-210	Sequence 210, App	C 218	12.4	56.4	5014	7	US-11-251-465-5	Sequence 5, Appli
C 146	12.6	57.3	1500	7	US-11-217-529-1568	Sequence 1568, Ap	C 219	12.4	56.4	5251	7	US-11-217-529-191127	Sequence 191127, A
C 147	12.6	57.3	1749	7	US-11-217-529-6123	Sequence 6123, Ap	C 220	12.4	56.4	5269	7	US-11-217-529-190883	Sequence 190883, A
C 148	12.6	57.3	1838	7	US-11-301-554-1897	Sequence 1897, Ap	C 221	12.4	56.4	5269	7	US-11-217-529-190885	Sequence 190885, A
C 149	12.6	57.3	2079	6	US-10-370-959-6	Sequence 6, Appli	C 222	12.4	56.4	5269	7	US-11-217-529-190899	Sequence 190899, A
C 150	12.6	57.3	2164	6	US-10-505-928-147	Sequence 147, App	C 223	12.4	56.4	5269	7	US-11-217-529-190913	Sequence 190913, A
C 151	12.6	57.3	2438	6	US-10-370-959-4	Sequence 4, Appli	C 224	12.4	56.4	5269	7	US-11-217-529-190944	Sequence 190944, A
C 152	12.6	57.3	2587	6	US-10-473-173-125	Sequence 125, App	C 225	12.4	56.4	5269	7	US-11-217-529-191008	Sequence 191008, A
C 153	12.6	57.3	2694	6	US-10-196-749-207	Sequence 207, App	C 226	12.4	56.4	5269	7	US-11-217-529-191076	Sequence 191076, A
C 154	12.6	57.3	2778	7	US-11-217-529-5649	Sequence 5649, Ap	C 227	12.4	56.4	5269	7	US-11-217-529-191082	Sequence 191082, A
C 155	12.6	57.3	3780	6	US-10-509-131-24	Sequence 24, Appl	C 228	12.4	56.4	5269	7	US-11-217-529-191115	Sequence 191115, A
C 156	12.6	57.3	3781	6	US-10-196-749-453	Sequence 453, App	C 229	12.4	56.4	5269	7	US-11-217-529-191136	Sequence 191136, A
C 157	12.6	57.3	4092	7	US-11-217-529-2502	Sequence 2502, Ap	C 230	12.4	56.4	5269	7	US-11-217-529-191171	Sequence 191171, A
C 158	12.6	57.3	4093	7	US-11-251-465-6	Sequence 6, Appli	C 231	12.4	56.4	5269	7	US-11-217-529-191171	Sequence 191171, A
C 159	12.6	57.3	4194	7	US-11-217-529-77339	Sequence 77339, A	C 232	12.4	56.4	5269	7	US-11-131-901-5	Sequence 5, Appli
C 160	12.6	57.3	5003	6	US-10-473-173-112	Sequence 112, App	C 233	12.4	56.4	6163	6	US-10-524-021-9	Sequence 9, Appli
C 161	12.6	57.3	6335	6	US-10-505-928-178	Sequence 178, App	C 234	12.4	56.4	6450	6	US-10-505-928-750	Sequence 750, App
C 162	12.6	57.3	6543	6	US-10-509-131-34	Sequence 34, Appl	C 235	12.4	56.4	7008	7	US-11-263-326-98	Sequence 98, Appl
C 163	12.6	57.3	7758	6	US-10-505-928-236	Sequence 236, App	C 236	12.4	56.4	7008	7	US-11-263-326-104	Sequence 104, App
C 164	12.6	57.3	11564	6	US-10-505-928-105	Sequence 105, App	C 237	12.4	56.4	7408	7	US-11-245-473-13	Sequence 13, Appl
C 165	12.6	57.3	151830	6	US-10-519-335-37	Sequence 37, Appl	C 238	12.4	56.4	15304	6	US-10-505-928-828	Sequence 828, Appl
C 166	12.4	56.4	25	7	US-11-217-529-105108	Sequence 105108, A	C 239	12.4	56.4	394191	6	US-10-506-549-3	Sequence 3, Appli
C 167	12.4	56.4	108	7	US-11-217-529-81840	Sequence 81840, A	C 240	12.2	55.5	25	7	US-11-217-529-103956	Sequence 103956, A
C 168	12.4	56.4	193	7	US-11-217-529-5752	Sequence 5752, Ap	C 241	12.2	55.5	25	7	US-11-217-529-155568	Sequence 155568, A
C 169	12.4	56.4	241	7	US-11-301-554-866	Sequence 866, App	C 242	12.2	55.5	51	7	US-11-143-642-2024	Sequence 2024, Ap
C 170	12.4	56.4	350	6	US-10-488-619-577	Sequence 577, App	C 243	12.2	55.5	99	7	US-11-217-529-174292	Sequence 174292, A
C 171	12.4	56.4	404	6	US-10-488-619-347	Sequence 347, App	C 244	12.2	55.5	111	7	US-11-217-529-166813	Sequence 166813, A

Sequence 1719, Ap
Sequence 81843, A
Sequence 205, App
Sequence 353, App
Sequence 847, App
Sequence 71, Appl
Sequence 174034, A
Sequence 3, Appl
Sequence 937, App
Sequence 1682, App
Sequence 2986, App
Sequence 6, Appl
Sequence 2411, App
Sequence 80548, A
Sequence 431, App
Sequence 3528, App
Sequence 20, Appl
Sequence 1054, App
Sequence 78884, A
Sequence 2083, App
Sequence 3534, App
Sequence 75884, A
Sequence 127, App
Sequence 10, Appl
Sequence 63, Appl
Sequence 78421, A
Sequence 8, Appl
Sequence 76376, A
Sequence 79704, A
Sequence 479, App
Sequence 76439, A
Sequence 25, Appl
Sequence 76568, A
Sequence 535, App
Sequence 5, Appl
Sequence 3162, App
Sequence 13, Appl
Sequence 3, Appl
Sequence 1, Appl
Sequence 163, App
Sequence 547, App
Sequence 613, App
Sequence 76244, A
Sequence 2220, App
Sequence 11, Appl
Sequence 22, Appl
Sequence 2533, App
Sequence 5833, App
Sequence 179, App
Sequence 77238, A
Sequence 78638, A
Sequence 261, App
Sequence 629, App
Sequence 208, App
Sequence 3, Appl

US-11-301-554-1719
US-11-217-529-61843
US-10-488-619-205
US-11-301-554-353
US-11-301-554-847
US-11-301-554-71
US-11-217-529-174034
US-11-131-901-3
US-11-301-554-937
US-10-488-619-1682
US-10-488-619-2986
US-11-317-983-6
US-11-217-529-2241
US-11-217-529-80548
US-10-196-749-431
US-11-217-529-3528
US-11-154-103-20
US-11-217-529-1054
US-11-217-529-77582
US-11-217-529-78884
US-11-217-529-2083
US-11-217-529-3534
US-11-217-529-75884
US-10-196-749-127
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US-11-256-428-63
US-11-217-529-78421
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US-11-106-014-13
US-11-244-678-3
US-11-244-678-1
US-11-145-307A-163
US-10-196-749-547
US-11-217-529-613
US-11-217-529-76244
US-11-217-529-2220
US-11-245-628-11
US-11-302-678-22
US-10-196-749-253
US-11-217-529-5833
US-10-196-749-179
US-11-217-529-77238
US-11-217-529-78638
US-10-196-749-261
US-10-505-928-629
US-10-505-928-208
US-11-066-633-3

ALIGNMENTS

RESULT 1
US-11-217-529-75858
; Sequence 75858, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75858
; LENGTH: 1923
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75858
Query Match 70.9%; Score 15.6; DB 7; Length 1923;
Best Local Similarity 81.8%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GAAAGCCCTTCGGGGGTGCTC 22
DB 1283 GCAATGCCCTTTGGGGGTGCTC 1304
RESULT 2
US-11-143-642-1563
; Sequence 1563, Application US/11143642
; Publication No. US20060099610A1
; GENERAL INFORMATION:
; APPLICANT: Jukka T. SALONEN et al.
; TITLE OF INVENTION: METHOD AND KIT FOR DETECTING A RISK OF ACUTE MYOCARDIAL INFARCTION
; FILE REFERENCE: 0933-0245PUS1
; CURRENT APPLICATION NUMBER: US/11/143,642
; CURRENT FILING DATE: 2005-06-03
; NUMBER OF SEQ ID NOS: 2039
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1563
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-143-642-1563
Query Match 67.3%; Score 14.8; DB 7; Length 51;
Best Local Similarity 88.9%; Pred. No. 21;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 AGGCTTTTCGGGGGTGCT 21
DB 32 AGGCTTTTCGGGGGTGCT 49
RESULT 3
US-10-488-619-487
; Sequence 487, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 487
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-488-619-487
Query Match 66.4%; Score 14.6; DB 6; Length 352;
Best Local Similarity 81.0%; Pred. No. 36;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GAAAGCCCTTCGGGGGTGCT 21

Db 168 GGAAGGCTCCGGGGTGCT 188
| | | | | | | | | | | | | | | | | |

RESULT 4
US-11-258-767-61
; Sequence 61, Application US/11258767
; Publication No. US20060094082A1
; GENERAL INFORMATION:
; APPLICANT: Varadhachary, Atul
; APPLICANT: Glynn, Peter
; APPLICANT: Petrak, Kare1
; APPLICANT: Engelmayer, Jose
; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/11/258,767
; PRIOR FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/622,176
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61
; LENGTH: 4896
; TYPE: DNA
; ORGANISM: HUMAN
US-11-258-767-61

Query Match 66.4%; Score 14.6; DB 7; Length 4896;
Best Local Similarity 81.0%; Pred. No. 52;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AAAGGCTTTTCGGGGTGCTC 22
| | | | | | | | | | | | | | | | | |
Db 336 AATGGCCTTGAGGGGTGCTC 356

RESULT 5
US-10-506-549-3/c
; Sequence 3, Application US/10506549
; Publication No. US20060100417A1
; GENERAL INFORMATION:
; APPLICANT: APPLERA CORPORATION
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001361-US
; CURRENT APPLICATION NUMBER: US/10/506,549
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/361,343
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 394191
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(394191)
; OTHER INFORMATION: n = A,T,C or G
US-10-506-549-3

Query Match 66.4%; Score 14.6; DB 6; Length 394191;
Best Local Similarity 81.0%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTTCGGGGTGCT 21
| | | | | | | | | | | | | | | | | |
Db 348930 GAGAGGCTTTCTGAGTGCT 348910

RESULT 6
US-10-473-173-344/c

; Sequence 344, Application US/10473173
; Publication No. US20060088823A1
; GENERAL INFORMATION:
; APPLICANT: VAN ANDEL INSTITUTE
; TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
; FILE REFERENCE: 38345-170094
; CURRENT APPLICATION NUMBER: US/10/473,173
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/279,411
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 498
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 344
; LENGTH: 415
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (186)..(186)
; OTHER INFORMATION: n can be a, c, g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (235)..(235)
; OTHER INFORMATION: n can be a, c, g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (242)..(242)
; OTHER INFORMATION: n can be a, c, g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (257)..(257)
; OTHER INFORMATION: n can be a, c, g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (319)..(319)
; OTHER INFORMATION: n can be a, c, g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (372)..(372)
; OTHER INFORMATION: n can be a, c, g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (385)..(385)
; OTHER INFORMATION: n can be a, c, g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (410)..(410)
; OTHER INFORMATION: n can be a, c, g or t
US-10-473-173-344

Query Match 64.5%; Score 14.2; DB 6; Length 415;
Best Local Similarity 84.2%; Pred. No. 58;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTTCGGGGTG 19
| | | | | | | | | | | | | | | | | |
Db 228 GAGAGCCCTTCAGGGTG 210

RESULT 7
US-10-488-619-2783
; Sequence 2783, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1

Qy

Db 509 AGGCCCTTCGGGGAAGCTC 491
||||| ||||| |||||

RESULT 11
US-11-145-307A-34/c
; Sequence 34, Application US/11145307A
; Publication No. US20060094035A1
; GENERAL INFORMATION:
; APPLICANT: Arcturus Bioscience, Inc.
; APPLICANT: Erlander, Mark G.
; APPLICANT: Ma, Xiao-Jun
; TITLE OF INVENTION: Identification of Tumors
; FILE REFERENCE: 022041-002020US
; CURRENT APPLICATION NUMBER: US/11/145,307A
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/577,084
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 2104
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-145-307A-34

Query Match 64.5%; Score 14.2; DB 7; Length 2104;
Best Local Similarity 84.2%; Pred. No. 73;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 AGGCCCTTCGGGGTGCTC 22
||||| ||||| |||||
Db 532 AGGCCCTTCGGGGAAGCTC 514

RESULT 12
US-11-217-529-80486/c
; Sequence 80486, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80486
; LENGTH: 963
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-80486

Query Match 63.6%; Score 14; DB 7; Length 963;
Best Local Similarity 77.3%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTCGGGGTGCTC 22
||||| ||||| |||||
Db 275 GTATAGCCTTCGAGGGTGCTC 254

RESULT 13
US-11-217-529-81650
; Sequence 81650, Application US/11217529
; Publication No. US20060099612A1

; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81650
; LENGTH: 1122
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-81650

Query Match 63.6%; Score 14; DB 7; Length 1122;
Best Local Similarity 77.3%; Pred. No. 84;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTCGGGGTGCTC 22
||||| ||||| |||||
Db 526 GTAGGCCCTTCGGGGATACAC 547

RESULT 14
US-11-217-529-82499/c
; Sequence 82499, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82499
; LENGTH: 1938
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82499

Query Match 63.6%; Score 14; DB 7; Length 1938;
Best Local Similarity 77.3%; Pred. No. 91;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTCGGGGTGCTC 22
||||| ||||| |||||
Db 504 GAAGAGCCTTCGGGGGAAGCTC 483

RESULT 15
US-11-145-307A-259
; Sequence 259, Application US/11145307A
; Publication No. US20060094035A1
; GENERAL INFORMATION:
; APPLICANT: Arcturus Bioscience, Inc.
; APPLICANT: Erlander, Mark G.
; APPLICANT: Ma, Xiao-Jun
; TITLE OF INVENTION: Identification of Tumors

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; FILE REFERENCE: 022041-002020US
; CURRENT APPLICATION NUMBER: US/11/145,307A
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/577,084
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 259
; LENGTH: 2384
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-145-307A-259

Query Match      63.6%; Score 14; DB 7; Length 2384;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 CCTTTCGGGGTGTC 20
Db      2244 CCTTTCGGGGTGTC 2257

RESULT 16
US-10-505-928-717
; Sequence 717, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 717
; LENGTH: 3401
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-717

Query Match      63.6%; Score 14; DB 6; Length 3401;
Best Local Similarity 77.3%; Pred. No. 99;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 GAAAGGCGTTTCGGGGTGCTC 22
Db      2758 GAAAGGCGTTTCACGGGCTGCTC 2779

RESULT 17
US-10-196-749-439/c
; Sequence 439, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Deenoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586

; FILE REFERENCE: 022041-002020US
; CURRENT APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 439
; LENGTH: 4277
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-749-439

Query Match      63.6%; Score 14; DB 6; Length 4277;
Best Local Similarity 77.3%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 GAAAGGCGTTTCGGGGTGCTC 22
Db      3465 GACAGGACTGTGCGGGGCTCTC 3444

RESULT 18
US-10-505-928-15/c
; Sequence 15, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 15
; LENGTH: 4933
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-15

Query Match      63.6%; Score 14; DB 6; Length 4933;
Best Local Similarity 77.3%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 GAAAGGCGTTTCGGGGTGCTC 22
Db      1852 GAGAGGCCGTTGGGTGGGCTC 1831

RESULT 19
US-10-505-928-88/c
; Sequence 88, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
```

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; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 88
; LENGTH: 4933
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-88

Query Match      63.6%; Score 14; DB 6; Length 4933;
Best Local Similarity 77.3%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTCGGGGTGCTC 22
Db 1852 GAGAGGCCGTTGGGGTGGGCTC 1831

RESULT 20
US-10-505-928-607/c
; Sequence 607, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 607
; LENGTH: 135090
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-607

Query Match      63.6%; Score 14; DB 6; Length 135090;
Best Local Similarity 77.3%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTCGGGGTGCTC 22
Db 33663 GATAGGCCCTTGGCAGTTGCTC 33642

RESULT 21
US-11-267-871-477
; Sequence 477, Application US/11267871
; Publication No. US20060094655A1
; GENERAL INFORMATION:
; APPLICANT: Guyon, Thierry
; APPLICANT: Borrelly, Gilles
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: MODIFIED GROWTH HORMONES
; FILE REFERENCE: 17109-015001/925
; CURRENT APPLICATION NUMBER: US/11/267,871
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: 60/706,697
; PRIOR FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: 60/625,652
; PRIOR FILING DATE: 2004-11-04
; NUMBER OF SEQ ID NOS: 719
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 477
; LENGTH: 76
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

US-11-267-871-477

Query Match      62.7%; Score 13.8; DB 7; Length 76;
Best Local Similarity 88.2%; Pred. No. 72;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAAGGCCTTCGGGGT 18
Db 43 AAAGGCCTTAGGAGGT 27

RESULT 23
US-11-267-871-478
; Sequence 478, Application US/11267871
; Publication No. US20060094655A1
; GENERAL INFORMATION:
; APPLICANT: Guyon, Thierry
; APPLICANT: Borrelly, Gilles
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: MODIFIED GROWTH HORMONES
; FILE REFERENCE: 17109-015001/925
; CURRENT APPLICATION NUMBER: US/11/267,871
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: 60/706,697
; PRIOR FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: 60/625,652
; PRIOR FILING DATE: 2004-11-04
; NUMBER OF SEQ ID NOS: 719
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 478
; LENGTH: 76
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

US-11-267-871-478

Query Match      62.7%; Score 13.8; DB 7; Length 76;
Best Local Similarity 88.2%; Pred. No. 72;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAAGGCCTTCGGGGT 18
Db 43 AAAGGCCTTAGGAGGT 27

RESULT 22
US-11-267-871-477/c
; Sequence 477, Application US/11267871
; Publication No. US20060094655A1
; GENERAL INFORMATION:
; APPLICANT: Guyon, Thierry
; APPLICANT: Borrelly, Gilles
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: MODIFIED GROWTH HORMONES
; FILE REFERENCE: 17109-015001/925
; CURRENT APPLICATION NUMBER: US/11/267,871
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: 60/706,697
; PRIOR FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: 60/625,652
; PRIOR FILING DATE: 2004-11-04
; NUMBER OF SEQ ID NOS: 719
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 477
; LENGTH: 76
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

US-11-267-871-477

Query Match      62.7%; Score 13.8; DB 7; Length 76;
Best Local Similarity 88.2%; Pred. No. 72;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAAGGCCTTCGGGGT 18
Db 34 AAAGGCCTTAGGAGGT 50
```

```
; OTHER INFORMATION: Primer
US-11-267-871-478

Query Match          62.7%; Score 13.8; DB 7; Length 76;
Best Local Similarity 88.2%; Pred. No. 72;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 AAAGGCCTTTCGGGGT 18
    ||||| ||| |||
Db  34 AAAGGCCTTTAGGAGT 50

RESULT 24
US-11-267-871-478/c
; Sequence 478, Application US/11267871
; Publication No. US20060094655A1
; GENERAL INFORMATION:
; APPLICANT: Guyon, Thierry
; APPLICANT: Borrelly, Gilles
; APPLICANT: Dittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: MODIFIED GROWTH HORMONES
; FILE REFERENCE: 17109-015001/925
; CURRENT APPLICATION NUMBER: US/11/267,871
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: 60/706,697
; PRIOR FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: 60/625,652
; PRIOR FILING DATE: 2004-11-04
; NUMBER OF SEQ ID NOS: 719
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 478
; LENGTH: 76
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-11-267-871-478

Query Match          62.7%; Score 13.8; DB 7; Length 76;
Best Local Similarity 88.2%; Pred. No. 72;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 AAAGGCCTTTCGGGGT 18
    ||||| ||| |||
Db  43 AAAGGCCTTTAGGAGT 27

RESULT 25
US-11-267-871-479
; Sequence 479, Application US/11267871
; Publication No. US20060094655A1
; GENERAL INFORMATION:
; APPLICANT: Guyon, Thierry
; APPLICANT: Borrelly, Gilles
; APPLICANT: Dittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: MODIFIED GROWTH HORMONES
; FILE REFERENCE: 17109-015001/925
; CURRENT APPLICATION NUMBER: US/11/267,871
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: 60/706,697
; PRIOR FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: 60/625,652
; PRIOR FILING DATE: 2004-11-04
; NUMBER OF SEQ ID NOS: 719
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 479
; LENGTH: 76
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Primer
US-10-505-928-577
; Sequence 577, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 577
; LENGTH: 3432
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-577

Query Match          62.7%; Score 13.8; DB 6; Length 3432;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  3 AAGGCCTTTCGGGGTG 19
    ||||| ||| |||
```


Db 2782 AAGGCCTTGGGGGGTG 2798

RESULT 28
US-10-489-730-10
; GENERAL INFORMATION:
; APPLICANT: Melino, Gennaro
; APPLICANT: Hayes, Ian
; APPLICANT: de Laurenzi, Vincenzo
; APPLICANT: Barcaroli, Daniela
; APPLICANT: Candi, Eleonora
; APPLICANT: Bernasola, Francesca
; APPLICANT: Tobler, Andreas
; APPLICANT: Novak, Urban
; TITLE OF INVENTION: Human Delta-N p73 Molecules and Uses Thereof
; FILE REFERENCE: 19319.002
; CURRENT APPLICATION NUMBER: US/10/489,730
; CURRENT FILING DATE: 2004-03-16
; PRIOR APPLICATION NUMBER: PCT/GB02/04238
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US 60/322,436
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 39
; OTHER INFORMATION: reverse complement of exons 14 through 1 as reported in GenBank A
US-10-489-730-10

Query Match 62.7%; Score 13.8; DB 6; Length 138941;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AAGGCCTTTCGGGGTG 19
|||||

Db 81269 AAGGCCTATCTGGGGTG 81285

RESULT 29
US-10-511-937-2651/c
; Sequence 2651, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2651
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-2651

Query Match 61.8%; Score 13.6; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AAGGCCTTTCGGGGTGCT 21
|||||

Db 24 AAAGCCATTGGTGGGGCT 5

RESULT 30
US-11-267-871-480
; Sequence 480, Application US/11267871
; Publication No. US20060094655A1
; GENERAL INFORMATION:
; APPLICANT: Guyon, Thierry
; APPLICANT: Borrelly, Gilles
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: MODIFIED GROWTH HORMONES
; FILE REFERENCE: 17109-015001/925
; CURRENT APPLICATION NUMBER: US/11/267,871
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: 60/706,697
; PRIOR FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: 60/625,652
; PRIOR FILING DATE: 2004-11-04
; NUMBER OF SEQ ID NOS: 719
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 480
; LENGTH: 76
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-11-267-871-480

Query Match 61.8%; Score 13.6; DB 7; Length 76;
Best Local Similarity 80.0%; Pred. No. 90;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AAAGCCTTTCGGGGTGCT 21
|||||

Db 34 AAAGCCTTTAGGAGCTGAT 53

RESULT 31
US-11-267-871-480/c
; Sequence 480, Application US/11267871
; Publication No. US20060094655A1
; GENERAL INFORMATION:
; APPLICANT: Guyon, Thierry
; APPLICANT: Borrelly, Gilles
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: MODIFIED GROWTH HORMONES
; FILE REFERENCE: 17109-015001/925
; CURRENT APPLICATION NUMBER: US/11/267,871
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: 60/706,697
; PRIOR FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: 60/625,652
; PRIOR FILING DATE: 2004-11-04
; NUMBER OF SEQ ID NOS: 719
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 480
; LENGTH: 76
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-11-267-871-480

Query Match 61.8%; Score 13.6; DB 7; Length 76;
Best Local Similarity 80.0%; Pred. No. 90;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AAAGCCTTTCGGGGTGCT 21
|||||

Db 43 AAAGCCTTTAGGAGCTGAT 24

```

; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 167012
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-167012

Query Match      61.8%; Score 13.6; DB 7; Length 420;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  2 AAAGCCCTTCGGGGTGCT 21
    ||||| ||||| ||||| |||||
Db  313 AAAGCCCTTTGGGGCGTT 294

RESULT 35
US-10-541-993-76/c
; Sequence 76, Application US/10541993
; Publication No. US20060099670A1
; GENERAL INFORMATION:
; APPLICANT: Matuschek, Markus
; APPLICANT: Heinekamp, Thorsten
; APPLICANT: Schmidt, Andre
; APPLICANT: Brakhage, Axel
; TITLE OF INVENTION: Method for the genetic modification of organisms of the genus
; TITLE OF INVENTION: Blakeslea, corresponding organisms, and the use of the same
; FILE REFERENCE: 13311-00010-US
; CURRENT APPLICATION NUMBER: US/10/541,993
; CURRENT FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: PCT/EP2004/000100
; PRIOR FILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: DE 103 00 649.4
; PRIOR FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: DE 103 41 272.7
; PRIOR FILING DATE: 2003-09-08
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 76
; LENGTH: 1170
; TYPE: DNA
; ORGANISM: Thermus thermophilus
US-10-541-993-76

Query Match      61.8%; Score 13.6; DB 6; Length 1170;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  3 AAGCCCTTCGGGGTGCTC 22
    ||||| ||||| ||||| |||||
Db  482 AGGCCCTTAAGGGCGTCTC 463

RESULT 36
US-10-511-937-598
; Sequence 598, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: James

; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2676
; LENGTH: 282
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-2676

Query Match      61.8%; Score 13.6; DB 7; Length 282;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  2 AAAGCCCTTCGGGGTGCT 21
    ||||| ||||| ||||| |||||
Db  74 AAAGCCCTTTGGGGCGTT 55

RESULT 33
US-10-488-619-1040
; Sequence 1040, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1040
; LENGTH: 393
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1040

Query Match      61.8%; Score 13.6; DB 6; Length 393;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  2 AAAGCCCTTCGGGGTGCT 21
    ||||| ||||| ||||| |||||
Db  73 AAAGGTCTCTGGAGGTGCT 92

RESULT 34
US-11-217-529-167012/c
; Sequence 167012, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: James
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```
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 598
; LENGTH: 1458
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-598

Query Match          61.8%; Score 13.6; DB 6; Length 1458;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTTCGGGGGTGC 20
   |||||
Db 1225 GTAAAGCCTTTCGGGTGCTC 1244

RESULT 37
US-10-511-937-398/c
; Sequence 398, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 398
; LENGTH: 1631
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-398

Query Match          61.8%; Score 13.6; DB 6; Length 1631;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AAAGGCCTTTCGGGGGTGCT 21
   |||||
Db 1379 AATGGCCTTTCAGTGTGCT 1360

RESULT 38
US-11-217-529-77050
; Sequence 77050, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77050
; LENGTH: 1950
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77050

Query Match          61.8%; Score 13.6; DB 7; Length 1950;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 AAGGCCTTTCGGGGGTGCTC 22
   |||||
Db 364 AAGGCCTTTCGGGAGTTCTC 383

RESULT 39
US-10-511-937-462/c
; Sequence 462, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 462
; LENGTH: 2615
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-462

Query Match          61.8%; Score 13.6; DB 6; Length 2615;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTTCGGGGGTGC 20
   |||||
Db 994 GAAGGCATTCGGGGCTCC 975
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RESULT 40

US-10-937-2820/c
; Sequence 2820, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2820
; LENGTH: 3003
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-2820

Query Match 61.8%; Score 13.6; DB 6; Length 3003;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AAAGCCTTCGGGGTGCT 21

Db 2918 AAAGCCATTGGGTGGGCT 2899

RESULT 41

US-11-217-529-989
; Sequence 989, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 989
; LENGTH: 3435
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-989

Query Match 61.8%; Score 13.6; DB 7; Length 3435;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AAAGCCTTCGGGGTGCT 21

Db 53 ATAGGCCTTCGGCGGTGT 72

RESULT 42

US-10-488-619-319/c
; Sequence 319, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 319
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(462)
; OTHER INFORMATION: n is g, c, a or t
US-10-488-619-319

Query Match 60.9%; Score 13.4; DB 6; Length 462;
Best Local Similarity 93.3%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAAGCCTTCGGG 15

Db 92 GAAAGCCTTCGGG 78

RESULT 43

US-10-511-937-1868
; Sequence 1868, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1868
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-1868

Query Match 60.0%; Score 13.2; DB 6; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GGCCTTCGGGGTGCTC 22

Db 3 GGCCTTCCTTGGGTCTC 20

RESULT 44
US-11-217-529-165666
; Sequence 165666, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOSHIO
; APPLICANT: ASHIKARI, TOMOHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 165666
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-165666

Query Match 60.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 AGCGCTTTCGGGGTGCT 21
| | | | | | | | | | | | | | | | | | | | | |
Db 7 AAGCCTTTCAGCGGTGCT 24

RESULT 45
US-11-267-871-397
; Sequence 397, Application US/11267871
; Publication No. US20060094655A1
; GENERAL INFORMATION:
; APPLICANT: Guyon, Thierry
; APPLICANT: Borrelly, Gilles
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: MODIFIED GROWTH HORMONES
; FILE REFERENCE: 17109-015001/925
; CURRENT APPLICATION NUMBER: US/11/267,871
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: 60/706,697
; PRIOR FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: 60/625,652
; PRIOR FILING DATE: 2004-11-04
; NUMBER OF SEQ ID NOS: 719
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 397
; LENGTH: 64
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-11-267-871-397

Query Match 60.0%; Score 13.2; DB 7; Length 64;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGCGCTTTCGGGGTG 19
| | | | | | | | | | | | | | | | | | | | | |
Db 28 AAAGCGCTTTCGGGTG 45

RESULT 46

US-11-267-871-397/c
; Sequence 397, Application US/11267871
; Publication No. US20060094655A1
; GENERAL INFORMATION:
; APPLICANT: Guyon, Thierry
; APPLICANT: Borrelly, Gilles
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: MODIFIED GROWTH HORMONES
; FILE REFERENCE: 17109-015001/925
; CURRENT APPLICATION NUMBER: US/11/267,871
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: 60/706,697
; PRIOR FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: 60/625,652
; PRIOR FILING DATE: 2004-11-04
; NUMBER OF SEQ ID NOS: 719
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 397
; LENGTH: 64
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-11-267-871-397

Query Match 60.0%; Score 13.2; DB 7; Length 64;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGCGCTTTCGGGGTG 19
| | | | | | | | | | | | | | | | | | | | | |
Db 37 AAAGCGCTTTCGGGTG 20

RESULT 47
US-11-301-554-300
; Sequence 300, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419

```

; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 300
; LENGTH: 185
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-301-554-300

Query Match      60.0%; Score 13.2; DB 7; Length 185;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 AAAGGCCTTCGGGGGTG 19
Db  130 AATGGCCTTCGTGGTG 147

RESULT 48
US-10-488-619-1087/c
; Sequence 1087, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT FILING DATE: 2004-03-01
; CURRENT APPLICATION NUMBER: US/10/488,619
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1087
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1087

Query Match      60.0%; Score 13.2; DB 6; Length 253;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 AAAGGCCTTCGGGGGTG 19
Db  223 AAAGGCCTTCGGGGGGG 206

RESULT 49
US-11-217-529-81832
; Sequence 81832, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81832
; LENGTH: 330
; TYPE: DNA

```

```

; ORGANISM: Saccharomyces pastorianus
US-11-217-529-81832

Query Match      60.0%; Score 13.2; DB 7; Length 330;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  1 GAAAGGCCTTCGGGGGTG 18
Db  244 GAAAGGCATTTGGGTGGT 261

RESULT 50
US-11-217-529-82742
; Sequence 82742, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82742
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82742

Query Match      60.0%; Score 13.2; DB 7; Length 399;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  4 AGGCCTTCGGGGGTGCT 21
Db  323 AAGCCTTCAGCGGTGCT 340

RESULT 51
US-11-301-554-373/c
; Sequence 373, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28

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/ PRIOR APPLICATION NUMBER: US 10/017,754
/ PRIOR FILING DATE: 2001-10-29
/ PRIOR APPLICATION NUMBER: US 09/902,941
/ PRIOR FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: US 09/849,626
/ PRIOR FILING DATE: 2001-05-03
/ PRIOR APPLICATION NUMBER: US 09/736,457
/ PRIOR FILING DATE: 2000-12-13
/ PRIOR APPLICATION NUMBER: US 09/702,705
/ PRIOR FILING DATE: 2000-10-30
/ PRIOR APPLICATION NUMBER: US 09/677,419
/ PRIOR FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: US 09/671,325
/ PRIOR FILING DATE: 2000-09-26
/ PRIOR APPLICATION NUMBER: US 09/658,824
/ PRIOR FILING DATE: 2000-09-08
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 2157
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 373
/ LENGTH: 467
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-301-554-373

Query Match          60.0%; Score 13.2; DB 7; Length 467;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTCGGGGTG 19
Db 148 AAAGCTCTCTCGGGTG 131

RESULT 52
US-10-514-738-19
/ Sequence 19, Application US/10514738
/ Publication No. US2006009353A1
/ GENERAL INFORMATION:
/ APPLICANT: DANG, NAM HOANG
/ APPLICANT: MORIMOTO, CHIKAO
/ TITLE OF INVENTION: CD26-BASED THERAPIES FOR CANCERS AND IMMUNE DISEASE
/ FILE REFERENCE: UTSC:7500S
/ CURRENT APPLICATION NUMBER: US/10/514,738
/ PRIOR FILING DATE: 2004-11-18
/ PRIOR APPLICATION NUMBER: PCT/US03/15499
/ PRIOR FILING DATE: 2003-05-15
/ PRIOR APPLICATION NUMBER: 60/381,606
/ PRIOR FILING DATE: 2002-05-17
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 19
/ LENGTH: 574
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-514-738-19

Query Match          60.0%; Score 13.2; DB 6; Length 574;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTCGGGGTG 19
Db 159 AATGGCTTCTCGGGGTG 176

RESULT 53
US-11-217-529-79160/c
/ Sequence 79160, Application US/11217529
/ Publication No. US20060099612A1
/ GENERAL INFORMATION:
/ APPLICANT: SUNTORY LIMITED
/ APPLICANT: NAKAO, YOSHIHIRO
/ APPLICANT: NAKAO, YOSHIHIRO
/ APPLICANT: KODAMA, YUKIKO
/ APPLICANT: FUJIMURA, TOMOKO
/ APPLICANT: ASHIKARI, TOSHIHIKO
/ TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ FILE REFERENCE: S-38-285
/ CURRENT APPLICATION NUMBER: US/11/217,529
/ CURRENT FILING DATE: 2005-09-02
/ PRIOR APPLICATION NUMBER: US 10/932,182
/ PRIOR FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
```

```
/ APPLICANT: NAKAMURA, NORIHIISA
/ APPLICANT: KODAMA, YUKIKO
/ APPLICANT: FUJIMURA, TOMOKO
/ APPLICANT: ASHIKARI, TOSHIHIKO
/ TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ FILE REFERENCE: S-38-285
/ CURRENT APPLICATION NUMBER: US/11/217,529
/ CURRENT FILING DATE: 2005-09-02
/ PRIOR APPLICATION NUMBER: US 10/932,182
/ PRIOR FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 79160
/ LENGTH: 723
/ TYPE: DNA
/ ORGANISM: Saccharomyces pastorianus
US-11-217-529-79160

Query Match          60.0%; Score 13.2; DB 7; Length 723;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTCGGGGTG 19
Db 95 AAAGGACTTTCAGGGTTG 78

RESULT 54
US-10-488-619-1381/c
/ Sequence 1381, Application US/10488619
/ Publication No. US20060099578A1
/ GENERAL INFORMATION:
/ APPLICANT: Greenlee, Winner and Sullivan, P.C.
/ TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations and Genotyping Arrays
/ FILE REFERENCE: 98-01 WO
/ CURRENT APPLICATION NUMBER: US/10/488,619
/ CURRENT FILING DATE: 2004-03-01
/ NUMBER OF SEQ ID NOS: 1040
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1381
/ LENGTH: 813
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-10-488-619-1381

Query Match          60.0%; Score 13.2; DB 6; Length 813;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTCGGGGTG 19
Db 457 AAAGCTCTCTCGGGGTG 440

RESULT 55
US-11-217-529-447/c
/ Sequence 447, Application US/11217529
/ Publication No. US20060099612A1
/ GENERAL INFORMATION:
/ APPLICANT: SUNTORY LIMITED
/ APPLICANT: NAKAO, YOSHIHIRO
/ APPLICANT: NAKAMURA, NORIHIISA
/ APPLICANT: KODAMA, YUKIKO
/ APPLICANT: FUJIMURA, TOMOKO
/ APPLICANT: ASHIKARI, TOSHIHIKO
/ TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ FILE REFERENCE: S-38-285
/ CURRENT APPLICATION NUMBER: US/11/217,529
/ CURRENT FILING DATE: 2005-09-02
/ PRIOR APPLICATION NUMBER: US 10/932,182
/ PRIOR FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
```

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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 447
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-447

Query Match          60.0%; Score 13.2; DB 7; Length 894;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAGAGCCTTTTCGGGGT 18
    |||||
Db 79 GAATGGCCTTTTCGGGGT 62

RESULT 56
US-11-301-554-1664
; Sequence 1664, Application US/11301554
; Publication No. US2006008527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1664
; LENGTH: 999
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2, 5, 10, 22, 83, 150, 176, 189, 264, 275, 283, 286, 302,
; LOCATION: 311, 318, 338, 374, 524, 528, 531, 536, 541, 606, 611, 614,
; LOCATION: 616, 621, 634, 635, 636, 644, 659, 682, 688, 702, 715, 723,
; LOCATION: 726, 768, 777, 779, 789, 796, 802, 810, 819, 831, 836
; OTHER INFORMATION: n = A,T,C or G
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 853, 854, 869, 874, 893, 900, 903, 911, 989, 999
; OTHER INFORMATION: n = A,T,C or G
US-11-301-554-1664

Query Match          60.0%; Score 13.2; DB 7; Length 999;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTTCGGGGTG 19
    |||||
Db 956 AAAGACCTTTTCGGGGG 973

RESULT 57
US-10-511-937-613/c
; Sequence 613, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fty, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 613
; LENGTH: 1263
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-613

Query Match          60.0%; Score 13.2; DB 6; Length 1263;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 GGCCTTTTCGGGGTGCTC 22
    |||||
Db 261 GGCCTTTAGGGGCTCTC 244

RESULT 58
US-11-217-529-2966/c
; Sequence 2966, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
```



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; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2966
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-2966

Query Match          60.0%; Score 13.2; DB 7; Length 1284;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCTTTTCGGGGGTG 19
||||| ||||| |||||
Db 185 AAAGCTCTTCGGGGGTG 168

RESULT 59
US-11-217-529-3591/c
; Sequence 3591, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3591
; LENGTH: 1902
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3591

Query Match          60.0%; Score 13.2; DB 7; Length 1902;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGGT 18
||||| ||||| |||||
Db 1039 GAATGGCTTTCTTGGGT 1022

RESULT 60
US-10-511-937-605
; Sequence 605, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24

; NUMBER OF SEQ ID NOS: 10196749
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 605
; LENGTH: 2338
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-605

Query Match          60.0%; Score 13.2; DB 6; Length 2338;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCTTTTCGGGGGTG 19
||||| ||||| |||||
Db 1285 AAAGCTCTTCCTGGGGTG 1302

RESULT 61
US-11-217-529-1652
; Sequence 1652, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIRO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1652
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1652

Query Match          60.0%; Score 13.2; DB 7; Length 2436;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCTTTTCGGGGGTG 19
||||| ||||| |||||
Db 1480 AATGGCTTTCAGGTTG 1497

RESULT 62
US-10-196-749-95
; Sequence 95, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC340
; CURRENT APPLICATION NUMBER: US/10/196,749
```

; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; SEQ ID NO 95
; LENGTH: 2579
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-749-95

Query Match 60.0%; Score 13.2; DB 6; Length 2579;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAGGCTTTTCGGGGTGTG 19
||||| ||||| |||||

Db 1570 AAGGCTTTTCAGGGATG 1587

RESULT 63
US-11-217-529-80783/c
; Sequence 80783, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80783
; LENGTH: 2760
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (2094)..(2094)
; OTHER INFORMATION: a, c, g, t, unknown, or other
US-11-217-529-80783

Query Match 60.0%; Score 13.2; DB 7; Length 2760;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGGCTTTTCGGGGTGTG 20
||||| ||||| |||||

Db 567 AAGGCCATTTGGGAGTGC 550

RESULT 64
US-11-217-529-80319/c
; Sequence 80319, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80319
; LENGTH: 2976
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-80319

Query Match 60.0%; Score 13.2; DB 7; Length 2976;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGTGTG 18
||||| ||||| |||||

Db 1484 GAACGGCTTTTCGTCGCT 1467

RESULT 65
US-10-505-928-836/c
; Sequence 836, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 836
; LENGTH: 3269
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-836

Query Match 60.0%; Score 13.2; DB 6; Length 3269;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 AGGCTTTTCGGGGTGTGCT 21
||||| ||||| |||||

Db 963 AGGCTTTTCGCGGGCT 946

RESULT 66
US-10-505-928-346/c
; Sequence 346, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

```
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; PRIOR FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 346
; LENGTH: 3396
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-505-928-346

Query Match          60.0%   Score 13.2; DB 6; Length 3396;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCTTTTCGGGGGTG 19
   |||||
Db 1193 AAAGGCTATTGTGGGTG 1176

RESULT 67
US-11-145-307A-255/c
; Sequence 255, Application US/11/145307A
; Publication No. US2006094035A1
; GENERAL INFORMATION:
; APPLICANT: Arcturus Bioscience, Inc.
; APPLICANT: Erlander, Mark G.
; APPLICANT: Ma, Xiao-Jun
; TITLE OF INVENTION: Identification of Tumors
; FILE REFERENCE: 022041-002020US
; CURRENT APPLICATION NUMBER: US/11/145,307A
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/577,084
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 255
; LENGTH: 3487
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-145-307A-255

Query Match          60.0%   Score 13.2; DB 7; Length 3487;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGGT 18
   |||||
Db 1872 GACAGACCTTTCAGGGGT 1855

RESULT 68
US-11-312-958-59
; Sequence 59, Application US/11/312958
; Publication No. US20060100152A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Rosenfeld, Julie Beth
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
; TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
; TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
; TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
; TITLE OF INVENTION: 13424 MOLECULES
; FILE REFERENCE: MPI02-027PIRNONMIN
; CURRENT APPLICATION NUMBER: US/11/312,958
; CURRENT FILING DATE: 2005-12-20
; PRIOR APPLICATION NUMBER: US/10/369,022
; PRIOR FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: US 60/360,495
```

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; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/370,121
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/373,010
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/373,908
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/377,717
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US 60/379,949
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/382,409
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/385,280
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/386,879
; PRIOR FILING DATE: 2002-06-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 3650
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (118)...(2013)
; US-11-312-958-59

Query Match          60.0%   Score 13.2; DB 7; Length 3650;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 GGCTTTTCGGGGGTGCTC 22
   |||||
Db 2304 GGCCATTTCAGGGGTGCAC 2321

RESULT 69
US-10-505-928-679/c
; Sequence 679, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 679
; LENGTH: 3711
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-505-928-679

Query Match          60.0%   Score 13.2; DB 6; Length 3711;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 AGGCTTTTCGGGGGTGCT 21
   |||||
Db 756 AGGCTTTCGGGGGTGCT 739

RESULT 70
US-10-473-173-18
; Sequence 18, Application US/10473173
; Publication No. US20060088823A1
; GENERAL INFORMATION:
; APPLICANT: VAN ANDEL INSTITUTE
```

```
; TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
; TITLE OF INVENTION: Carcinoma: Prognosis and Drug Target Identification
; FILE REFERENCE: 38345-170094
; CURRENT APPLICATION NUMBER: US/10/473,173
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/279,411
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 498
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 3806
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-473-173-18

Query Match      60.0%; Score 13.2; DB 6; Length 3806;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTTCGGGGT 18
   ||||| ||| |||||
Db 852 GAAAGGCTTTCTCGGGT 869

RESULT 71
US-11-066-633-3/c
; Sequence 3, Application US/11066633
; Publication No. US2006094031A1
; GENERAL INFORMATION:
; APPLICANT: Stowers Institute for Medical Research
; APPLICANT: Sauer, Brian L.
; TITLE OF INVENTION: Alpha-subscript L-Arabinofuranosidase Histochemical Reporter Gene
; FILE REFERENCE: 097287
; CURRENT APPLICATION NUMBER: US/11/066,633
; CURRENT FILING DATE: 2005-02-25
; PRIOR FILING DATE: 2004-11-04
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 4122
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-11-066-633-3

Query Match      60.0%; Score 13.2; DB 7; Length 4122;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 AGGCTTTTCGGGGTGTCT 21
   ||||| ||||| |||||
Db 1855 AAGCTCCCGGGGTGCT 1838

RESULT 72
US-10-511-937-629
; Sequence 629, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
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; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 629
; LENGTH: 7391
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-629

Query Match      60.0%; Score 13.2; DB 6; Length 7391;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GGCCTTTTCGGGGTGTCT 22
   ||||| ||||| |||||
Db 7105 GGCCTTTTCGGGTCTC 7122

RESULT 73
US-10-511-937-2852/c
; Sequence 2852, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2852
; LENGTH: 7603
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-2852

Query Match      60.0%; Score 13.2; DB 6; Length 7603;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGGCTTTTCGGGGTGTG 19
   ||||| ||||| |||||
Db 670 AGATGCTTTTCGTGGGTG 653

RESULT 74
US-10-519-335-37
; Sequence 37, Application US/10519335
; Publication No. US20060099210A1
; GENERAL INFORMATION:
; APPLICANT: Cavarec, Laurent
; APPLICANT: Chumakov, Ilya
; APPLICANT: Destenaves, Benoit
; APPLICANT: Gonthier, Catherine
```

```
, APPLICANT: Elias, Isabelle
, TITLE OF INVENTION: NOVEL KCNQ POLYPEPTIDES, MODULATORS THEREOF, AND THEIR USES IN TH
, FILE REFERENCE: G-194US03PCT
, CURRENT FILING DATE: 2004-12-22
, PRIOR FILING DATE: 2002-06-25
, NUMBER OF SEQ ID NOS: 47
, SOFTWARE: PatentIn version 3.1
, SEQ ID NO 37
, LENGTH: 151830
, TYPE: DNA
, ORGANISM: Homo sapiens
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (10)..(10)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (60402)..(60402)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (61110)..(61110)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (98207)..(98207)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (98208)..(98208)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (98209)..(98209)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (98210)..(98210)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (98211)..(98211)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (99743)..(99743)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (108055)..(108055)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (109094)..(109094)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (109125)..(109125)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (118900)..(118900)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (119052)..(119052)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (119053)..(119112)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (119121)..(119121)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (119123)..(119123)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (141674)..(141674)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (142063)..(142063)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (142137)..(142137)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (142967)..(142967)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (143077)..(143077)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (143506)..(143506)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (143587)..(143587)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (143629)..(143629)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (149079)..(149079)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (5363)..(5363)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (8080)..(8080)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (10296)..(10296)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (14528)..(14528)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (15336)..(15336)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (15457)..(15457)
, OTHER INFORMATION: n = a or c or g or t
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (16288)..(16288)
, OTHER INFORMATION: n = a or c or g or t
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FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16306)..(16307)
; OTHER INFORMATION: n = a or c or g or t
FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16316)..(16316)
; OTHER INFORMATION: n = a or c or g or t
FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16397)..(16397)
; OTHER INFORMATION: n = a or c or g or t
FEATURE:
; NAME/KEY: misc feature
; LOCATION: (56012)..(56012)
; OTHER INFORMATION: n = a or c or g or t
FEATURE:
; NAME/KEY: misc feature
; LOCATION: (57662)..(57662)
; OTHER INFORMATION: n = a or c or g or t
FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(54)
; OTHER INFORMATION: exon 1
FEATURE:
; NAME/KEY: exon
; LOCATION: (55)..(124)
; OTHER INFORMATION: exon 1
FEATURE:
; NAME/KEY: exon
; LOCATION: (91147)..(91244)
; OTHER INFORMATION: exon 2
FEATURE:
; NAME/KEY: exon
; LOCATION: (93669)..(93834)
; OTHER INFORMATION: exon 3
FEATURE:
; NAME/KEY: exon
; LOCATION: (96310)..(96422)
; OTHER INFORMATION: exon 4
FEATURE:
; NAME/KEY: exon
; LOCATION: (99546)..(99723)
; OTHER INFORMATION: exon 5
FEATURE:
; NAME/KEY: exon
; LOCATION: (125441)..(125605)

Query Match 60.0%; Score 13.2; DB 6; Length 151830;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GGCCCTTCGGGGTGCTC 22

Db 40233 GGCCCTTCGGGGTGCTC 40250

RESULT 75

US-11-217-529-48200
; Sequence 48200, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 125441
; LENGTH: 25

; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 48200
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-48200

Query Match 59.1%; Score 13; DB 7; Length 25;
Best Local Similarity 76.2%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AAAGGCCTTCGGGGTGCTC 22

Db 2 AAAGTCCTTCAGCGATGTC 22

RESULT 76

US-11-217-529-95163/c
; Sequence 95163, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 95163
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-95163

Query Match 59.1%; Score 13; DB 7; Length 25;
Best Local Similarity 76.2%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AAAGGCCTTCGGGGTGCTC 22

Db 24 ACAGGCCTTCAGGGGTTTC 4

RESULT 77

US-11-217-529-110861/c
; Sequence 110861, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 110861
; LENGTH: 25

```
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-110861

Query Match          59.1%; Score 13; DB 7; Length 25;
Best Local Similarity 76.2%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AAAGGCCTTCGGGGGTGCTC 22
    ||||| ||| ||||| |||||
Db 21 AAAGTCATTAGGGGATTCTC 1

RESULT 78
US-11-217-529-193133/c
; Sequence 193133, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 193133
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-193133

Query Match          59.1%; Score 13; DB 7; Length 25;
Best Local Similarity 76.2%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTCGGGGGTGCT 21
    ||||| ||||| ||||| |||||
Db 24 GAAAGTATTTCGGCGTGCT 4

RESULT 79
US-10-473-173-422
; Sequence 422, Application US/10473173
; Publication No. US2006008823A1
; GENERAL INFORMATION:
; APPLICANT: VAN ANDEL INSTITUTE
; TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
; TITLE OF INVENTION: Carcinoma: Prognosis and Drug Target Identification
; FILE REFERENCE: 38345-170094
; CURRENT APPLICATION NUMBER: US/10/473,173
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/279,411
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 498
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 422
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-473-173-422

Query Match          59.1%; Score 13; DB 6; Length 455;
Best Local Similarity 76.2%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTCGGGGGTGCT 21
```

```
Db 321 GCAAGGCATTTCAGGGATGCT 341

RESULT 80
US-11-217-529-3817
; Sequence 3817, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 3817
; LENGTH: 519
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3817

Query Match          59.1%; Score 13; DB 7; Length 519;
Best Local Similarity 76.2%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AAAGGCCTTCGGGGGTGCTC 22
    ||||| ||||| ||||| |||||
Db 26 AAAGTCTTTTCAGCGATGTC 46

RESULT 81
US-10-488-619-772/c
; Sequence 772, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 772
; LENGTH: 524
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-488-619-772

Query Match          59.1%; Score 13; DB 6; Length 524;
Best Local Similarity 76.2%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTCGGGGGTGCT 21
    ||||| ||||| ||||| |||||
Db 465 GAAAGCCCTCTTGGGGGCAC 445

RESULT 82
US-10-488-619-2860/c
; Sequence 2860, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
```

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RESULT 84
US-11-217-529-190988/c
; Sequence 190988, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIRO
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 190988
; LENGTH: 838
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-190988

```

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RESULT 86
US-11-217-529-77851/c
; Sequence 77851, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIISHA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77851
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77851

```

```

Query Match      59.1%; Score 13; DB 7; Length 924;
Best Local Similarity 76.2%; Pred. NO. 2.6e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```


Qy 2 AAAGCCCTTCGGGGGTGCTC 22
||||| ||| ||| ||| |||
Db 714 AAAGTCCATTAGGGGATTCTC 694

RESULT 87

US-11-217-529-591/c
; Sequence 591, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 591
; LENGTH: 966
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-591

Query Match 59.1%; Score 13; DB 7; Length 966;
Best Local Similarity 76.2%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AAAGCCCTTCGGGGGTGCTC 22
||||| ||| ||| ||| |||
Db 94 ACAGCCCTTCAGGGGAGCGC 74

RESULT 88

US-11-217-529-77610/c
; Sequence 77610, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 77610
; LENGTH: 975
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77610

Query Match 59.1%; Score 13; DB 7; Length 975;
Best Local Similarity 76.2%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AAAGCCCTTCGGGGGTGCTC 22
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Db 54 AAGAACTTTCGGGGGTGCTC 34

RESULT 89

US-11-301-554-1664/c
; Sequence 1664, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1664
; LENGTH: 999
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2, 5, 10, 22, 83, 150, 176, 189, 264, 275, 283, 286, 302,
; LOCATION: 311, 318, 338, 374, 524, 528, 531, 536, 541, 606, 611, 614,
; LOCATION: 616, 621, 634, 635, 636, 644, 659, 682, 688, 702, 715, 723,
; LOCATION: 726, 768, 777, 779, 789, 796, 802, 810, 819, 831, 836
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 853, 854, 869, 874, 893, 900, 903, 911, 989, 999
; OTHER INFORMATION: n = A,T,C or G
US-11-301-554-1664

Query Match 59.1%; Score 13; DB 7; Length 999;
Best Local Similarity 76.2%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AAAGCCCTTCGGGGGTGCTC 22
||||| ||| ||| ||| |||
Db 965 AAAGTCTTTTGGGGTTACCC 945

RESULT 90

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US-11-217-529-3014
; Sequence 3014, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3014
; LENGTH: 1299
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3014

Query Match          59.1%; Score 13; DB 7; Length 1299;
Best Local Similarity 76.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 AAAGGCCTTTCGGGGTGCTC 22
Db      841 AATGGTCTTTTGGCGGTGATC 861
      ||||| ||||| ||||| |||||

RESULT 91
US-11-217-529-76451/c
; Sequence 76451, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76451
; LENGTH: 1329
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76451

Query Match          59.1%; Score 13; DB 7; Length 1329;
Best Local Similarity 76.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 AAAGGCCTTTCGGGGTGCTC 22
Db      986 ACAGGCCTTTGAGGGGTTTC 966
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RESULT 92
US-11-242-505A-11/c
; Sequence 11, Application US/11242505A
; Publication No. US20060099656A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
```

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; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; FILE REFERENCE: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
; FILE REFERENCE: MPI2001-288P1RCP10MNM
; CURRENT APPLICATION NUMBER: US/11/242,505A
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US 10/290,078
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/347,949
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/320,351
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,606
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1431
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1431)
US-11-242-505A-11

Query Match          59.1%; Score 13; DB 7; Length 1431;
Best Local Similarity 76.2%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 GAAAGGCCTTTCGGGGTGCT 21
Db      977 GAAAGACCTGTGCGGGTCT 957
      ||||| ||||| ||||| |||||

RESULT 93
US-10-508-063A-2/c
; Sequence 2, Application US/10508063A
; Publication No. US2006008832A1
; GENERAL INFORMATION:
; APPLICANT: Deutsches Krebsforschungszentrum
; APPLICANT: ANGEL, Peter
; APPLICANT: FURSTENBERGER, Gerhard
; APPLICANT: BREITENBACH, Ute
; APPLICANT: RICHTER, Harmut
; APPLICANT: HESS, Jochen
; APPLICANT: TUCKERMAN, Jan
; TITLE OF INVENTION: TAP-70, A NOVEL MARKER FOR EPITHELIAL TUMORS
; FILE REFERENCE: 31304-701.831
; CURRENT APPLICATION NUMBER: US/10/508,063A
; CURRENT FILING DATE: 2004-09-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-508-063A-2

Query Match          59.1%; Score 13; DB 6; Length 1695;
Best Local Similarity 76.2%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 AAAGGCCTTTCGGGGTGCTC 22
Db      616 AAAGGCCTTCAGGAGGCCTC 596
      ||||| ||||| ||||| |||||

RESULT 94
US-11-217-529-77917
; Sequence 77917, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
```

```
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US 10/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77917
; LENGTH: 1731
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1323)..(1373)
; OTHER INFORMATION: a, c, g, t, unknown, or other
US-11-217-529-77917

Query Match          59.1%; Score 13; DB 7; Length 1731;
Best Local Similarity 76.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTCGGGGTGCT 21
Db 202 GCAGGGCCTTTTGGTGGTGT 222

RESULT 95
US-11-242-505A-10/c
; Sequence 10, Application US/11242505A
; Publication No. US20060099656A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
; FILE REFERENCE: MPI2001-288P1RCP10MNM
; CURRENT APPLICATION NUMBER: US/11/242,505A
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US 10/290,078
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/347,949
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/320,351
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,606
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1821
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-242-505A-10

Query Match          59.1%; Score 13; DB 7; Length 1821;
Best Local Similarity 76.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTCGGGGTGCT 21
Db 1011 GAAAGACCTGTGCGGGGTCT 991

RESULT 96
US-11-217-529-76600/c
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; Sequence 76600, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76600
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76600

Query Match          59.1%; Score 13; DB 7; Length 2007;
Best Local Similarity 76.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTCGGGGTGCT 21
Db 1665 GAAAGGCCTTTTGAGTGTGAT 1645

RESULT 97
US-10-511-937-384/c
; Sequence 384, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 384
; LENGTH: 2106
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-384

Query Match          59.1%; Score 13; DB 6; Length 2106;
Best Local Similarity 76.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTCGGGGTGCT 21
Db 1955 GATAGGCCACGCGGGGTACT 1935
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```

RESULT 100
US-10-505-928-124/c
; Sequence 124, Application US/10505928
; Publication No. US2006008532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL CELL

```

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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 02:23:06 ; Search time 1887.72 Seconds
(without alignments)
1829.273 Million cell updates/sec

Title: US-10-665-708-11

Perfect score: 54

Sequence: 1 gaaattataatcgactacta.....tgtgcaatattcccaactgc 54

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Listing first 300 summaries

Database :

GenEmbl:

1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	54	2	AR438643 Sequence
2	54	100.0	54	2	AX166845 Sequence
3	42	77.8	58	2	AR438640 Sequence
4	42	77.8	58	2	AX166842 Sequence
5	41	75.9	57	2	AR438642 Sequence
6	41	75.9	57	2	AX166844 Sequence
7	40	74.1	59	2	AR438641 Sequence
8	40	74.1	59	2	AX166843 Sequence
9	37.6	69.6	54	2	AR344820 Sequence
10	37.6	69.6	54	2	AR720137 Sequence
11	37.6	69.6	54	2	AX397775 Sequence
12	37	68.5	53	2	AR344853 Sequence
13	37	68.5	53	2	AR720170 Sequence
14	37	68.5	53	2	AX397808 Sequence
15	37	68.5	57	2	CS072196 Sequence
16	37	68.5	57	2	CS072206 Sequence
17	37	68.5	57	2	AR438639 Sequence
18	37	68.5	57	2	AR559011 Sequence

AR559021 Sequence
AX166841 Sequence
AR344813 Sequence
AR720130 Sequence
AX397768 Sequence
AR344817 Sequence
AR720134 Sequence
AX397772 Sequence
AR344845 Sequence
AR344847 Sequence
AR720162 Sequence
AR720164 Sequence
AX397800 Sequence
AX397802 Sequence
DD177972 Method fo
AX802102 Sequence
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AR307460 Sequence
AR594174 Sequence
AR344821 Sequence
AR720138 Sequence
AX397776 Sequence
AR344854 Sequence
AR438644 Sequence
AR720171 Sequence
AX166846 Sequence
AX397809 Sequence
AR344846 Sequence
AR720163 Sequence
AX397801 Sequence
AR344844 Sequence
AR720161 Sequence
AX397799 Sequence
AR719674 Sequence
AR344849 Sequence
AR720166 Sequence
AX397804 Sequence
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AR307441 Sequence
AR594155 Sequence
AR344856 Sequence
AR720173 Sequence
AX397811 Sequence
CS072195 Sequence
CS072205 Sequence
AR559010 Sequence
AR559020 Sequence
BD236961 Nucleic a
AR307447 Sequence
AR594161 Sequence
AR647675 Sequence
AX498431 Sequence
AF521666 Cloning v
AX202478 Sequence
CS072203 Sequence
AR344815 Sequence
AR438668 Sequence
AR559018 Sequence
AR647685 Sequence
AR720132 Sequence
AX166870 Sequence
AX397770 Sequence
AX498441 Sequence
CS008909 Sequence
AR193645 Sequence
AR352369 Sequence
AX768001 Sequence
AX768013 Sequence
AX299239 Sequence
BD080457 Methods f
AR703437 Sequence
AR344852 Sequence
AR720169 Sequence

92	33	61.1	51	2	AX397807	AX397807 Sequence	165	33	61.1	144	2	BD070051	BD070051 In vitro
93	33	61.1	52	2	BD237698	BD237698 Therapeut	166	33	61.1	144	2	AR448927	AR448927 Sequence
94	33	61.1	52	2	AR344850	AR344850 Sequence	167	33	61.1	153	2	BD263446	BD263446 Compositi
95	33	61.1	52	2	AR720167	AR720167 Sequence	168	33	61.1	153	2	BD263448	BD263448 Compositi
96	33	61.1	52	2	AX278216	AX278216 Sequence	169	33	61.1	159	8	M23201	M23201 Synthetic c
97	33	61.1	52	2	AX397805	AX397805 Sequence	170	33	61.1	186	2	AR123825	AR123825 Sequence
98	33	61.1	53	2	AR344848	AR344848 Sequence	171	33	61.1	187	2	AR004778	AR004778 Sequence
99	33	61.1	53	2	AR720165	AR720165 Sequence	172	33	61.1	187	2	I13578	I13578 Sequence 7
100	33	61.1	53	2	AX397803	AX397803 Sequence	173	33	61.1	193	2	BD182014	BD182014 Process f
101	33	61.1	55	2	AR070661	AR070661 Sequence	174	33	61.1	193	2	BD263444	BD263444 Compositi
102	33	61.1	55	2	AR135557	AR135557 Sequence	175	33	61.1	204	2	BD185651	BD185651 Methods f
103	33	61.1	55	2	AR157492	AR157492 Sequence	176	33	61.1	216	2	BD185797	BD185797 Methods f
104	33	61.1	55	2	BD243358	BD243358 Protectio	177	33	61.1	216	2	AX766172	AX766172 Sequence
105	33	61.1	55	2	I25934	I25934 Sequence 14	178	33	61.1	216	2	AX766177	AX766177 Sequence
106	33	61.1	55	2	AR344855	AR344855 Sequence	179	33	61.1	217	2	BD187663	BD187663 Methods f
107	33	61.1	55	2	AR720172	AR720172 Sequence	180	33	61.1	217	2	BD187686	BD187686 Methods f
108	33	61.1	55	2	AX397810	AX397810 Sequence	181	33	61.1	217	2	BD189715	BD189715 Methods f
109	33	61.1	56	2	BD237699	BD237699 Therapeut	182	33	61.1	244	2	BD187664	BD187664 Methods f
110	33	61.1	56	2	AX278217	AX278217 Sequence	183	33	61.1	244	2	BD187687	BD187687 Methods f
111	33	61.1	57	2	AR647674	AR647674 Sequence	184	33	61.1	244	2	BD189716	BD189716 Methods f
112	33	61.1	57	2	AX498430	AX498430 Sequence	185	33	61.1	278	2	AR009724	AR009724 Sequence
113	33	61.1	58	2	DD177965	DD177965 Method fo	186	33	61.1	303	2	CQ788787	CQ788787 Sequence
114	33	61.1	58	2	AX802095	AX802095 Sequence	187	33	61.1	303	2	CS109167	CS109167 Sequence
115	33	61.1	59	2	CS072194	CS072194 Sequence	188	33	61.1	310	8	M23200	M23200 Synthetic c
116	33	61.1	59	2	CS072204	CS072204 Sequence	189	33	61.1	374	2	BD177595	BD177595 RNA-DNA c
117	33	61.1	59	2	AR559009	AR559009 Sequence	190	33	61.1	398	2	CQ829254	CQ829254 Sequence
118	33	61.1	59	2	AR559019	AR559019 Sequence	191	33	61.1	412	2	E15946	E15946 T7 promoter
119	33	61.1	60	2	I12131	I12131 Sequence 36	192	33	61.1	424	5	S70622	S70622 G1 phase-sp
120	33	61.1	62	2	I41301	I41301 Sequence 36	193	33	61.1	431	2	CQ829253	CQ829253 Sequence
121	33	61.1	63	2	AR193637	AR193637 Sequence	194	33	61.1	451	3	S69320	S69320 X=represor
122	33	61.1	63	2	AR352361	AR352361 Sequence	195	33	61.1	511	2	BD187666	BD187666 Methods f
123	33	61.1	66	2	AX576371	AX576371 Sequence	196	33	61.1	511	2	BD187689	BD187689 Methods f
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125	33	61.1	67	2	AR703436	AR703436 Sequence	198	33	61.1	599	2	CQ829256	CQ829256 Sequence
126	33	61.1	71	2	AX451979	AX451979 Sequence	199	33	61.1	632	2	CQ829255	CQ829255 Sequence
127	33	61.1	71	2	AR208505	AR208505 Sequence	200	33	61.1	652	2	BD187665	BD187665 Methods f
128	33	61.1	75	2	AR208505	AR208505 Sequence	201	33	61.1	652	2	BD187688	BD187688 Methods f
129	33	61.1	75	2	AR473646	AR473646 Sequence	202	33	61.1	652	2	BD189717	BD189717 Methods f
130	33	61.1	75	2	AR689681	AR689681 Sequence	203	33	61.1	656	2	A92429	A92429 Sequence 5
131	33	61.1	75	2	AX708347	AX708347 Sequence	204	33	61.1	656	2	BD022744	BD022744 Live Heli
132	33	61.1	75	2	AX708361	AX708361 Sequence	205	33	61.1	717	2	A36847	A36847 Sequence 1
133	33	61.1	77	2	AX451980	AX451980 Sequence	206	33	61.1	844	2	BD187662	BD187662 Methods f
134	33	61.1	77	2	AX458693	AX458693 Sequence	207	33	61.1	844	2	BD187685	BD187685 Methods f
135	33	61.1	84	2	CQ829204	CQ829204 Sequence	208	33	61.1	844	2	BD189714	BD189714 Methods f
136	33	61.1	88	2	BD012958	BD012958 A method	209	33	61.1	905	2	CQ829260	CQ829260 Sequence
137	33	61.1	88	2	E37843	E37843 Process for	210	33	61.1	924	8	SYNHG1	M63852 Rat high mo
138	33	61.1	89	2	A50149	A50149 Sequence 6	211	33	61.1	938	2	CQ829259	CQ829259 Sequence
139	33	61.1	96	2	BD160834	BD160834 Method fo	212	33	61.1	945	2	A36849	A36849 Sequence 3
140	33	61.1	96	2	BD167972	BD167972 Method of	213	33	61.1	967	2	AR224425	AR224425 Sequence
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142	33	61.1	96	2	CS016506	CS016506 Sequence	215	33	61.1	1118	2	CS038990	CS038990 Sequence
143	33	61.1	96	2	CS018792	CS018792 Sequence	216	33	61.1	1170	2	AX022820	AX022820 Sequence
144	33	61.1	100	8	SYNTRHDDR	M73804 Synthetic h	217	33	61.1	1367	2	CQ829258	CQ829258 Sequence
145	33	61.1	102	2	BD263457	BD263457 Compositi	218	33	61.1	1400	2	CQ829257	CQ829257 Sequence
146	33	61.1	102	2	BD263459	BD263459 Compositi	219	33	61.1	2467	2	AX451983	AX451983 Sequence
147	33	61.1	102	2	BD263461	BD263461 Compositi	220	33	61.1	2467	2	AX458696	AX458696 Sequence
148	33	61.1	104	2	E01421	E01421 Synthetic D	221	33	61.1	2504	2	CQ796820	CQ796820 Sequence
149	33	61.1	104	2	I05066	I05066 Sequence 12	222	33	61.1	2566	2	AX260259	AX260259 Sequence
150	33	61.1	104	2	I08128	I08128 Sequence 1	223	33	61.1	2599	2	CQ796832	CQ796832 Sequence
151	33	61.1	104	2	AR014457	AR014457 Sequence	224	33	61.1	2617	2	CQ796831	CQ796831 Sequence
152	33	61.1	109	2	BD174706	BD174706 Method fo	225	33	61.1	2730	15	PE781F1P	X62499 E.coli plas
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154	33	61.1	110	2	BD174715	BD174715 Labeling	227	33	61.1	2812	8	SYNPT12V	L08949 pT712 cloni
155	33	61.1	110	2	BD176577	BD176577 Reagent f	228	33	61.1	2818	8	SYNPT711V	L08950 pT713 cloni
156	33	61.1	110	2	BD176586	BD176586 Method of	229	33	61.1	2828	8	CVPRSET6D	X54205 Cloning vec
157	33	61.1	117	2	BD012964	BD012964 A method	230	33	61.1	2828	8	CVPRSET6D	X54205 Cloning vec
158	33	61.1	118	2	CQ904470	CQ904470 Sequence	231	33	61.1	2829	8	CVPRSET5C	X54204 Cloning vec
159	33	61.1	118	2	AR201918	AR201918 Sequence	232	33	61.1	2829	8	CVPRSET5C	X54208 Cloning vec
160	33	61.1	120	2	BD263443	BD263443 Compositi	233	33	61.1	2830	8	CVPRSET5B	X54203 Cloning vec
161	33	61.1	135	2	A87397	A87397 Sequence 5	234	33	61.1	2830	8	CVPRSET6B	X54207 Cloning vec
162	33	61.1	135	2	BD070048	BD070048 In vitro	235	33	61.1	2831	8	CVPRSET5A	X54202 Cloning vec
163	33	61.1	136	2	BD182009	BD182009 Process f	236	33	61.1	2831	8	CVPRSET6A	X54206 Cloning vec
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RESULT 3
AR438640
LOCUS AR438640 58 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 8 from patent US 6564081.

RESULT 1			
AR438643			
LOCUS	AR438643	54 bp	DNA
DEFINITION	Sequence 11 from patent US 6664081.		
ACCESSION	AR438643		
			PAT 20-FEB-2004

TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: US 6664081-A 8 16-DEC-2003;
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA
FEATURES
source
1. .58
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 77.8%; Score 42; DB 2; Length 58;
Best Local Similarity 98.1%; Pred. No. 5.8e+04;
Matches 53; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATTTCCCACTGC 54
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Db 1 GAAATTAATACGACTCACTATAGGAGACCA- TGTGCAATATTTCCCACTGC 53

RESULT 4

AXI166842
LOCUS AXI166842 58 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 8 from Patent WO0144510.
ACCESSION AXI166842
VERSION AXI166842.1 GI:14596445

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE

1 Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
Rodrigue,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: WO 0144510-A 8 21-JUN-2001;
Gen-Probe Incorporated (US); Biomerieux S.A. (FR)

FEATURES

source
Location/Qualifiers

1. .58
/organism="synthetic construct"
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/note="primer oligonucleotide"
1. .33

promoter

ORIGIN

Query Match 77.8%; Score 42; DB 2; Length 58;
Best Local Similarity 98.1%; Pred. No. 5.8e+04;
Matches 53; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATTTCCCACTGC 54
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCA- TGTGCAATATTTCCCACTGC 53

RESULT 5

AXI166842
LOCUS AXI166842 57 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 10 from patent US 6664081.
ACCESSION AR438642
VERSION AR438642.1 GI:42663566

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
1 (bases 1 to 57)
Unclassified.

AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
Rodrigue,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: US 6664081-A 10 16-DEC-2003;
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA

FEATURES

source
1. .57
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 75.9%; Score 41; DB 2; Length 57;
Best Local Similarity 94.7%; Pred. No. 7.9e+04;
Matches 54; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 54
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Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATTTCCCACTGC 57

RESULT 6

AXI166844
LOCUS AXI166844 57 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 10 from Patent WO0144510.
ACCESSION AXI166844
VERSION AXI166844.1 GI:14596447

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE

1 Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
Rodrigue,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: WO 0144510-A 10 21-JUN-2001;
Gen-Probe Incorporated (US); Biomerieux S.A. (FR)

FEATURES

source
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer oligonucleotide"
1. .33

promoter

ORIGIN

Query Match 75.9%; Score 41; DB 2; Length 57;
Best Local Similarity 94.7%; Pred. No. 7.9e+04;
Matches 54; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 54
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RESULT 7

AXI166841
LOCUS AXI166841 59 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 9 from patent US 6664081.
ACCESSION AR438641
VERSION AR438641.1 GI:42663565

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
1 (bases 1 to 59)
Unclassified.

AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
Rodrigue,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: US 6664081-A 9 16-DEC-2003;
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA

FEATURES

source
Location/Qualifiers
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/mol_type="genomic DNA"

ORIGIN

Query Match 74.1%; Score 40; DB 2; Length 59;
Best Local Similarity 93.1%; Pred. No. 1e+05;
Matches 54; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 54
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Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATTTCCCACTGC 58

RESULT 8
AX166843
LOCUS AX166843 59 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 9 from Patent WO0144510.
ACCESSION AX166843
VERSION AX166843.1 GI:14596446
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
OTHER SEQUENCES; artificial sequences.
REFERENCE 1
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and Rodriguez,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: WO 0144510-A 9 21-JUN-2001;
Gen-Probe Incorporated (US) ; Biomerieux S.A. (FR)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer oligonucleotide"
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Qy 1 GAAATTAATACGACTCACTATAGGAGACCA----CATGTGCAATATTTCCCACTGC 54
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Db 1 GAAATTAATACGACTCACTATAGGAGACCACTATAGGAGACCACTATATTTCCCACTGC 58
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RESULT 9
AR344820
LOCUS AR344820 54 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 9 from patent US 6582920.
ACCESSION AR344820
VERSION AR344820.1 GI:33740901
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 54)
AUTHORS Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
TITLE Amplification of HIV-1 RT sequences for detection of sequences associated with drug-resistance mutations
JOURNAL Patent: US 6582920-A 9 24-JUN-2003;
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
FEATURES
source Location/Qualifiers
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/mol_type="genomic DNA"
ORIGIN
Query Match 69.6%; Score 37.6; DB 2; Length 54;
Best Local Similarity 90.9%; Pred. No. 2.3e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Db 1 GAAATTAATACGACTCACTATAGGAGACCACTATAGGAGACCACTATATTT 44
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RESULT 10
AR720137
LOCUS AR720137 54 bp DNA linear PAT 07-OCT-2005
DEFINITION Sequence 9 from patent US 6946254.
ACCESSION AR720137
VERSION AR720137.1 GI:77371202

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 54)
AUTHORS Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
TITLE Amplification of HIV-1 gag sequences for detection of sequences associated with drug-resistance mutations
JOURNAL Patent: US 6946254-A 9 20-SEP-2005;
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
FEATURES
source Location/Qualifiers
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Best Local Similarity 90.9%; Pred. No. 2.3e+05; Mismatches 4; Indels 0; Gaps 0;
Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTATAGGAGACCACTATATTT 44
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Db 1 GAAATTAATACGACTCACTATAGGAGACCACTATAGGAGACCACTATATTT 44
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RESULT 11
AX397775
LOCUS AX397775 54 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 9 from Patent WO0220852.
ACCESSION AX397775
VERSION AX397775.1 GI:21260649
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
OTHER SEQUENCES; artificial sequences.
REFERENCE 1
AUTHORS Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
TITLE Amplification of hiv-1 sequences for detection of sequences associated with drug-resistance mutations
JOURNAL Patent: WO 0220852-A 9 14-MAR-2002;
Gen-Probe Incorporated Patent Dept (US) ; Biomerieux S.A. (FR)
FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Oligonucleotide primer for Reverse Transcriptase target sequence"
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ORIGIN
Query Match 69.6%; Score 37.6; DB 2; Length 54;
Best Local Similarity 90.9%; Pred. No. 2.3e+05; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTATAGGAGACCACTATATTT 44
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Db 1 GAAATTAATACGACTCACTATAGGAGACCACTATAGGAGACCACTATATTT 44
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RESULT 12
AR344853
LOCUS AR344853 53 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 42 from patent US 6582920.
ACCESSION AR344853
VERSION AR344853.1 GI:33740934
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 53)
AUTHORS Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
TITLE Amplification of HIV-1 RT sequences for detection of sequences

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associated with drug-resistance mutations
Patent: US 6582920-A 42 24-JUN-2003;
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
FEATURES
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        /mol_type="genomic DNA"
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Query Match      68.5%; Score 37; DB 2; Length 53;
Best Local Similarity 88.9%; Pred. No. 2.8e+05;
Matches 40; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCACTATAGGAGACCAACATCTTGCAATATT 45
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RESULT 13
LOCUS      ART20170          53 bp      DNA      linear      PAT 07-OCT-2005
DEFINITION Sequence 42 from patent US 6946254.
ACCESSION  AR720170
VERSION     AR720170.1 GI:77371235
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 53)
AUTHORS   Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
TITLE     Amplification of HIV-1 gag sequences for detection of sequences
          associated with drug-resistance mutations
JOURNAL   Patent: US 6946254-A 42 20-SEP-2005;
          Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
FEATURES   Location/Qualifiers
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Query Match      68.5%; Score 37; DB 2; Length 53;
Best Local Similarity 88.9%; Pred. No. 2.8e+05;
Matches 40; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCACTATAGGAGACCAACATCTTGCAATATT 45
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Db 1 GAAATTAATACGACTCACTATAGGAGACCAACATCTTGATAAATT 45
    |||||
RESULT 14
LOCUS      AX397808          53 bp      DNA      linear      PAT 27-MAY-2002
DEFINITION Sequence 42 from Patent WO0220852.
ACCESSION  AX397808
VERSION     AX397808.1 GI:21260682
KEYWORDS   .
SOURCE     synthetic construct
          other sequences; artificial sequences.
ORGANISM   1
REFERENCE  1
AUTHORS   Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
TITLE     Amplification of hiv-1 sequences for detection of sequences
          associated with drug-resistance mutations
JOURNAL   Patent: WO 0220852-A 42 14-MAR-2002;
          Gen-Probe Incorporated Patent Dept (US) ; Biomerieux S.A. (FR)
FEATURES   Location/Qualifiers
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associated with drug-resistance mutations
Patent: US 6582920-A 42 24-JUN-2003;
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
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Query Match      68.5%; Score 37; DB 2; Length 53;
Best Local Similarity 88.9%; Pred. No. 2.8e+05;
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Qy 1 GAAATTAATACGACTCACTATAGGAGACCAACATCTTGCAATATT 45
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Db 1 GAAATTAATACGACTCACTATAGGAGACCAACATCTTGATAAATT 45
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RESULT 15
LOCUS      CS072196          57 bp      DNA      linear      PAT 05-MAY-2005
DEFINITION Sequence 3 from Patent WO2001044511.
ACCESSION  CS072196
VERSION     CS072196.1 GI:63089421
KEYWORDS   .
SOURCE     synthetic construct
          other sequences; artificial sequences.
ORGANISM   1
REFERENCE  1
AUTHORS   Brentano,S.T. and Lankford,R.L.
TITLE     Methods and compositions for detection of mycobacterium avium
          complex species
JOURNAL   Patent: WO 2001044511-A 3 21-JUN-2001;
          Gen-Probe Incorporated (US)
FEATURES   Location/Qualifiers
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              /note="Description of Artificial Sequence: synthetic
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Query Match      68.5%; Score 37; DB 2; Length 57;
Best Local Similarity 91.2%; Pred. No. 2.7e+05;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
Qy 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTGTGCAATATCCCCACT 52
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Db 1 GAAATTAATACGACTCACTATAGGAGACCACTATGTGCAATATCCCCACT 57
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RESULT 16
LOCUS      CS072206/c          57 bp      DNA      linear      PAT 05-MAY-2005
DEFINITION Sequence 13 from Patent WO2001044511.
ACCESSION  CS072206
VERSION     CS072206.1 GI:63089431
KEYWORDS   .
SOURCE     synthetic construct
          synthetic construct
          other sequences; artificial sequences.
ORGANISM   1
REFERENCE  1
AUTHORS   Brentano,S.T. and Lankford,R.L.
TITLE     Methods and compositions for detection of mycobacterium avium
          complex species
JOURNAL   Patent: WO 2001044511-A 13 21-JUN-2001;
          Gen-Probe Incorporated (US)
FEATURES   Location/Qualifiers
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ORIGIN
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Best Local Similarity 91.2%; Pred. No. 2.7e+05;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
Qy 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTGTGCAATATCCCCACT 52
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Db 1 GAAATTAATACGACTCACTATAGGAGACCACTATGTGCAATATCCCCACT 57
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RESULT 16
LOCUS      CS072206/c          57 bp      DNA      linear      PAT 05-MAY-2005
DEFINITION Sequence 13 from Patent WO2001044511.
ACCESSION  CS072206
VERSION     CS072206.1 GI:63089431
KEYWORDS   .
SOURCE     synthetic construct
          synthetic construct
          other sequences; artificial sequences.
ORGANISM   1
REFERENCE  1
AUTHORS   Brentano,S.T. and Lankford,R.L.
TITLE     Methods and compositions for detection of mycobacterium avium
          complex species
JOURNAL   Patent: WO 2001044511-A 13 21-JUN-2001;
          Gen-Probe Incorporated (US)
FEATURES   Location/Qualifiers
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Best Local Similarity 91.2%; Pred. No. 2.7e+05;
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Db 1 GAAATTAATACGACTCACTATAGGAGACCACTATGTGCAATATCCCCACT 57
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Qy 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTTCCCACT 52
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Db 57 GAAATTAATACGACTCACTATAGGAGACCAAGCCAGCCATTGTGCAATATTTCCCACT 1

RESULT 17
AR438639
LOCUS AR438639 57 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 7 from patent US 6664081.
ACCESSION AR438639
VERSION AR438639.1 GI:42663563
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 57)
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
Rodrigue,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: US 6664081-A 7 16-DEC-2003;
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA
FEATURES
source
1..57
/organism="unknown"
/mol_type="genomic DNA"

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Query Match 68.5%; Score 37; DB 2; Length 57;
Best Local Similarity 91.2%; Pred. No. 2.7e+05;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTTCCCACT 52
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Db 1 GAAATTAATACGACTCACTATAGGAGACCAAGCCAGCCATTGTGCAATATTTCCCACT 57

RESULT 18
AR559011
LOCUS AR559011 57 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 3 from patent US 6747141.
ACCESSION AR559011
VERSION AR559011.1 GI:53966350
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 57)
AUTHORS Brentano,S.T. and Lankford,R.L.
TITLE Methods and compositions for detection of mycobacterium avium
complex species
JOURNAL Patent: US 6747141-A 3 08-JUN-2004;
Gen-Probe Incorporated; San Diego, CA
FEATURES
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/mol_type="genomic DNA"

ORIGIN
Query Match 68.5%; Score 37; DB 2; Length 57;
Best Local Similarity 91.2%; Pred. No. 2.7e+05;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTTCCCACT 52
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCAAGCCAGCCATTGTGCAATATTTCCCACT 57

RESULT 19
AR559021/c
LOCUS AR559021 57 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 13 from patent US 6747141.
ACCESSION AR559021
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VERSION AR559021.1 GI:53966360
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 57)
AUTHORS Brentano,S.T. and Lankford,R.L.
TITLE Methods and compositions for detection of mycobacterium avium
complex species
JOURNAL Patent: US 6747141-A 13 08-JUN-2004;
Gen-Probe Incorporated; San Diego, CA
FEATURES
source
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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 68.5%; Score 37; DB 2; Length 57;
Best Local Similarity 91.2%; Pred. No. 2.7e+05;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTTCCCACT 52
|||||
Db 57 GAAATTAATACGACTCACTATAGGAGACCAAGCCAGCCATTGTGCAATATTTCCCACT 1

RESULT 20
AX166841
LOCUS AX166841 57 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 7 from Patent WO0144510.
ACCESSION AX166841
VERSION AX166841.1 GI:14596444
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
Rodrigue,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: WO 0144510-A 7 21-JUN-2001;
Gen-Probe Incorporated (US) ; Blomerieux S.A. (FR)
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source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer oligonucleotide"

ORIGIN
promoter
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Query Match 68.5%; Score 37; DB 2; Length 57;
Best Local Similarity 91.2%; Pred. No. 2.7e+05;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTTCCCACT 52
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCAAGCCAGCCATTGTGCAATATTTCCCACT 57

RESULT 21
AR344813
LOCUS AR344813 37 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 2 from patent US 6582920.
ACCESSION AR344813
VERSION AR344813.1 GI:33740894
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 37)
AUTHORS Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
TITLE Amplification of HIV-1 RT sequences for detection of sequences
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associated with drug-resistance mutations
 Patent: US 6582920-A 2 24-JUN-2003;
 Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA

FEATURES
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 /mol_type="genomic DNA"

ORIGIN

Query Match 66.7%; Score 36; DB 2; Length 37;
 Best Local Similarity 100.0%; Pred. No. 5e+05;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36
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 Db 1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36

RESULT 22
 AR720130
 LOCUS AR720130 37 bp DNA linear PAT 07-OCT-2005
 DEFINITION Sequence 2 from patent US 6946254.
 ACCESSION AR720130
 VERSION AR720130.1 GI:77371195
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 37)
 AUTHORS Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
 TITLE Amplification of HIV-1 gag sequences for detection of sequences associated with drug-resistance mutations
 JOURNAL Patent: US 6946254-A 2 20-SEP-2005;
 Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA

FEATURES
 source
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 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 66.7%; Score 36; DB 2; Length 37;
 Best Local Similarity 100.0%; Pred. No. 5e+05;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36
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 Db 1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36

RESULT 23
 AX397768
 LOCUS AX397768 37 bp DNA linear PAT 27-MAY-2002
 DEFINITION Sequence 2 from Patent WO0220852.
 ACCESSION AX397768
 VERSION AX397768.1 GI:21260642
 KEYWORDS .
 SOURCE synthetic construct
 ORGANISM synthetic construct
 other sequences; artificial sequences.

REFERENCE 1
 AUTHORS Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
 TITLE Amplification of hiv-1 sequences for detection of sequences associated with drug-resistance mutations
 JOURNAL Patent: WO 0220852-A 2 14-MAR-2002;
 Gen-Probe Incorporated Patent Dept (US) ; Biomerieux S.A. (FR)

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 1. .37
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="T7 promoter sequence"
 1. .29

promoter
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Query Match 66.7%; Score 36; DB 2; Length 37;
 Best Local Similarity 100.0%; Pred. No. 5e+05;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36
 |||||
 Db 1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36

RESULT 24
 AR344817
 LOCUS AR344817 54 bp DNA linear PAT 17-AUG-2003
 DEFINITION Sequence 6 from patent US 6582920.
 ACCESSION AR344817
 VERSION AR344817.1 GI:33740898
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 54)
 AUTHORS Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
 TITLE Amplification of HIV-1 RT sequences for detection of sequences associated with drug-resistance mutations
 JOURNAL Patent: US 6582920-A 6 24-JUN-2003;
 Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA

FEATURES
 source
 1. .54
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 66.7%; Score 36; DB 2; Length 54;
 Best Local Similarity 100.0%; Pred. No. 3.7e+05;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36
 |||||
 Db 1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36

RESULT 25
 AR720134
 LOCUS AR720134 54 bp DNA linear PAT 07-OCT-2005
 DEFINITION Sequence 6 from patent US 6946254.
 ACCESSION AR720134
 VERSION AR720134.1 GI:77371199
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 54)
 AUTHORS Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
 TITLE Amplification of HIV-1 gag sequences for detection of sequences associated with drug-resistance mutations
 JOURNAL Patent: US 6946254-A 6 20-SEP-2005;
 Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA

FEATURES
 source
 1. .54
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 66.7%; Score 36; DB 2; Length 54;
 Best Local Similarity 100.0%; Pred. No. 3.7e+05;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36
 |||||
 Db 1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36

RESULT 26

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AX397772
LOCUS AX397772 54 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 6 from Patent WO220852.
ACCESSION AX397772
VERSION AX397772.1 GI:21260646
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of HIV-1 sequences for detection of sequences
associated with drug-resistance mutations
JOURNAL Patent: WO 0220852-A 6 14-MAR-2002;
Gen-Probe Incorporated Patent Dept (US); Biomerieux S.A. (FR)
FEATURES
source
1..54
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer for Gag target sequence"
promoter 1..33
modified_base 46
/note="Nebularine"
/mod_base=OTHER
ORIGIN
Query Match 66.7%; Score 36; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 3.7e+05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36
|||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36
|||||
RESULT 27
AR344845
LOCUS AR344845 53 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 34 from patent US 6582920.
ACCESSION AR344845
VERSION AR344845.1 GI:33740926
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of HIV-1 RT sequences for detection of sequences
associated with drug-resistance mutations
JOURNAL Patent: US 6582920-A 34 24-JUN-2003;
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
FEATURES
source
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Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 66.3%; Score 35.8; DB 2; Length 53;
Best Local Similarity 94.9%; Pred. No. 4e+05;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTC 39
|||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCACTGATGC 39
|||||
RESULT 28
AR344847
LOCUS AR344847 53 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 36 from patent US 6582920.
ACCESSION AR344847
VERSION AR344847.1 GI:33740928

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KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of HIV-1 RT sequences for detection of sequences
associated with drug-resistance mutations
JOURNAL Patent: US 6582920-A 36 24-JUN-2003;
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
FEATURES
source
1..53
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 66.3%; Score 35.8; DB 2; Length 53;
Best Local Similarity 94.9%; Pred. No. 4e+05;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTC 39
|||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCACTGATGC 39
|||||
RESULT 29
AR720162
LOCUS AR720162 53 bp DNA linear PAT 07-OCT-2005
DEFINITION Sequence 34 from patent US 6946254.
ACCESSION AR720162
VERSION AR720162.1 GI:77371227
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of HIV-1 gag sequences for detection of sequences
associated with drug-resistance mutations
JOURNAL Patent: US 6946254-A 34 20-SEP-2005;
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
FEATURES
source
1..53
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 66.3%; Score 35.8; DB 2; Length 53;
Best Local Similarity 94.9%; Pred. No. 4e+05;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTC 39
|||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCACTGATGC 39
|||||
RESULT 30
AR720164
LOCUS AR720164 53 bp DNA linear PAT 07-OCT-2005
DEFINITION Sequence 36 from patent US 6946254.
ACCESSION AR720164
VERSION AR720164.1 GI:77371229
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of HIV-1 gag sequences for detection of sequences
associated with drug-resistance mutations
JOURNAL Patent: US 6946254-A 36 20-SEP-2005;
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match          66.3%; Score 35.8; DB 2; Length 53;
Best Local Similarity 94.9%; Pred. No. 4e+05;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAATTATACGACTCACTATAGGAGACCACATTGTGC 39
|||||
Db 1 GAAATTATACGACTCACTATAGGAGACCACATTGTGC 39
|||||

RESULT 31
AX397800
LOCUS          AX397800          53 bp          DNA          linear          PAT 27-MAY-2002
DEFINITION     Sequence 36 from Patent WO0220852.
ACCESSION      AX397800
VERSION        AX397800.1 GI:21260674
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Yang,Y.Y., Brentano,S.T., Babola O., Tran,N. and Vernet,G.
TITLE          Amplification of hiv-1 sequences for detection of sequences
               associated with drug-resistance mutations
JOURNAL        Patent: WO 0220852-A 36 14-MAR-2002;
               Gen-Probe Incorporated Patent Dept (US) ; Biomerieux S.A. (FR)
FEATURES       Location/Qualifiers
               source
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               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Oligonucleotide primer for Gag target sequence"
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               modified_base 45
               /note="Nebularine"
               /mod_base=OTHER

ORIGIN
Query Match          66.3%; Score 35.8; DB 2; Length 53;
Best Local Similarity 94.9%; Pred. No. 4e+05;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAATTATACGACTCACTATAGGAGACCACATTGTGC 39
|||||
Db 1 GAAATTATACGACTCACTATAGGAGACCACATTGTGC 39
|||||

RESULT 32
AX397802
LOCUS          AX397802          53 bp          DNA          linear          PAT 27-MAY-2002
DEFINITION     Sequence 36 from Patent WO0220852.
ACCESSION      AX397802
VERSION        AX397802.1 GI:21260676
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Yang,Y.Y., Brentano,S.T., Babola O., Tran,N. and Vernet,G.
TITLE          Amplification of hiv-1 sequences for detection of sequences
               associated with drug-resistance mutations
JOURNAL        Patent: WO 0220852-A 36 14-MAR-2002;
               Gen-Probe Incorporated Patent Dept (US) ; Biomerieux S.A. (FR)
FEATURES       Location/Qualifiers
               source
               1. .53
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Oligonucleotide primer for Gag target sequence"

promoter          1. .33
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match          66.3%; Score 35.8; DB 2; Length 53;
Best Local Similarity 94.9%; Pred. No. 4e+05;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAATTATACGACTCACTATAGGAGACCACATTGTGC 39
|||||
Db 1 GAAATTATACGACTCACTATAGGAGACCACATTGTGC 39
|||||

RESULT 33
DD177972
LOCUS          DD177972          53 bp          DNA          linear          PAT 19-DEC-2005
DEFINITION     Method for the detection and/or identification of the original
               animal species in animal matter contained in a sample.
ACCESSION      DD177972
VERSION        DD177972.1 GI:83962997
KEYWORDS       JP 2005514037-A/241.
SOURCE         unidentified
ORGANISM       unclassified sequences.
REFERENCE      1 (bases 1 to 53)
AUTHORS        Pijemu,N.B., Babola,O., Douvaren,S., Lacroix,B. and Mabilat,C.
TITLE          Method for the detection and/or identification of the original
               animal species in animal matter contained in a sample
JOURNAL        Patent: JP 2005514037-A 241 19-MAY-2005;
               Bio Merieux
COMMENT        OS amorice sequence CBHT7 20
               PD JP 2005514037-A/241
               PF 19-MAY-2005
               PF 10-JAN-2003 JP 2003558206
               PF 10-JAN-2002 FR 02/00265
               PI nathalie bero pijemu,odile babola,sabine douvaren,bruno PI
               lacroix,
               PI claudie mabilat
               CC
               FH Key Location/Qualifiers.
               1. .53
               /organism="unidentified"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32644"

ORIGIN
Query Match          65.6%; Score 35.4; DB 2; Length 53;
Best Local Similarity 86.7%; Pred. No. 4.6e+05;
Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GAAATTATACGACTCACTATAGGAGACCACATTGTGCATATT 45
|||||
Db 1 GAAATTATACGACTCACTATAGGAGACCACAGAAATGATATT 45
|||||

RESULT 34
AX802102
LOCUS          AX802102          53 bp          DNA          linear          PAT 24-NOV-2003
DEFINITION     Sequence 241 from Patent WO03057913.
ACCESSION      AX802102
VERSION        AX802102.1 GI:38501026
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       synthetic construct
               other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Mabilat,C., Desvarenne,S., Babola,O., Lacroix,B. and bello Pigem,N.
TITLE          Method for the detection and/or identification of the original
               animal species in animal matter contained in a sample
JOURNAL        Patent: WO 03057913-A 241 17-JUL-2003;
               BIO MERIEUX (FR)
FEATURES       Location/Qualifiers
               source
               1. .53
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REFERENCE 1. (US 5,110,531)
 AUTHORS Yang, Y. Y., Brentano, S. T., Babola, O., Tran, N. and Vernet, G.
 TITLE Amplification of HIV-1 RT sequences for detection of sequences associated with drug-resistance mutations
 JOURNAL Patent: US 5182920-A 10 24-JUN-2003;
 FEATURES Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
 source Location/Qualifiers
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 /organism="unknown"
 /mol_type="genomic DNA"
 ORIGIN
 Query Match 65.6%; Score 35.4; DB 2; Length 55;
 Best Local Similarity 97.3%; Pred. No. 4.4e+05;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


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Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTGT 37
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTGT 37

RESULT 39
LOCUS AR720138 55 bp DNA linear PAT 07-OCT-2005
DEFINITION Sequence 10 from patent US 6946254.
ACCESSION AR720138
VERSION AR720138.1 GI:77371203
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 55)
AUTHORS Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
TITLE Amplification of HIV-1 gag sequences for detection of sequences
associated with drug-resistance mutations
JOURNAL Patent: US 6946254-A 10 20-SEP-2005;
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
FEATURES
source
1..55
/mol_type="genomic DNA"
ORIGIN

Query Match 65.6%; Score 35.4; DB 2; Length 55;
Best Local Similarity 97.3%; Pred. No. 4.4e+05;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTGT 37
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTGT 37

RESULT 40
AX397776 55 bp DNA linear PAT 27-MAY-2002
LOCUS AX397776
DEFINITION Sequence 10 from Patent WO0220852.
ACCESSION AX397776
VERSION AX397776.1 GI:21260650
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
TITLE Amplification of hiv-1 sequences for detection of sequences
associated with drug-resistance mutations
JOURNAL Patent: WO 0220852-A 10 14-MAR-2002;
Gen-Probe Incorporated patent Dept (US) ; Biomerieux S.A. (FR)
FEATURES
source
1..55
/mol_type="synthetic construct"
/db_xref="taxon:32630"
/notice="Oligonucleotide primer for Reverse Transcriptase
target sequence"
promoter
1..33
ORIGIN

Query Match 65.6%; Score 35.4; DB 2; Length 55;
Best Local Similarity 97.3%; Pred. No. 4.4e+05;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTGT 37
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTGT 37

RESULT 41
AX344854

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LOCUS AR344854 52 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 43 from patent US 6582920.
ACCESSION AR344854
VERSION AR344854.1 GI:33740935
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 52)
AUTHORS Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
TITLE Amplification of HIV-1 RT sequences for detection of sequences
associated with drug-resistance mutations
JOURNAL Patent: US 6582920-A 43 24-JUN-2003;
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
FEATURES
source
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/mol_type="genomic DNA"
ORIGIN

Query Match 64.8%; Score 35; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 5.2e+05;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTT 35
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTT 35

RESULT 42
AR438644 52 bp DNA linear PAT 20-FEB-2004
LOCUS AR438644
DEFINITION Sequence 12 from patent US 6664081.
ACCESSION AR438644
VERSION AR438644.1 GI:42663568
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 52)
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
Rodrigue,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
Patent: US 6664081-A 12 16-DEC-2003;
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA
FEATURES
source
1..52
/mol_type="genomic DNA"
ORIGIN

Query Match 64.8%; Score 35; DB 2; Length 52;
Best Local Similarity 80.4%; Pred. No. 5.2e+05;
Matches 41; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATTCGCCAC 51
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Db 1 GAAATTAATACGACTCACTATAGGAGACCACTGCATCAGCTTGC GCC 51

RESULT 43
AR720171 52 bp DNA linear PAT 07-OCT-2005
LOCUS AR720171
DEFINITION Sequence 43 from patent US 6946254.
ACCESSION AR720171
VERSION AR720171.1 GI:77371236
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 52)
AUTHORS Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
TITLE Amplification of HIV-1 gag sequences for detection of sequences

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associated with drug-resistance mutations
 Patent: US 6946254-A 43 20-SEP-2005;
 Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA

JOURNAL

FEATURES
 source
 1..52
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 64.8%; Score 35; DB 2; Length 52;
 Best Local Similarity 100.0%; Pred. No. 5.2e+05;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACACATT 35
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 Db 1 GAAATTAATACGACTCACTATAGGAGACACATT 35

RESULT 44

AX166846
 LOCUS AX166846 52 bp DNA linear PAT 04-JUL-2001
 DEFINITION Sequence 12 from Patent WO0144510.
 ACCESSION AX166846
 VERSION AX166846.1 GI:14596449
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 other sequences; artificial sequences.

REFERENCE

AUTHORS Brentano, S.T., Jucker, M.T., Delgado, F.D., Cleuziat, P. and
 Rodrigue, M.
 TITLE Nucleic acid amplification and detection of mycobacterium species
 JOURNAL Patent: WO 0144510-A 12 21-JUN-2001;
 Gen-Probe Incorporated (US); Biomerieux S.A. (FR)
 FEATURES
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 1..52
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="primer oligonucleotide"

ORIGIN

Query Match 64.8%; Score 35; DB 2; Length 52;
 Best Local Similarity 80.4%; Pred. No. 5.2e+05;
 Matches 41; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

promoter
 1..33

ORIGIN

QY 1 GAAATTAATACGACTCACTATAGGAGACACATTGTCGAATATTC 51
 |||||
 Db 1 GAAATTAATACGACTCACTATAGGAGACACATGCATCAGGCTTGGCGCC 51

RESULT 45

AX397809
 LOCUS AX397809 52 bp DNA linear PAT 27-MAY-2002
 DEFINITION Sequence 43 from Patent WO0220852.
 ACCESSION AX397809
 VERSION AX397809.1 GI:21260683
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 other sequences; artificial sequences.

REFERENCE

AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.
 TITLE Amplification of hiv-1 sequences for detection of sequences
 associated with drug-resistance mutations
 JOURNAL Patent: WO 0220852-A 43 14-MAR-2002;
 Gen-Probe Incorporated Patent Dept (US); Biomerieux S.A. (FR)
 FEATURES
 source
 1..52
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"

/note="Oligonucleotide primer for Reverse Transcriptase
 target sequence"
 1..33

promoter

ORIGIN

Query Match 64.8%; Score 35; DB 2; Length 52;
 Best Local Similarity 100.0%; Pred. No. 5.2e+05;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACACATT 35
 |||||
 Db 1 GAAATTAATACGACTCACTATAGGAGACACATT 35

RESULT 46

AR344846
 LOCUS AR344846 53 bp DNA linear PAT 17-AUG-2003
 DEFINITION Sequence 35 from patent US 6582920.
 ACCESSION AR344846
 VERSION AR344846.1 GI:33740927
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 other sequences; artificial sequences.

REFERENCE

AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.
 TITLE Amplification of HIV-1 RT sequences for detection of sequences
 associated with drug-resistance mutations
 JOURNAL Patent: US 6582920-A 35 24-JUN-2003;
 Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
 FEATURES
 source
 1..53
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 64.4%; Score 34.8; DB 2; Length 53;
 Best Local Similarity 84.8%; Pred. No. 5.5e+05;
 Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACACATTGTCGAATATTC 46
 |||||
 Db 1 GAAATTAATACGACTCACTATAGGAGACACAGGCTGCTCTTC 46

RESULT 47

AR720163
 LOCUS AR720163 53 bp DNA linear PAT 07-OCT-2005
 DEFINITION Sequence 35 from patent US 6946254.
 ACCESSION AR720163
 VERSION AR720163.1 GI:77371228
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 other sequences; artificial sequences.

REFERENCE

AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.
 TITLE Amplification of HIV-1 gag sequences for detection of sequences
 associated with drug-resistance mutations
 JOURNAL Patent: US 6946254-A 35 20-SEP-2005;
 Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
 FEATURES
 source
 1..53
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 64.4%; Score 34.8; DB 2; Length 53;
 Best Local Similarity 84.8%; Pred. No. 5.5e+05;
 Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACACATTGTCGAATATTC 46
 |||||

Db 1 GAAATTAATACGACTCACTATAGGAGACACAGGGTGGCTCCTTC 46

RESULT 48
AX397801
LOCUS AR397801 53 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 35 from Patent WO0220852.
ACCESSION AX397801
VERSION AX397801.1 GI:21260675
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Yang, Y. Y., Brentano, S. T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of hiv-1 sequences for detection of sequences associated with drug-resistance mutations
JOURNAL Patent: WO 0220852-A 35 14-MAR-2002;
Gen-Probe Incorporated Patent Dept (US) ; Biomerieux S.A. (FR)
FEATURES
source Location/Qualifiers
1..53
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer for Gag target sequence"
promoter 1..33
ORIGIN
Query Match 64.4%; Score 34.8; DB 2; Length 53;
Best Local Similarity 84.8%; Pred. No. 5.5e+05;
Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCACTATAGGAGACACATGTCATATTC 46
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACACAGGGTGGCTCCTTC 46
|||||

RESULT 49
AR344844
LOCUS AR344844 54 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 33 from patent US 6582920.
ACCESSION AR344844
VERSION AR344844.1 GI:33740925
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 54)
AUTHORS Yang, Y. Y., Brentano, S. T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of HIV-1 RT sequences for detection of sequences associated with drug-resistance mutations
JOURNAL Patent: US 6582920-A 33 24-JUN-2003;
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
FEATURES
source Location/Qualifiers
1..54
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 63.7%; Score 34.4; DB 2; Length 54;
Best Local Similarity 97.2%; Pred. No. 6.1e+05;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCACTATAGGAGACACCATG 36
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACACCATG 36
|||||

RESULT 50
AR720161
LOCUS AR720161 54 bp DNA linear PAT 07-OCT-2005
DEFINITION Sequence 33 from patent US 6946254.
ACCESSION AR720161

VERSION AR720161.1 GI:77371226
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 54)
AUTHORS Yang, Y. Y., Brentano, S. T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of HIV-1 gag sequences for detection of sequences associated with drug-resistance mutations
JOURNAL Patent: US 6946254-A 33 20-SEP-2005;
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
FEATURES
source Location/Qualifiers
1..54
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 63.7%; Score 34.4; DB 2; Length 54;
Best Local Similarity 97.2%; Pred. No. 6.1e+05;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCACTATAGGAGACACCATG 36
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACACCATG 36
|||||

RESULT 51
AX397799
LOCUS AX397799 54 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 33 from Patent WO0220852.
ACCESSION AX397799
VERSION AX397799.1 GI:21260673
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Yang, Y. Y., Brentano, S. T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of hiv-1 sequences for detection of sequences associated with drug-resistance mutations
JOURNAL Patent: WO 0220852-A 33 14-MAR-2002;
Gen-Probe Incorporated Patent Dept (US) ; Biomerieux S.A. (FR)
FEATURES
source Location/Qualifiers
1..54
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer for Gag target sequence"
promoter 1..33
ORIGIN
Query Match 63.7%; Score 34.4; DB 2; Length 54;
Best Local Similarity 97.2%; Pred. No. 6.1e+05;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCACTATAGGAGACACCATG 36
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACACCATG 36
|||||

RESULT 52
AR719674
LOCUS AR719674 62 bp DNA linear PAT 07-OCT-2005
DEFINITION Sequence 48 from patent US 6943242.
ACCESSION AR719674
VERSION AR719674.1 GI:77370598
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 62)
AUTHORS Samartzidou, H., Turner, L., Daniel, S. and Houts, T.
TITLE Design of artificial genes for use as controls in gene expression

/db_xref="taxon:32630"

ORIGIN

Query Match 63.0%; Score 34; DB 2; Length 54;
Best Local Similarity 80.0%; Pred. No. 6.9e+05;
Matches 40; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 2 AAATTAATACGACTCCTATAGGGAGACCACATTGTGCAATATCCCCAC 51
|||||
Db 2 AAATTAATACGACTCCTATAGGGAGACCACAGGGTGAACCTGGCCAC 51
|||||

RESULT 57
LOCUS AR307441 54 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 30 from patent US 6551778.
ACCESSION AR307441
VERSION AR307441.1 GI:31697980
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 54)
AUTHORS Harvey,R.C. and Clark,T.J. Jr.
TITLE Nucleic acid sequences for detecting genetic markers for cancer in a biological sample
JOURNAL Patent: US 6551778-A 30 22-APR-2003;
FEATURES Location/Qualifiers
source 1..54
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 63.0%; Score 34; DB 2; Length 54;
Best Local Similarity 80.0%; Pred. No. 6.9e+05;
Matches 40; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 2 AAATTAATACGACTCCTATAGGGAGACCACATTGTGCAATATCCCCAC 51
|||||
Db 2 AAATTAATACGACTCCTATAGGGAGACCACAGGGTGAACCTGGCCAC 51
|||||

RESULT 58
LOCUS AR594155 54 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 30 from patent US 6811985.
ACCESSION AR594155
VERSION AR594155.1 GI:56643660
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 54)
AUTHORS Harvey,R.C. and Clark,T.J. Jr.
TITLE Nucleic acid sequences for detecting genetic markers for cancer in a biological sample
JOURNAL Patent: US 6811985-A 30 02-NOV-2004;
FEATURES Location/Qualifiers
source 1..54
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 63.0%; Score 34; DB 2; Length 54;
Best Local Similarity 80.0%; Pred. No. 6.9e+05;
Matches 40; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 2 AAATTAATACGACTCCTATAGGGAGACCACATTGTGCAATATCCCCAC 51
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Db 2 AAATTAATACGACTCCTATAGGGAGACCACAGGGTGAACCTGGCCAC 51
|||||

RESULT 59

LOCUS AR344856 55 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 45 from patent US 6582920.
ACCESSION AR344856
VERSION AR344856.1 GI:33740937
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 55)
AUTHORS Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
TITLE Amplification of HIV-1 RT sequences for detection of sequences associated with drug-resistance mutations
JOURNAL Patent: US 6582920-A 45 24-JUN-2003;
FEATURES Location/Qualifiers
source 1..55
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 63.0%; Score 34; DB 2; Length 55;
Best Local Similarity 100.0%; Pred. No. 6.8e+05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCCTATAGGGAGACCACAT 34
|||||
Db 1 GAAATTAATACGACTCCTATAGGGAGACCACAT 34
|||||

RESULT 60

LOCUS AR720173 55 bp DNA linear PAT 07-OCT-2005
DEFINITION Sequence 45 from patent US 6946254.
ACCESSION AR720173
VERSION AR720173.1 GI:77371238
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 55)
AUTHORS Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
TITLE Amplification of HIV-1 gag sequences for detection of sequences associated with drug-resistance mutations
JOURNAL Patent: US 6946254-A 45 20-SEP-2005;
FEATURES Location/Qualifiers
source 1..55
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 63.0%; Score 34; DB 2; Length 55;
Best Local Similarity 100.0%; Pred. No. 6.8e+05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCCTATAGGGAGACCACAT 34
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Db 1 GAAATTAATACGACTCCTATAGGGAGACCACAT 34
|||||

RESULT 61

LOCUS AX397811 55 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 45 from Patent WO0220852.
ACCESSION AX397811
VERSION AX397811.1 GI:21260685
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of hiv-1 sequences for detection of sequences associated with drug-resistance mutations
JOURNAL Patent: WO 0220852-A 45 14-MAR-2002;
FEATURES Gen-Probe Incorporated Patent Dept (US) ; Biomerieux S.A. (FR)
source Location/Qualifiers
1..55
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide primer for Reverse Transcriptase target sequence"
promoter 1..33
ORIGIN
Query Match 63.0%; Score 34; DB 2; Length 55;
Best Local Similarity 100.0%; Pred. No. 6.8e+05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCCTATATAGGAGACCACAT 34
Db 1 GAAATTAATACGACTCCTATATAGGAGACCACAT 34
RESULT 62
CS072195
LOCUS CS072195 61 bp DNA linear PAT 05-MAY-2005
DEFINITION Sequence 2 from Patent WO2001044511.
ACCESSION CS072195
VERSION CS072195.1 GI:63089420
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Brentano, S.T. and Lankford, R.L.
TITLE Methods and compositions for detection of mycobacterium avium complex species
JOURNAL Patent: WO 2001044511-A 2 21-JUN-2001;
FEATURES Gen-Probe Incorporated (US)
source Location/Qualifiers
1..61
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: synthetic promoter-primer"
ORIGIN
Query Match 63.0%; Score 34; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCCTATATAGGAGACCACAT 34
Db 1 GAAATTAATACGACTCCTATATAGGAGACCACAT 34
RESULT 63
CS072205/c
LOCUS CS072205 61 bp DNA linear PAT 05-MAY-2005
DEFINITION Sequence 12 from Patent WO2001044511.
ACCESSION CS072205
VERSION CS072205.1 GI:63089430
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Brentano, S.T. and Lankford, R.L.
TITLE Methods and compositions for detection of mycobacterium avium complex species

JOURNAL Patent: WO 2001044511-A 12 21-JUN-2001;
FEATURES Gen-Probe Incorporated (US)
source Location/Qualifiers
1..61
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: synthetic probe"
ORIGIN
Query Match 63.0%; Score 34; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCCTATATAGGAGACCACAT 34
Db 61 GAAATTAATACGACTCCTATATAGGAGACCACAT 28
RESULT 64
AR559010
LOCUS AR559010 61 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 2 from patent US 6747141.
ACCESSION AR559010
VERSION AR559010.1 GI:53966349
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 61)
AUTHORS Brentano, S.T. and Lankford, R.L.
TITLE Methods and compositions for detection of mycobacterium avium complex species
JOURNAL Patent: US 6747141-A 2 08-JUN-2004;
FEATURES Gen-Probe Incorporated; San Diego, CA
source Location/Qualifiers
1..61
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 63.0%; Score 34; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCCTATATAGGAGACCACAT 34
Db 1 GAAATTAATACGACTCCTATATAGGAGACCACAT 34
RESULT 65
AR559020/c
LOCUS AR559020 61 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 12 from patent US 6747141.
ACCESSION AR559020
VERSION AR559020.1 GI:53966359
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 61)
AUTHORS Brentano, S.T. and Lankford, R.L.
TITLE Methods and compositions for detection of mycobacterium avium complex species
JOURNAL Patent: US 6747141-A 12 08-JUN-2004;
FEATURES Gen-Probe Incorporated; San Diego, CA
source Location/Qualifiers
1..61
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

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Query Match          63.0%; Score 34; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACAT 34
    |||||
Db 61 GAAATTAATACGACTCACTATAGGAGACCACAT 28

RESULT 66
BD236961
LOCUS          52 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION    Nucleic acid sequence for detecting genetic marker for cancer in
ACCESSION    BD236961
VERSION      BD236961.1 GI:33046731
KEYWORDS     JP 2002535014-A/36.
SOURCE       synthetic construct
ORGANISM     other sequences; artificial sequences.
REFERENCE    1 (bases 1 to 52)
AUTHORS     Harvey,R.C. and Jr,T.J.C.
TITLE       Nucleic acid sequence for detecting genetic marker for cancer in
            biological samples
JOURNAL      Patent: JP 2002535014-A 36 22-OCT-2002;
COMMENT      GEN PROBE INC
            OS Artificial Sequence
            PN JP 2002535014-A/36
            PD 22-OCT-2002
            PF 28-JAN-2000 JP 2000596180
            PI RICHARD C HARVEY, THOMAS J CLARK JR
            PC C12N15/09,C12Q1/68,C12N15/00
            CC Description of Artificial Sequence: synthetic construct FH
            Key promoter
            FT Location/Qualifiers
               1..52
               /organism="synthetic construct"
               /mol_type="genomic DNA"
               /db_xref="taxon:32630"

ORIGIN
Query Match          62.6%; Score 33.8; DB 2; Length 52;
Best Local Similarity 94.6%; Pred. No. 7.5e+05;
Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAATTAATACGACTCACTATAGGAGACCATTGTG 38
    |||||
Db 2 AAATTAATACGACTCACTATAGGAGACCATTCTG 38

RESULT 67
AR307447
LOCUS          52 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION    Sequence 36 from patent US 6551778.
ACCESSION    AR307447
VERSION      AR307447.1 GI:31697986
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 52)
AUTHORS     Harvey,R.C. and Clark,T.J. Jr.
TITLE       Nucleic acid sequences for detecting genetic markers for cancer in
            a biological sample
JOURNAL      Patent: US 6551778-A 36 22-APR-2003;
            Gen-Probe Incorporated; San Diego, CA
FEATURES     Location/Qualifiers
               1..52
               /organism="unknown"
               /mol_type="genomic DNA"

ORIGIN
Query Match          62.6%; Score 33.8; DB 2; Length 52;
Best Local Similarity 94.6%; Pred. No. 7.5e+05;
Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAATTAATACGACTCACTATAGGAGACCATTGTG 38
    |||||
Db 2 AAATTAATACGACTCACTATAGGAGACCATTCTG 38

RESULT 69
AR647675
LOCUS          58 bp      DNA      linear      PAT 20-APR-2005
DEFINITION    Sequence 19 from patent US 6870045.
ACCESSION    AR647675
VERSION      AR647675.1 GI:62786794
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 58)
AUTHORS     Yang,Y.Y. and Burrell,T.A.
TITLE       Kits for detecting HIV-2
            Patent: US 6870045-A 19 22-MAR-2005;
            Gen-Probe Incorporated; San Diego, CA
FEATURES     Location/Qualifiers
               1..58
               /organism="unknown"
               /mol_type="genomic DNA"

ORIGIN
Query Match          61.5%; Score 33.2; DB 2; Length 58;
Best Local Similarity 92.1%; Pred. No. 8.3e+05;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCATTGTG 38
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACCCTG 38

RESULT 70
AX498431
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Query Match          62.6%; Score 33.8; DB 2; Length 52;
Best Local Similarity 94.6%; Pred. No. 7.5e+05;
Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAATTAATACGACTCACTATAGGAGACCATTGTG 38
    |||||
Db 2 AAATTAATACGACTCACTATAGGAGACCATTCTG 38
```

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RESULT 68
AR594161
LOCUS          52 bp      DNA      linear      PAT 15-DEC-2004
DEFINITION    Sequence 36 from patent US 6811985.
ACCESSION    AR594161
VERSION      AR594161.1 GI:56643666
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 52)
AUTHORS     Harvey,R.C. and Clark,T.J. Jr.
TITLE       Nucleic acid sequences for detecting genetic markers for cancer in
            a biological sample
JOURNAL      Patent: US 6811985-A 36 02-NOV-2004;
            Gen-Probe Incorporated; San Diego, CA
FEATURES     Location/Qualifiers
               1..52
               /organism="unknown"
               /mol_type="genomic DNA"

ORIGIN
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Query Match          62.6%; Score 33.8; DB 2; Length 52;
Best Local Similarity 94.6%; Pred. No. 7.5e+05;
Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAATTAATACGACTCACTATAGGAGACCATTGTG 38
    |||||
Db 2 AAATTAATACGACTCACTATAGGAGACCATTCTG 38
```

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RESULT 69
AR647675
LOCUS          58 bp      DNA      linear      PAT 20-APR-2005
DEFINITION    Sequence 19 from patent US 6870045.
ACCESSION    AR647675
VERSION      AR647675.1 GI:62786794
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 58)
AUTHORS     Yang,Y.Y. and Burrell,T.A.
TITLE       Kits for detecting HIV-2
            Patent: US 6870045-A 19 22-MAR-2005;
            Gen-Probe Incorporated; San Diego, CA
FEATURES     Location/Qualifiers
               1..58
               /organism="unknown"
               /mol_type="genomic DNA"

ORIGIN
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Query Match          61.5%; Score 33.2; DB 2; Length 58;
Best Local Similarity 92.1%; Pred. No. 8.3e+05;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCATTGTG 38
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACCCTG 38

RESULT 70
AX498431
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LOCUS AX498431 58 bp DNA linear PAT 26-SEP-2002
 DEFINITION Sequence 19 from Patent WO234951.
 ACCESSION AX498431
 VERSION AX498431.1 GI:23343309
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Yang,Y.Y. and Burrell,T.A.
 TITLE Compositions and methods for detecting human immunodeficiency virus
 2 (hiv-2)
 JOURNAL Patent: WO 0234951-A 19 02-MAY-2002;
 Gen-Probe Incorporated (US)
 FEATURES
 source
 1..58
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="17 promoter primer having a promoter sequence
 appended at the 5' end of an HIV-2 complementary primer
 sequence"

ORIGIN
 Query Match 61.5%; Score 33.2; DB 2; Length 58;
 Best Local Similarity 92.1%; Pred. No. 8.3e+05;
 Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTACCTATAGGAGACACCATTTGTG 38
 |||||
 DB 1 GAAATTAATACGACTACCTATAGGAGACACCATTTGTG 38
 |||||

RESULT 71
 AF521666 4356 bp DNA circular SYN 04-DEC-2002
 LOCUS Cloning vector pLOI2065 complete sequence.
 DEFINITION
 ACCESSION AF521666
 VERSION AF521666.1 GI:21780275
 KEYWORDS
 SOURCE Cloning vector pLOI2065
 ORGANISM Cloning vector pLOI2065
 other sequences; artificial sequences; vectors.
 REFERENCE 1 (bases 1 to 4356)
 AUTHORS Underwood,S.A., Zhou,S., Causey,T.B., Yomano,L.P., Shanmugam,K.T.
 and Ingram,L.O.
 TITLE Genetic Changes To Optimize Carbon Partitioning between Ethanol and
 Biosynthesis in Ethanologenic *Escherichia coli*
 JOURNAL Appl. Environ. Microbiol. 68 (12), 6263-6272 (2002)
 PUBMED 12450851
 REFERENCE 2 (bases 1 to 4356)
 AUTHORS Yomano,L.P. and Ingram,L.O.
 TITLE Direct Submission
 JOURNAL Submitted (13-JUN-2002) Microbiology & Cell Science, University of
 Florida, POBox 110700, Museum Rd., Gainesville, FL 32611, USA
 FEATURES
 source
 1..4356
 /organism="Cloning vector pLOI2065"
 /mol_type="genomic DNA"
 /db_xref="taxon:280595"
 456..510
 /bound_moiety="flipase"
 complement(711..1901)
 /gene="tet"
 complement(711..1901)
 /gene="tet"
 /note="tetracycline resistance protein"
 /codon_start=1
 /transl_table=11
 /product="tet"
 /protein_id="AAW77666.1"
 /db_xref="GI:21780276"
 /translation="MKSNNALIVILGTVTLDVAVGIGLVMPVLFGLLRDIIVHSDSIASH

protein_bind
 2013..2047
 /bound_moiety="flipase"
 rep_origin
 2537..3125
 /note="ColE1 ori"
 gene
 complement(3296..4156)
 /gene="bla"
 CDS
 complement(3296..4156)
 /gene="bla"
 /note="ampicillin resistance protein"
 /codon_start=1
 /transl_table=11
 /product="beta-lactamase"
 /protein_id="AAM77667.1"
 /db_xref="GI:21780277"
 /translation="MSIQHPRVALIPFFAAFLPVFAHPETLVKVKDAEDOLGARVGY
 IELDLSKILLESFRRPERFPMWSTFKVLLGAVLSRIDAGQEQOLGRIRHYSDNDLVE
 YSPVTERKHLTDGMTVRELCSAAITMSNTAANLLLTIGGPKELTAFVHNMGDHWRL
 DRWEPELNEAIPNDERDTMPVAMATLRKLLTGLLTLASRQQLIDWMEADKVAAGL
 LRSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVYITGTSQATMDERNQIA
 EIGASLKHWH"

ORIGIN
 Query Match 61.5%; Score 33.2; DB 8; Length 4356;
 Best Local Similarity 75.9%; Pred. No. 2.8e+04;
 Matches 41; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTACCTATAGGAGACACCATTTGCAATATTCCCACTGC 54
 |||||
 DB 2089 GAAATTAATACGACTACCTATAGGAGACCGGAATTCGTAATCATGTCATAGC 2142
 |||||

RESULT 72
 AX202478 5731 bp DNA linear PAT 30-AUG-2001
 LOCUS Sequence 66 from Patent WO0152620.
 DEFINITION
 ACCESSION AX202478
 VERSION AX202478.1 GI:15392206
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Barbas,C.F., Stege,J.T., Guan,X. and Dalmia,B.
 TITLE Methods and compositions to modulate expression in plants
 JOURNAL Patent: WO 0152620-A 66 26-JUL-2001;
 The Scripps Research Institute (US) ; SYNGENTA AGRICULTURAL
 DISCOVERY, INC. (CA)
 FEATURES
 Location/Qualifiers
 1..5731
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="2C7-SID"

ORIGIN
 Query Match 61.5%; Score 33.2; DB 2; Length 5731;
 Best Local Similarity 75.9%; Pred. No. 2.3e+04;
 Matches 41; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTACCTATAGGAGACACCATTTGCAATATTCCCACTGC 54
 |||||
 DB 858 GAAATTAATACGACTACCTATAGGAGACCGGAATTCGTAATCATGTCATAGC 911
 |||||

RESULT 73
 CS072203

LOCUS CS072203 33 bp DNA linear PAT 05-MAY-2005
DEFINITION Sequence 10 from Patent WO2001044511.
ACCESSION CS072203
VERSION CS072203.1 GI:63089428
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 Brentano,S.T. and Lankford,R.L.
AUTHORS Methods and compositions for detection of mycobacterium avium
TITLE complex species
JOURNAL Patent: WO 2001044511-A 10 21-JUN-2001;
Gen-Probe Incorporated (US)
FEATURES Location/Qualifiers
source 1..33
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: promoter"
ORIGIN
Query Match 61.1%; Score 33; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAAATTATACGACTCACTATAGGAGACCACA 33
|||||
Db 1 GAAATTATACGACTCACTATAGGAGACCACA 33
|||||
RESULT 74
AR344815
LOCUS AR344815 33 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 4 from patent US 6582920.
ACCESSION AR344815
VERSION AR344815.1 GI:33740896
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
TITLE Amplification of HIV-1 RT sequences for detection of sequences
associated with drug-resistance mutations
JOURNAL Patent: US 6582920-A 4 24-JUN-2003;
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
FEATURES Location/Qualifiers
source 1..33
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 61.1%; Score 33; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAAATTATACGACTCACTATAGGAGACCACA 33
|||||
Db 1 GAAATTATACGACTCACTATAGGAGACCACA 33
|||||
RESULT 75
AR438668
LOCUS AR438668 33 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 36 from patent US 6664081.
ACCESSION AR438668
VERSION AR438668.1 GI:42663592
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)

AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
Rodrigue,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: US 6664081-A 36 16-DEC-2003;
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA
FEATURES Location/Qualifiers
source 1..33
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 61.1%; Score 33; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAAATTATACGACTCACTATAGGAGACCACA 33
|||||
Db 1 GAAATTATACGACTCACTATAGGAGACCACA 33
|||||
RESULT 76
AR559018
LOCUS AR559018 33 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 10 from patent US 6747141.
ACCESSION AR559018
VERSION AR559018.1 GI:53966357
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Brentano,S.T. and Lankford,R.L.
TITLE Methods and compositions for detection of mycobacterium avium
complex species
JOURNAL Patent: US 6747141-A 10 08-JUN-2004;
Gen-Probe Incorporated; San Diego, CA
FEATURES Location/Qualifiers
source 1..33
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 61.1%; Score 33; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAAATTATACGACTCACTATAGGAGACCACA 33
|||||
Db 1 GAAATTATACGACTCACTATAGGAGACCACA 33
|||||
RESULT 77
AR647685
LOCUS AR647685 33 bp DNA linear PAT 20-APR-2005
DEFINITION Sequence 29 from patent US 6870045.
ACCESSION AR647685
VERSION AR647685.1 GI:62786804
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Yang,Y.Y. and Burrell,T.A.
TITLE Kits for detecting HIV-2
JOURNAL Patent: US 6870045-A 29 22-MAR-2005;
Gen-Probe Incorporated; San Diego, CA
FEATURES Location/Qualifiers
source 1..33
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 61.1%; Score 33; DB 2; Length 33;

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Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 78
LOCUS AR720132 33 bp DNA linear PAT 07-OCT-2005
DEFINITION Sequence 4 from patent US 6946254.
ACCESSION AR720132
VERSION AR720132.1 GI:77371197
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 33)
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of HIV-1 gag sequences for detection of sequences
associated with drug-resistance mutations
JOURNAL Patent: US 6946254-A 4 20-SEP-2005;
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
FEATURES
source
1..33
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 61.1%; Score 33; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 79
LOCUS AX166870 33 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 36 from Patent WO0144510.
ACCESSION AX166870
VERSION AX166870.1 GI:14596472
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Brentano, S.T., Jucker, M.T., Delgado, F.D., Cleuziat, P. and
Rodrigue, M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: WO 0144510-A 36 21-JUN-2001;
Gen-Probe Incorporated (US) ; Biomerieux S.A. (FR)
FEATURES
source
1..33
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="promoter"

ORIGIN
Query Match 61.1%; Score 33; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 80
LOCUS AX397770 33 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 4 from Patent WO0220852.
ACCESSION AX397770
VERSION AX397770.1 GI:21260644
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of hiv-1 sequences for detection of sequences
associated with drug-resistance mutations
JOURNAL Patent: WO 0220852-A 4 14-MAR-2002;
Gen-Probe Incorporated Patent Dept (US) ; Biomerieux S.A. (FR)
FEATURES
source
1..33
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="T7 promoter sequence"
1..33
promoter
ORIGIN
Query Match 61.1%; Score 33; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 81
LOCUS AX498441 33 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 29 from Patent WO0234951.
ACCESSION AX498441
VERSION AX498441.1 GI:23343319
KEYWORDS
SOURCE Human immunodeficiency virus 2 (HIV-2)
ORGANISM Human immunodeficiency virus 2
Viruses; Retro-transcribing viruses; Retroviridae;
Orthoretrovirinae; Lentivirus; Primate lentivirus group.
REFERENCE
1
AUTHORS Yang, Y.Y. and Burrell, T.A.
TITLE Compositions and methods for detecting human immunodeficiency virus
2 (hiv-2)
JOURNAL Patent: WO 0234951-A 29 02-MAY-2002;
Gen-Probe Incorporated (US)
FEATURES
source
1..33
/organism="Human immunodeficiency virus 2"
/mol_type="unassigned DNA"
/db_xref="taxon:11709"

ORIGIN
Query Match 61.1%; Score 33; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 82
LOCUS CS008909 41 bp DNA linear PAT 11-FEB-2005
DEFINITION Sequence 6 from Patent WO2005007886.
ACCESSION CS008909
VERSION CS008909.1 GI:59669518
KEYWORDS

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```

SOURCE      synthetic construct
ORGANISM     synthetic construct
REFERENCE    other sequences; artificial sequences.
1
AUTHORS      Scott,C. and Walker,B.
TITLE        Method
JOURNAL      Patent: WO 2005007896-A 6 27-JAN-2005;
              The Queen's University of Belfast (GB)
              Location/Qualifiers
FEATURES     source
              1..41
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Artificial sequence"

ORIGIN
Query Match      61.1%; Score 33; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
    |||||
Db 5 GAAATTAATACGACTCACTATAGGAGACCACA 37

RESULT 83
AR193645
LOCUS          AR193645          41 bp      DNA      linear      PAT 20-APR-2002
DEFINITION     Sequence 15 from patent US 6348315.
ACCESSION      AR193645
VERSION        AR193645.1 GI:20240237
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 41)
AUTHORS        Pluckthun,A., Hanes,J. and Jermutus,L.
TITLE          Polysome display in the absence of functional ssrA-RNA
JOURNAL        Patent: US 6348315-A 15 19-FEB-2002;
              Location/Qualifiers
FEATURES       source
              1..41
              /organism="unknown"
              /mol_type="unassigned DNA"

ORIGIN
Query Match      61.1%; Score 33; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
    |||||
Db 5 GAAATTAATACGACTCACTATAGGAGACCACA 37

RESULT 84
AR352369
LOCUS          AR352369          41 bp      DNA      linear      PAT 17-AUG-2003
DEFINITION     Sequence 15 from patent US 6589741.
ACCESSION      AR352369
VERSION        AR352369.1 GI:33757503
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 41)
AUTHORS        Pluckthun,A., Hanes,J. and Jermutus,L.
TITLE          Polysome display in the absence of functional ssrA-RNA
JOURNAL        Patent: US 6589741-A 15 08-JUL-2003;
              University of Zurich; Zurich;
              EPX;
              Location/Qualifiers
FEATURES       source
              1..41
              /organism="unknown"

SOURCE      synthetic construct
ORGANISM     synthetic construct
REFERENCE    other sequences; artificial sequences.
1
AUTHORS      Scott,C. and Walker,B.
TITLE        Method
JOURNAL      Patent: WO 2005007896-A 6 27-JAN-2005;
              The Queen's University of Belfast (GB)
              Location/Qualifiers
FEATURES     source
              1..41
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Artificial sequence"

ORIGIN
Query Match      61.1%; Score 33; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
    |||||
Db 5 GAAATTAATACGACTCACTATAGGAGACCACA 37

RESULT 85
AX768001
LOCUS          AX768001          41 bp      DNA      linear      PAT 02-JUL-2003
DEFINITION     Sequence 3 from Patent EP1316616.
ACCESSION      AX768001
VERSION        AX768001.1 GI:32436681
KEYWORDS       unidentified
SOURCE         unidentified
ORGANISM       unidentified
REFERENCE      1
AUTHORS        Nemetz,C., Buchberger,B., Watzele,M., Mutter,W., Roeder,A. and
              Wessner,S.
TITLE          Method for producing linear dna fragments for the in vitro
              expression of proteins
JOURNAL        Patent: EP 1316616-A 3 04-JUN-2003;
              Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
              Location/Qualifiers
FEATURES       source
              1..41
              /organism="unidentified"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32644"
              /note="Primer"

ORIGIN
Query Match      61.1%; Score 33; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 86
AX768013
LOCUS          AX768013          41 bp      DNA      linear      PAT 02-JUL-2003
DEFINITION     Sequence 15 from Patent EP1316616.
ACCESSION      AX768013
VERSION        AX768013.1 GI:32436693
KEYWORDS       unidentified
SOURCE         unidentified
ORGANISM       unidentified
REFERENCE      1
AUTHORS        Nemetz,C., Buchberger,B., Watzele,M., Mutter,W., Roeder,A. and
              Wessner,S.
TITLE          Method for producing linear dna fragments for the in vitro
              expression of proteins
JOURNAL        Patent: EP 1316616-A 15 04-JUN-2003;
              Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
              Location/Qualifiers
FEATURES       source
              1..41
              /organism="unidentified"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32644"
              /note="Primer"

ORIGIN
Query Match      61.1%; Score 33; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
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Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTATACGACTCACTATAGGAGACCACA 33
Db 1 GAAATTATACGACTCACTATAGGAGACCACA 33

RESULT 87
AX299239
LOCUS AX299239 49 bp DNA linear PAT 26-NOV-2001
DEFINITION Sequence 2 from Patent WO0183734.
ACCESSION AX299239
VERSION AX299239.1 GI:17129110
KEYWORDS Enterobacteria phage T7
SOURCE Enterobacteria phage T7
ORGANISM Enterobacteria phage T7
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae; T7-like viruses.

REFERENCE 1
AUTHORS Nilsson, N.
TITLE Expression vector libraries
JOURNAL Patent: WO 0183734-A 2 08-NOV-2001;
Bioinvent International AB (SE)
FEATURES
source 1..49
/organism="Enterobacteria phage T7"
/mol_type="unassigned DNA"
/db_xref="taxon:10760"

ORIGIN
Query Match 61.1%; Score 33; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTATACGACTCACTATAGGAGACCACA 33
Db 1 GAAATTATACGACTCACTATAGGAGACCACA 33

RESULT 88
BD080457
LOCUS BD080457 50 bp DNA linear PAT 27-AUG-2002
DEFINITION Methods for protein screening.
ACCESSION BD080457
VERSION BD080457.1 GI:22626060
KEYWORDS JP 2001514850-A/14.
SOURCE unidentified
ORGANISM unidentified
unclassified sequences.

REFERENCE 1 (bases 1 to 50)
AUTHORS Carr, F.J., Carter, G., Hamilton, A.A., Adair, F.S. and Williams, S.
TITLE Methods for protein screening
JOURNAL Patent: JP 2001514850-A 14 18-SEP-2001;
BIOVATION LTD
COMMENT OS Unidentified
PN JP 2001514850-A/14
PD 18-SEP-2001
PF 03-SEP-1998 JP 2000508788
PR 03-SEP-1997 GB 9718552.4 18-SEP-1997 GB 9719834.5 PR
24-SEP-1997 GB 9720184.2 29-SEP-1997 GB 9720522.3 PR
29-SEP-1997 GB 9720525.6 29-SEP-1997 GB 9720523.1 PR
29-SEP-1997 GB 9720524.9 30-DEC-1997 US 60/070063 PR
30-DEC-1997 US 60/070062, 30-DEC-1997 US 60/070037 PR
30-DEC-1997 US 60/070050, 22-JAN-1998 GB 9801255.2 PR
25-FEB-1998 GB 9803828.4, 14-APR-1998 GB 9807760.5 PR
23-MAY-1998 GB 9811130.5
PI FRANCIS JOSEPH CARR, GRAHAM CARTER, ANITA ANNE HAMILTON, FIONA
PI SUZANNE ADAIR,
PI STEVEN WILLIAMS
PC C12N15/09, C07K17/00, C12N11/14, C12P21/00, C12Q1/68//C07K14/16,
PC C07K14/54,
PC C07K16/00, C12N15/00
CC Methods for protein screening

FEATURES
source 1..50
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 61.1%; Score 33; DB 2; Length 50;
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LOCUS AR703437 50 bp DNA linear PAT 20-SEP-2005
DEFINITION Sequence 15 from patent US 6927025.
ACCESSION AR703437
VERSION AR703437.1 GI:75921308
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 50)
AUTHORS Carr, F.J., Carter, G., Hamilton, A.A., Adair, F.S. and Williams, S.
TITLE Methods for protein screening
JOURNAL Patent: US 6927025-A 15 09-AUG-2005;
Biovation Limited; Aberdeen;
GBX;
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Db 15 GAAATTATACGACTCACTATAGGAGACCACA 47

RESULT 90
AR344852
LOCUS AR344852 51 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 41 from patent US 6582920.
ACCESSION AR344852
VERSION AR344852.1 GI:33740933
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 51)
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of HIV-1 RT sequences for detection of sequences associated with drug-resistance mutations
JOURNAL Patent: US 6582920-A 41 24-JUN-2003;
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
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Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 91
LOCUS AR720169 51 bp DNA linear PAT 07-OCT-2005
DEFINITION Sequence 41 from patent US 6946254.
ACCESSION AR720169
VERSION AR720169.1 GI:77371234
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 51)
AUTHORS Yang, Y. Y., Brentano, S. T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of HIV-1 gag sequences for detection of sequences
associated with drug-resistance mutations
JOURNAL Patent: US 6946254-A 41 20-SEP-2005;
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
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Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 92
LOCUS AX397807 51 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 41 from Patent WO0220852.
ACCESSION AX397807
VERSION AX397807.1 GI:21260681
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Yang, Y. Y., Brentano, S. T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of hiv-1 sequences for detection of sequences
associated with drug-resistance mutations
JOURNAL Patent: WO 0220852-A 41 14-MAR-2002;
Gen-Probe Incorporated Patent Dept (US) ; Biomerieux S.A. (FR)
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Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

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RESULT 93
LOCUS BD237698 52 bp DNA linear PAT 17-JUL-2003
DEFINITION Therapeutically active proteins in plants.
ACCESSION BD237698
VERSION BD237698.1 GI:33047468
KEYWORDS JP 2002526116-A/27.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 52)
AUTHORS Heifetz, P. B., Goff, S. A., Tuttle, A. B. and Wenk, M. E. G.
TITLE Therapeutically active proteins in plants
JOURNAL Patent: JP 2002526116-A 27 20-AUG-2002;
SYNGENTA PARTICIPATIONS AG
COMMENT OS Artificial Sequence
PN JP 2002526116-A/27
PD 20-AUG-2002
PF 05-OCT-1999 JP 2000574707
PR 07-OCT-1998 US 09/167362, 07-OCT-1998 US 09/168231 PI
PETER BERNARD HEIFETZ, STEPHEN ARTHUR GOFF, ANNMARIE BLOOM PI
TUTTLE,
PI MONIKA ELSE GRIOT WENK
PC A01H5/00, A23L1/30, A61K38/00, A61K38/16, A61K38/22, PC
A61K38/28
PC A61K38/43, A61K39/00, A61K39/35, A61P29/00, A61P37/00, A61P37/06,
PC A61P37/08,
PC C12N5/10, C12N15/09// (C12N5/10, C12R1:91), C12N15/00, C12N5/00, PC
A61K37/02,
PC A61K37/26, A61K37/48, A61K37/04, A61K37/24, (C12N5/00, C12R1:91) CC
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Db 10 GAAATTAATACGACTCACTATAGGAGACCACA 42

RESULT 94
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DEFINITION Sequence 39 from patent US 6582920.
ACCESSION AR344850
VERSION AR344850.1 GI:33740931
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 52)
AUTHORS Yang, Y. Y., Brentano, S. T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of HIV-1 RT sequences for detection of sequences
associated with drug-resistance mutations
JOURNAL Patent: US 6582920-A 39 24-JUN-2003;
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
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RESULT 95
LOCUS AR720167 52 bp DNA linear PAT 07-OCT-2005
DEFINITION Sequence 39 from patent US 6946254.
ACCESSION AR720167
VERSION AR720167.1 GI:77371232
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 52)
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of HIV-1 gag sequences for detection of sequences
associated with drug-resistance mutations
JOURNAL Patent: US 6946254-A 39 20-SEP-2005;
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 9.6e+05;
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Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 96
LOCUS AX278216 52 bp DNA linear PAT 01-NOV-2001
DEFINITION Sequence 27 from Patent WO0177353.
ACCESSION AX278216
VERSION AX278216.1 GI:16605267
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1
AUTHORS Helfetz, P.B., Goff, S.A., Tuttle, A.B. and Griot-Wenk, M.E.
TITLE Expression of pollen allergens in plasmids
JOURNAL Patent: WO 0177353-A 27 18-OCT-2001;
Syngenta Participations AG (CH)
FEATURES
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Location/Qualifiers
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QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
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Best Local Similarity 100.0%; Pred. No. 9.6e+05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 98
LOCUS AR344848 53 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 37 from patent US 6582920.
ACCESSION AR344848
VERSION AR344848.1 GI:33740929
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 53)
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of HIV-1 RT sequences for detection of sequences
associated with drug-resistance mutations
JOURNAL Patent: US 6582920-A 37 24-JUN-2003;
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
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RESULT 99
LOCUS AR720165 53 bp DNA linear PAT 07-OCT-2005
DEFINITION Sequence 37 from patent US 6946254.
ACCESSION AR720165
VERSION AR720165.1 GI:77371230
KEYWORDS
SOURCE Unknown.

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ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 53)
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of HIV-1 gag sequences for detection of sequences associated with drug-resistance mutations
JOURNAL Patent: US 6946254-A 37 20-SEP-2005;
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
FEATURES
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AX397803
LOCUS AX397803 53 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 37 from Patent WO0220852.
ACCESSION AX397803
VERSION AX397803.1 GI:21260677
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of hiv-1 sequences for detection of sequences associated with drug-resistance mutations
JOURNAL Patent: WO 0220852-A 37 14-MAR-2002;
Gen-Probe Incorporated Patent Dept (US) ; Biomerieux S.A. (FR)
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Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
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GenCore version 5.1.8
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	54	100.0	54	14	Aea08217 M. tuberc
4	42	77.8	58	4	AAD11258 Mycobacte
5	42	77.8	58	10	ADG88339 Mycobacte
6	42	77.8	58	14	Aea08214 M. tuberc
7	41	75.9	57	4	AAD11260 Mycobacte
8	41	75.9	57	10	ADG88341 Mycobacte
9	41	75.9	57	14	Aea08216 M. tuberc
10	40	74.1	59	4	AAD11259 Mycobacte
11	40	74.1	59	10	ADG88340 Mycobacte
12	40	74.1	59	14	Aea08215 M. tuberc
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14	37.6	69.6	54	6	AAL45471 HIV-1 pol
15	37.6	69.6	54	12	ADI18918 HIV-1 pol
16	37	68.5	53	6	ABK53142 HIV-1 rev
17	37	68.5	53	6	AAL45504 HIV-1 pol
18	37	68.5	53	12	ADI18951 HIV-1 pol

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37	68.5	57	4	AAD11013	Promoter-
37	68.5	57	4	AAD11257	Mycobacte
37	68.5	57	10	ADG88338	Mycobacte
37	68.5	57	14	AEA08213	M. tuberc
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36	66.7	37	12	ADI18911	T7 promot
36	66.7	37	12	ADI18911	T7 promot
36	66.7	54	6	ABK53106	HIV-1 gag
36	66.7	54	6	AAL45468	HIV-1 gag
36	66.7	54	12	ADI18915	HIV-1 gag
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35.8	66.3	53	6	ABK53134	HIV-1 gag
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35.8	66.3	53	6	AAL45498	HIV-1 gag
35.8	66.3	53	12	ADI18945	HIV-1 gag
35.8	66.3	53	12	ADI18943	HIV-1 gag
35.4	65.6	53	10	ADH79436	PCR prime
35.4	65.6	54	3	AAA76220	Human pro
35.4	65.6	55	6	ABK53110	HIV-1 rev
35.4	65.6	55	6	AAL45472	HIV-1 pol
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35	64.8	52	10	ADG88343	Mycobacte
35	64.8	52	12	ADI18952	HIV-1 pol
35	64.8	52	14	AEA08218	M. tuberc
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34.8	64.4	53	6	AAL45497	HIV-1 gag
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34.4	63.7	54	6	ABK53133	HIV-1 gag
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34	63.0	53	6	AAL45500	HIV-1 pol
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34	63.0	61	4	AAD11012	Promoter-
33.8	62.6	52	3	AAA76204	Human pro
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33.2	61.5	5731	4	AAD11615	Six finger
33	61.1	33	4	AAD11020	Bacteriop
33	61.1	33	4	AAD11286	Bacteriop
33	61.1	33	6	ABK53104	T7 promot
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33	61.1	49	6	ABL53868	Phage t7
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33	61.1	51	2	AAK85760	PCR prime
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33	61.1	52	5	AAD21601	Phage RNA
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97	33	61.1	55	6	ABK53144	Abk53144 HIV-1 rev	170	33	61.1	190	6	ABL56948	AbL56948 Galactose
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105	33	61.1	58	10	ADH79429	Adh79429 PCR prime	177	33	61.1	216	8	ABZ80275	Abz80275 Peptide-1
106	33	61.1	59	4	ADH11021	Adh11021 Probe #1	178	33	61.1	216	8	ABZ80276	Abz80276 Peptide-1
107	33	61.1	59	4	ADH11011	Adh11011 Promoter-	179	33	61.1	217	10	ADP55564	Adp55564 Cell-free
108	33	61.1	60	10	ADD69693	Add69693 Nucleic a	180	33	61.1	217	10	ADJ66007	Adj66007 5' DNA fr
109	33	61.1	60	10	ADD69692	Add69692 T7 RNA pr	181	33	61.1	222	6	ABQ82240	Abq82240 Plasmid p
110	33	61.1	62	2	AAQ57040	Aaq57040 M. tuberc	182	33	61.1	222	6	ABQ82238	Abq82238 Plasmid p
111	33	61.1	63	2	AAV70233	Aav70233 scFv anti	183	33	61.1	222	6	ABQ82236	Abq82236 Plasmid p
112	33	61.1	66	8	ABA00556	Aba00556 Sense pri	184	33	61.1	227	12	ADK71959	Adk71959 PCR prime
113	33	61.1	66	10	ABV76279	Abv76279 Green flu	185	33	61.1	227	12	ADQ54850	Adq54850 PCR prime
114	33	61.1	67	2	AAK25961	Aak25961 Capture d	186	33	61.1	227	13	ADS92548	Ads92548 PCR prime
115	33	61.1	71	6	ABN83684	Abn83684 T7 promot	187	33	61.1	227	14	AEC56031	Aec56031 BAG5 doma
116	33	61.1	74	12	ADLI16931	Adl16931 Pseudomon	188	33	61.1	227	14	AEC56018	Aec56018 BAG3 doma
117	33	61.1	75	2	AAK81449	Aak81449 PCR prime	189	33	61.1	228	12	ADM28957	Adm28957 PCR prime
118	33	61.1	75	8	ABQ77329	Abq77329 Bovine H-	190	33	61.1	244	10	ADP55565	Adp55565 Cell-free
119	33	61.1	75	8	AAL50784	Aal50784 Exonuclea	191	33	61.1	244	10	ADP66008	Adp66008 5' DNA fr
120	33	61.1	75	12	ADLI16916	Adl16916 Pseudomon	192	33	61.1	254	14	ADZ39855	Adz39855 T7 P-Nhis
121	33	61.1	84	12	ADQ30930	Adq30930 Hairpin l	193	33	61.1	254	14	ADZ02844	Adz02844 T7 P-Nhis
122	33	61.1	85	10	ADF86217	Adf86217 PCR prime	194	33	61.1	258	2	AAQ41868	Aaq41868 T7 late g
123	33	61.1	85	14	AEEO1636	Aee01636 Primer #3	195	33	61.1	287	15	AEF92004	Aef92004 Expressio
124	33	61.1	88	3	AAA60713	Aaa60713 T7 promot	196	33	61.1	299	12	ADL71887	Adl71887 Vector pE
125	33	61.1	88	4	AAF75873	Aaf75873 Oligonuc	197	33	61.1	299	15	AEF92006	Aef92006 Expressio
126	33	61.1	89	2	AAQ92012	Aaq92012 Oligomer	198	33	61.1	303	12	ADU27300	Adu27300 Nucleotid
127	33	61.1	89	2	AAT30154	Aat30154 Elements	200	33	61.1	350	9	ADB67799	Adb67799 DNA seque
128	33	61.1	89	2	AAV00260	Aav00260 Cloned T7	201	33	61.1	374	10	ADC64892	Adc64892 Polynucle
129	33	61.1	89	2	AAK01917	Aak01917 Bacteriop	202	33	61.1	374	14	ADM64744	Adm64744 Transport
130	33	61.1	90	2	AAK85755	Aak85755 Oligonuc	203	33	61.1	374	14	ADY75079	Ady75079 T7 RNA po
131	33	61.1	93	5	AAF82145	Aaf82145 T7 promot	204	33	61.1	398	12	ADQ30980	Adq30980 Hairpin l
132	33	61.1	96	6	ABK88323	Abk88323 T4 RNA li	205	33	61.1	407	14	ADM64743	Adm64743 Transport
133	33	61.1	96	6	ABK67969	Abk67969 Mutant DN	206	33	61.1	408	13	ADV34922	Adv34922 Recombina
134	33	61.1	96	9	ADB67790	Adb67790 DNA seque	207	33	61.1	412	2	AAV22974	Aav22974 Nucleic a
135	33	61.1	96	10	ADC64886	Adc64886 T7 promot	208	33	61.1	412	2	AAV70648	Aav70648 Human tau
136	33	61.1	96	14	ADM64747	Adm64747 Transport	209	33	61.1	424	12	ADQ17264	Adq17264 Human sof
137	33	61.1	96	14	ADX44479	Adx44479 pT7-FF re	210	33	61.1	424	12	ADQ22024	Adq22024 Human sof
138	33	61.1	102	3	AAC55508	Aac55508 Destinati	211	33	61.1	431	12	ADQ30979	Adq30979 Hairpin l
139	33	61.1	102	3	AAC55505	Aac55505 Destinati	212	33	61.1	450	2	AAQ80820	Aaq80820 Gene X ci
140	33	61.1	102	3	AAC55511	Aac55511 Destinati	213	33	61.1	495	14	AEEO1637	Aee01637 Undefined
141	33	61.1	104	1	AAK70013	Aak70013 Sequence	214	33	61.1	511	10	ADP55567	Adp55567 Cell-free
142	33	61.1	104	2	AAQ46833	Aaq46833 G10L sequ	215	33	61.1	511	10	ADJ66010	Adj66010 5' DNA fr
143	33	61.1	109	2	AAQ46833	Aaq46833 G10L sequ	216	33	61.1	599	12	ADQ30982	Adq30982 Hairpin l
144	33	61.1	110	6	AAL50148	Aal50148 Protein l	217	33	61.1	604	13	ADRI10590	Adri10590 Template
145	33	61.1	110	8	ABZ22169	Abz22169 T7 promot	218	33	61.1	632	12	ADQ30981	Adq30981 Hairpin l
146	33	61.1	117	4	AAF75879	Aaf75879 Oligonuc	219	33	61.1	640	6	ABV99931	Abv99931 Leptin-re
147	33	61.1	120	3	AAC55482	Aac55482 Destinati	220	33	61.1	644	5	AAI71848	Aai71848 Recombina
148	33	61.1	124	12	ADK71953	Adk71953 PCR prime	221	33	61.1	651	10	ADD69689	Add69689 Nucleic a
149	33	61.1	124	12	ADM96345	Adm96345 PCR prime	222	33	61.1	652	10	ADP55566	Adp55566 Cell-free
150	33	61.1	134	2	AAQ05915	Aaq05915 Upstream	223	33	61.1	654	10	ADJ66009	Adj66009 5' DNA fr
151	33	61.1	135	2	AAV59148	Aav59148 Peptide l	224	33	61.1	654	10	ADJ66009	Adj66009 5' DNA fr
152	33	61.1	136	8	AAL51534	Aal51534 Cell-free	225	33	61.1	654	10	ADJ66009	Adj66009 5' DNA fr
153	33	61.1	139	9	ADF86211	Adf86211 DNA oligo	226	33	61.1	701	15	AEF92014	Aef92014 Vector pi
154	33	61.1	143	9	ADB16304	Adb16304 Cleavase	227	33	61.1	713	15	AEF92016	Aef92016 Vector pi
155	33	61.1	144	2	AAV59151	Aav59151 Peptide l	228	33	61.1	728	2	AAQ55301	Aaq55301 Truncated
156	33	61.1	144	6	ADE53338	Ade53338 FEN-1 rel	229	33	61.1	782	2	AAV60837	Aav60837 Partial s
157	33	61.1	144	9	ADB16309	Adb16309 Vector pE	230	33	61.1	821	15	AEF92035	Aef92035 Vector pi
158	33	61.1	144	10	ADC02516	Adc02516 Vector pE	231	33	61.1	844	10	ADP55563	Adp55563 Cell-free
159	33	61.1	144	10	ADD69702	Add69702 Nucleic a	232	33	61.1	844	10	ADJ66006	Adj66006 5' DNA fr
160	33	61.1	146	2	AAK85763	Aak85763 Nucleotid	233	33	61.1	870	2	AAV58934	Aav58934 Humanised
161	33	61.1	147	10	ADD69703	Add69703 Nucleic a	234	33	61.1	905	12	ADQ30986	Adq30986 Hairpin l
162	33	61.1	153	3	AAC55490	Aac55490 Destinati	235	33	61.1	923	2	AAZ38850	Aaz38850 Human gra
163	33	61.1	153	3	AAC55487	Aac55487 Destinati	236	33	61.1	938	12	ADQ30985	Adq30985 Hairpin l
164	33	61.1	160	10	ADF86213	Adf86213 DNA oligo	237	33	61.1				

238 33 61.1 945 2 AAQ55302
239 33 61.1 967 2 AAX08992
240 33 1046 15 AEF92018 Vector pI
241 33 1058 15 AEF92020
242 33 1065 14 AEB71489
243 33 1077 15 AEF92033
244 33 1118 14 ADX86078
245 33 1170 2 AAX79941
246 33 1367 12 ADQ30984
247 33 1377 3 AAA37622
248 33 1400 12 ADQ30983
249 33 1440 3 AAZ98631
250 33 1661 3 AAA37637
251 33 1782 3 AAA37642
252 33 2021 14 ADY83721
253 33 2096 3 AAA37643
254 33 2467 6 ABB83686
255 33 2504 12 ADO33524
256 33 2566 4 ABB50173
257 33 2566 4 ABB49929
258 33 2566 4 ABB85864
259 33 2599 12 ADO33536
260 33 2617 12 ADO33535
261 33 2838 4 AAX91148
262 33 2852 14 AED43482
263 33 2856 4 AAF31388
264 33 2869 4 AAF31387
265 33 3056 14 AEB50618
266 33 3153 2 AAV26523
267 33 3160 2 AAV26480
268 33 3225 8 ABZ70676
269 33 3342 15 AEE32892
270 33 3342 15 AEE76014
271 33 3342 15 AEE27371
272 33 3383 15 AEE27370
273 33 3396 14 ADU87426
274 33 3396 14 ADZ67253
275 33 3451 13 ADT04775
276 33 3473 8 ABZ57850
277 33 3473 8 ABZ80274
278 33 3713 8 ACA61474
279 33 3836 15 AEE32893
280 33 3836 15 AEE76015
281 33 3857 15 AEE32894
282 33 3857 15 AEE76016
283 33 3879 14 ADV51154
284 33 3890 14 ADV51155
285 33 3892 15 AEF87314
286 33 3895 14 ADV51156
287 33 3900 14 ADV51157
288 33 3984 2 AAT07310
289 33 4009 2 AAQ92326
290 33 4019 15 AEE32895
291 33 4019 15 AEE76017
292 33 4050 14 AED95556
293 33 4100 4 AAH43600
294 33 4100 6 AAD22480
295 33 4100 8 ACA64103
296 33 4294 2 AAQ92325
297 33 4415 15 AEF87313
298 33 4488 4 AAD09266
299 33 4641 2 AAQ40294
300 33 4682 4 AAH43599

ALIGNMENTS

RESULT 1
ID AAD11261 standard; DNA; 54 BP.
XX
AC AAD11261;

XX 11-SEP-2003 (revised)
DT 24-SEP-2001 (first entry)
XX Mycobacterium 16S rRNA amplifying T7 promoter-primer #5.
XX Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
KW Mycobacterium other than tuberculosis; MOTT; PCR primer; T7 promoter; ss.
OS Enterobacteria phage T7.
OS Mycobacterium sp.
OS Chimeric.
XX Key Location/Qualifiers
FH promoter 1..33
FT /*tag= a
FT /label= T7_promoter
XX WO200144510-A2.
XX 21-JUN-2001.
XX 17-DEC-1999; 99WO-US030346.
XX 17-DEC-1999; 99WO-US030346.
XX (GENP-) GEN-PROBE INC.
XX (INNR) BIOMERIEUX SA.
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2001-398170/42.
XX Detecting Mycobacterium species, involves in vitro amplification of 16S
XX rRNA or DNA encoding RNA in nucleic acid amplification mixture using
XX specific primers, and detecting the amplified nucleic acid.
XX Claim 1; Page 34; 44pp; English.
XX The invention relates to a method of detecting Mycobacterium species,
XX that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
XX encoding 16S rRNA in an in vitro nucleic acid amplification mixture
XX comprising a polymerase, and at least two primers, and then detecting the
XX amplified nucleic acid. The method is relatively simple and useful for
XX detecting the presence of various Mycobacterium species in a biological
XX sample, and thus important for diagnosis of infections resulting from
XX them. The method is especially important for screening opportunistic
XX infections caused by M. tuberculosis or a Mycobacterium other than
XX tuberculosis (MOTT). The present sequence is a T7 promoter-primer used
XX for amplifying Mycobacterium 16S rRNA. (Updated on 11-SEP-2003 to
XX standardise OS field)
XX Sequence 54 BP; 18 A; 14 C; 9 G; 13 T; 0 U; 0 Other;
XX Query Match 100.0%; Score 54; DB 4; Length 54;
XX Best Local Similarity 100.0%; Pred. No. 1..1e-11;
XX Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTACTATAGGAGACCATTTGCAATATATCCCACTGC 54
DB 1 GAAATTAATACGACTACTATAGGAGACCATTTGCAATATATCCCACTGC 54
RESULT 2
ADG88342
ID ADG88342 standard; DNA; 54 BP.
XX
AC ADG88342;
XX
DT 11-MAR-2004 (first entry)
XX
DE Mycobacterium amplifying PCR primer #11.
XX

```

KW In vitro amplification; PCR; primer; ss.
XX Mycobacterium sp.
OS
XX US2003165824-A1.
XX
XX 04-SEP-2003.
XX
XX 15-DEC-2000; 2000US-00738274.
XX
XX 17-DEC-1999; 99US-0172190P.
XX
XX (BREN/) BRENTANO S T.
XX (JUCK/) JUCKER M T.
XX (DELG/) DELGADO F D.
XX (CLEU/) CLEUZIAT P.
XX (RODR/) RODRIGUE M.
XX
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2003-898044/82.
XX
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX in a biological sample comprises performing in vitro nucleic acid
XX amplification and detection of amplified products.
XX
XX Claim 1; SEQ ID NO 11; 20pp; English.
XX
XX The present invention relates to a method of detecting Mycobacterium
XX species present in a biological sample. The method involves using in
XX vitro nucleic acid amplification and detection of amplified products. The
XX invention is useful for diagnostic detection of pathogenic bacteria such
XX as Mycobacterium species. The present sequence is the Mycobacterium
XX tuberculosis (ATCC 27294) 16S ribosomal RNA (16S:rRNA) amplifying T7
XX promoter PCR primer. This T7 promoter primer sequence include a T7
XX promoter sequence attached to the portion of the primer sequence that
XX binds to the target or its complement.
XX
XX Sequence 54 BP; 18 A; 14 C; 9 G; 13 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 54; DB 10; Length 54;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-11;
XX Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 GAAATTAATACGACTCTACTATAGGAGACACATTGTGCAATATTTCCCACTGC 54
XX |||||||
XX Db 1 GAAATTAATACGACTCTACTATAGGAGACACATTGTGCAATATTTCCCACTGC 54
XX |||||||

RESULT 3
AEA08217
ID AEA08217 standard; DNA; 54 BP.
XX
XX AEA08217;
XX
XX 14-JUL-2005 (first entry)
XX
XX M. tuberculosis 16S:rRNA amplifying T7 promoter PCR primer, SEQ ID NO: 11.
XX
XX Microorganism detection; DNA amplification; 16s ribosomal RNA; 16s rRNA;
XX PCR; primer; ss.
XX
XX Mycobacterium tuberculosis; ATCC 27294.
XX
XX Enterobacteria phage T7.
XX
XX US2005100915-A1.
XX
XX 12-MAY-2005.
XX
XX 18-SEP-2003; 2003US-00665708.
XX
XX 17-DEC-1999; 99US-0172190P.
XX
XX 15-DEC-2000; 2000US-00738274.
XX
XX (BREN/) BRENTANO S T.
XX (JUCK/) JUCKER M T.
XX (DELG/) DELGADO F D.

In vitro amplification; PCR; primer; ss.
Mycobacterium sp.
US2003165824-A1.
04-SEP-2003.
15-DEC-2000; 2000US-00738274.
17-DEC-1999; 99US-0172190P.
(BREN/) BRENTANO S T.
(JUCK/) JUCKER M T.
(DELG/) DELGADO F D.
(CLEU/) CLEUZIAT P.
(RODR/) RODRIGUE M.
Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
WPI; 2003-898044/82.
Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
in a biological sample comprises performing in vitro nucleic acid
amplification and detection of amplified products.
Claim 1; SEQ ID NO 11; 20pp; English.
The present invention relates to a method of detecting Mycobacterium
species present in a biological sample. The method involves using in
vitro nucleic acid amplification and detection of amplified products. The
invention is useful for diagnostic detection of pathogenic bacteria such
as Mycobacterium species. The present sequence is the Mycobacterium
tuberculosis (ATCC 27294) 16S ribosomal RNA (16S:rRNA) amplifying T7
promoter PCR primer. This T7 promoter primer sequence include a T7
promoter sequence attached to the portion of the primer sequence that
binds to the target or its complement.
Sequence 54 BP; 18 A; 14 C; 9 G; 13 T; 0 U; 0 Other;
Query Match 100.0%; Score 54; DB 10; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCTACTATAGGAGACACATTGTGCAATATTTCCCACTGC 54
|||||
Db 1 GAAATTAATACGACTCTACTATAGGAGACACATTGTGCAATATTTCCCACTGC 54
|||||

RESULT 4
AAD11258
ID AAD11258 standard; DNA; 58 BP.
XX
XX AAD11258;
XX
XX 11-SEP-2003 (revised)
XX 24-SEP-2001 (first entry)
XX
XX Mycobacterium 16S rRNA amplifying T7 promoter-primer #2.
XX
XX Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
XX Mycobacterium other than tuberculosis; MOTT; PCR primer; T7 promoter; ss.
XX
XX Enterobacteria phage T7.
XX Mycobacterium sp.
XX Chimeric.
XX
XX Key Location/Qualifiers
XX promoter 1..33
XX /*tag= a
XX /label= T7_promoter
XX
XX WO200144510-A2.
XX
XX 21-JUN-2001.
XX
XX 17-DEC-1999; 99WO-US030346.
XX
XX 17-DEC-1999; 99WO-US030346.
XX
XX (GENP-) GEN-PROBE INC.
XX (INNR ) BIOMERIEUX SA.
XX
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2001-398170/42.
XX
XX Detecting Mycobacterium species, involves in vitro amplification of 16S

```

PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using
PT specific primers, and detecting the amplified nucleic acid.

XX Claim 1; Page 33; 44pp; English.

XX The invention relates to a method of detecting Mycobacterium species,
CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture
CC comprising a polymerase, and at least two primers, and then detecting the
CC amplified nucleic acid. The method is relatively simple and useful for
CC detecting the presence of various Mycobacterium species in a biological
CC sample, and thus important for diagnosis of infections resulting from
CC them. The method is especially important for screening opportunistic
CC infections caused by M. tuberculosis or a Mycobacterium other than
CC tuberculosis (MOTT). The present sequence is a T7 promoter-primer used
CC for amplifying Mycobacterium 16S rRNA. (Updated on 11-SEP-2003 to
CC standardise OS field)

XX Sequence 58 BP; 18 A; 16 C; 10 G; 14 T; 0 U; 0 Other;

Query Match 77.8%; Score 42; DB 4; Length 58;
Best Local Similarity 98.1%; Pred. No. 7.6e-07;
Matches 53; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 GAAATTAATACGACTCACTATAGGAGACACATTGTGCAATATTTCCCACTGC 54
|||||
DB 1 GAAATTAATACGACTCACTATAGGAGACACATTGTGCAATATTTCCCACTGC 53

RESULT 5

ADG88339
ID ADG88339 standard; DNA; 58 BP.

XX

AC ADG88339;

DT 11-MAR-2004 (first entry)

XX Mycobacterium amplifying PCR primer #8.

DE In vitro amplification; PCR; primer; ss.

XX Mycobacterium sp.

OS US2003165824-A1.

XX

PN 04-SEP-2003.

XX

PD 15-DEC-2000; 2000US-00738274.

XX

PF 17-DEC-1999; 99US-0172190P.

XX

PR (BREN/) BRENTANO S T.

XX

PA (JUCK/) JUCKER M T.

XX

PA (DELG/) DELGADO F D.

XX

PA (CLEU/) CLEUZIAZ P.

XX

PA (RODR/) RODRIGUE M.

XX

PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;

WPI; 2003-898044/82.

DR

XX

XX

PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present

PT in a biological sample comprises performing in vitro nucleic acid

PT amplification and detection of amplified products.

XX

PS Claim 1; SEQ ID NO 8; 20pp; English.

XX

XX

CC The present invention relates to a method of detecting Mycobacterium

CC species present in a biological sample comprises performing an in vitro

CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and

CC detecting the amplified Mycobacterium nucleic acid. The present sequence

CC is Mycobacterium amplifying PCR primer.

XX

SQ Sequence 58 BP; 18 A; 16 C; 10 G; 14 T; 0 U; 0 Other;

Query Match 77.8%; Score 42; DB 10; Length 58;
Best Local Similarity 98.1%; Pred. No. 7.6e-07;
Matches 53; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 GAAATTAATACGACTCACTATAGGAGACACATTGTGCAATATTTCCCACTGC 54
|||||
DB 1 GAAATTAATACGACTCACTATAGGAGACACATTGTGCAATATTTCCCACTGC 53

RESULT 6

AEA08214

ID AEA08214 standard; DNA; 58 BP.

XX

AC AEA08214;

XX

DT 14-JUL-2005 (first entry)

XX

DE M. tuberculosis 16SrRNA amplifying T7 promoter PCR primer, SEQ ID NO: 8.

XX Microorganism detection; DNA amplification; 16S ribosomal RNA; 16S rRNA;

KW PCR; primer; ss.

XX

OS Mycobacterium tuberculosis; ATCC 27294.

XX Enterobacteria phage T7.

XX

PN US2005100915-A1.

XX

PD 12-MAY-2005.

XX

PF 18-SEP-2003; 2003US-00665708.

XX

PR 17-DEC-1999; 99US-0172190P.

XX

PR 15-DEC-2000; 2000US-00738274.

XX

PA (BREN/) BRENTANO S T.

XX

PA (JUCK/) JUCKER M T.

XX

PA (DELG/) DELGADO F D.

XX

PA (CLEU/) CLEUZIAZ P.

XX

PA (RODR/) RODRIGUE M.

XX

PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;

XX

WPI; 2005-345392/35.

XX

DR

XX

XX

PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present

PT in a biological sample, comprises using in vitro nucleic acid

PT amplification and detection of amplified products.

XX

XX

PS Example 1; SEQ ID NO 8; 21pp; English.

XX

XX

CC The present invention relates to a method of detecting Mycobacterium

CC species present in a biological sample. The method involves using in

CC vitro nucleic acid amplification and detection of amplified products. The

CC invention is useful for diagnostic detection of pathogenic bacteria such

CC as Mycobacterium species. The present sequence is the Mycobacterium

CC tuberculosis (ATCC 27294) 16S ribosomal RNA (16SrRNA) amplifying T7

CC promoter PCR primer. This T7 promoter primer sequence include a T7

CC promoter sequence attached to the portion of the primer sequence that

CC binds to the target or its complement.

XX

XX

SQ Sequence 58 BP; 18 A; 16 C; 10 G; 14 T; 0 U; 0 Other;

Query Match 77.8%; Score 42; DB 14; Length 58;

Best Local Similarity 98.1%; Pred. No. 7.6e-07;

Matches 53; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 GAAATTAATACGACTCACTATAGGAGACACATTGTGCAATATTTCCCACTGC 54

|||||

DB 1 GAAATTAATACGACTCACTATAGGAGACACATTGTGCAATATTTCCCACTGC 53

```

RESULT 7
AAD11260
ID AAD11260 standard; DNA; 57 BP.
XX
AC AAD11260;
XX
XX 11-SEP-2003 (revised)
DT 24-SEP-2001 (first entry)
XX
DE Mycobacterium 16S rRNA amplifying T7 promoter-primer #4.
XX
XX Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
KW Mycobacterium other than tuberculosis; MOTT; PCR primer; T7 promoter; ss.
XX
XX Enterobacteria phage T7.
OS Mycobacterium sp.
OS Chimeric.
XX
XX Key Location/Qualifiers
FT promoter 1..33
FT /*tag= a
FT /label= T7_promoter
XX
XX WO200144510-A2.
XX
XX 21-JUN-2001.
XX
XX 17-DEC-1999; 99WO-US030346.
XX
XX 17-DEC-1999; 99WO-US030346.
XX
XX (GENP-) GEN-PROBE INC.
XX (INNR ) BIOMERIEUX SA.
XX
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2001-398170/42.
XX
XX Detecting Mycobacterium species, involves in vitro amplification of 16S
PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using
PT specific primers, and detecting the amplified nucleic acid.
XX
XX Claim 1; Page 34; 44pp; English.
XX
XX The invention relates to a method of detecting Mycobacterium species,
CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture
CC comprising a polymerase, and at least two primers, and then detecting the
CC amplified nucleic acid. The method is relatively simple and useful for
CC detecting the presence of various Mycobacterium species in a biological
CC sample, and thus important for diagnosis of infections resulting from
CC them. The method is especially important for screening opportunistic
CC infections caused by M. tuberculosis or a Mycobacterium other than
CC tuberculosis (MOTT). The present sequence is a T7 promoter-primer used
CC for amplifying Mycobacterium 16S rRNA. (Updated on 11-SEP-2003 to
CC standardise OS field)
XX
XX Sequence 57 BP; 19 A; 16 C; 9 G; 13 T; 0 U; 0 Other;
SQ
Query Match 75.9%; Score 41; DB 4; Length 57;
Best Local Similarity 94.7%; Pred. No. 1.9e-06;
Matches 54; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Oy 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATATCCCACTGC 54
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATATCCCACTGC 57

RESULT 8
ADG88341
ID ADG88341 standard; DNA; 57 BP.
XX
AC ADG88341;
XX
XX 11-MAR-2004 (first entry)
DE Mycobacterium amplifying PCR primer #10.
XX
XX In vitro amplification; PCR; primer; ss.
XX
XX Mycobacterium sp.
XX
XX US2003165824-A1.
XX
XX 04-SEP-2003.
XX
XX 15-DEC-2000; 2000US-00738274.
XX
XX 17-DEC-1999; 99US-0172190P.
XX
XX (BREN/) BRENTANO S T.
XX (JUCK/) JUCKER M T.
XX (DELG/) DELGADO F D.
XX (CLEU/) CLEUZIAT P.
XX (RODR/) RODRIGUE M.
XX
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2003-898044/82.
XX
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample comprises performing in vitro nucleic acid
PT amplification and detection of amplified products.
XX
XX Claim 1; SEQ ID NO 10; 20pp; English.
XX
XX The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample comprises performing an in vitro
CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
CC detecting the amplified Mycobacterium nucleic acid. The present sequence
CC is Mycobacterium amplifying PCR primer.
XX
XX Sequence 57 BP; 19 A; 16 C; 9 G; 13 T; 0 U; 0 Other;
SQ
Query Match 75.9%; Score 41; DB 10; Length 57;
Best Local Similarity 94.7%; Pred. No. 1.9e-06;
Matches 54; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Oy 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATATCCCACTGC 54
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATATCCCACTGC 57

RESULT 9
AEA08216
ID AEA08216 standard; DNA; 57 BP.
XX
XX AEA08216;
XX
XX 14-JUL-2005 (first entry)
XX
XX M. tuberculosis 16SrRNA amplifying T7 promoter PCR primer, SEQ ID NO: 10.
DE Microorganism detection; DNA amplification; 16S ribosomal RNA; 16S rRNA;
KW PCR; primer; ss.
XX
XX Mycobacterium tuberculosis; ATCC 27294.
OS Enterobacteria phage T7.
XX
XX US2005100915-A1.
XX
XX 12-MAY-2005.
XX
XX 18-SEP-2003; 2003US-00665708.
XX
XX 17-DEC-1999; 99US-0172190P.
PR

```

PR 15-DEC-2000; 2000US-00738274.
 XX (BREN/) BRENTANO S T.
 PA (JUCK/) JUCKER M T.
 PA (DELG/) DELGADO F D.
 PA (CLEU/) CLEUZIAT P.
 PA (RODR/) RODRIGUE M.
 XX
 PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
 XX WPI; 2005-345392/35.
 DR
 XX
 XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
 PT in a biological sample, comprises using in vitro nucleic acid
 PT amplification and detection of amplified products.
 XX
 PS Example 1; SEQ ID NO 10; 21pp; English.
 XX
 CC The present invention relates to a method of detecting Mycobacterium
 CC species present in a biological sample. The method involves using in
 CC vitro nucleic acid amplification and detection of amplified products. The
 CC invention is useful for diagnostic detection of pathogenic bacteria such
 CC as Mycobacterium species. The present sequence is the Mycobacterium
 CC tuberculosis (ATCC 27294) 16S ribosomal RNA (16S rRNA) amplifying T7
 CC promoter PCR primer. This T7 promoter primer sequence include a T7
 CC promoter sequence attached to the portion of the primer sequence that
 CC binds to the target or its complement.
 XX
 SQ Sequence 57 BP; 19 A; 16 C; 9 G; 13 T; 0 U; 0 Other;
 Query Match 75.9%; Score 41; DB 14; Length 57;
 Best Local Similarity 94.7%; Pred. NO. 1.9e-06;
 Matches 54; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
 QY 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 54
 Db 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 57
 RESULT 10
 AAD11259
 ID AAD11259 standard; DNA; 59 BP.
 XX AC AAD11259;
 XX
 DT 11-SEP-2003 (revised)
 DT 24-SEP-2001 (first entry)
 XX
 DE Mycobacterium 16S rRNA amplifying T7 promoter-primer #3.
 XX
 KW Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
 KW Mycobacterium other than tuberculosis; MOTT; PCR primer; T7 promoter; ss.
 XX
 OS Enterobacteria phage T7.
 OS Mycobacterium sp.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT promoter 1..33
 FT /*tag= a
 FT /label= T7_promoter
 XX
 PN WO200144510-A2.
 XX
 PD 21-JUN-2001.
 XX
 PF 17-DEC-1999; 99WO-US030346.
 XX
 PR 17-DEC-1999; 99WO-US030346.
 XX
 XX (GENP-) GEN-PROBE INC.
 PA (INMR) BIOMERIEUX SA.
 XX

PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
 XX WPI; 2001-398170/42.
 XX
 PT Detecting Mycobacterium species, involves in vitro amplification of 16S
 PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using
 PT specific primers, and detecting the amplified nucleic acid.
 XX
 XX Claim 1; Page 34; 44pp; English.
 XX
 CC The invention relates to a method of detecting Mycobacterium species,
 CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
 CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture
 CC comprising a polymerase, and at least two primers, and then detecting the
 CC amplified nucleic acid. The method is relatively simple and useful for
 CC detecting the presence of various Mycobacterium species in a biological
 CC sample, and thus important for diagnosis of infections resulting from
 CC them. The method is especially important for screening opportunistic
 CC infections caused by M. tuberculosis or a Mycobacterium other than
 CC tuberculosis (MOTT). The present sequence is a T7 promoter-primer used
 CC for amplifying Mycobacterium 16S rRNA. (Updated on 11-SEP-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 59 BP; 19 A; 17 C; 9 G; 14 T; 0 U; 0 Other;
 Query Match 74.1%; Score 40; DB 4; Length 59;
 Best Local Similarity 93.1%; Pred. No. 4.8e-06;
 Matches 54; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
 QY 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 54
 Db 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 58
 RESULT 11
 ADG88340
 ID ADG88340 standard; DNA; 59 BP.
 XX AC ADG88340;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Mycobacterium amplifying PCR primer #9.
 XX
 KW In vitro amplification; PCR; primer; ss.
 XX
 OS Mycobacterium sp.
 XX
 PN US2003165824-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 15-DEC-2000; 2000US-00738274.
 XX
 PR 17-DEC-1999; 99US-0172190P.
 XX
 PA (BREN/) BRENTANO S T.
 PA (JUCK/) JUCKER M T.
 PA (DELG/) DELGADO F D.
 PA (CLEU/) CLEUZIAT P.
 PA (RODR/) RODRIGUE M.
 XX
 PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
 XX WPI; 2003-898044/82.
 DR
 XX
 XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
 PT in a biological sample comprises performing in vitro nucleic acid
 PT amplification and detection of amplified products.
 XX
 PS Claim 1; SEQ ID NO 9; 20pp; English.
 XX
 CC The present invention relates to a method of detecting Mycobacterium

CC species present in a biological sample comprises performing an in vitro
 CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
 CC detecting the amplified Mycobacterium nucleic acid. The present sequence
 CC is Mycobacterium amplifying PCR primer.
 XX
 SQ Sequence 59 BP; 19 A; 17 C; 9 G; 14 T; 0 U; 0 Other;

Query Match 74.1%; Score 40; DB 10; Length 59;
 Best Local Similarity 93.1%; Pred. No. 4.8e-06;
 Matches 54; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA----CATGTGCAATATTCCTCCACTGC 54
 Db 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATGTGCAATATTCCTCCACTGC 58

RESULT 12
 AEA08215 ID AEA08215 standard; DNA; 59 BP.
 XX
 AC AEA08215;
 XX
 DT 14-JUL-2005 (first entry)
 XX
 DE M. tuberculosis 16S rRNA amplifying T7 promoter PCR primer, SEQ ID NO: 9.
 XX
 KW Microorganism detection; DNA amplification; 16S ribosomal RNA; 16S rRNA;
 KW PCR; primer; ss.
 XX
 OS Mycobacterium tuberculosis; ATCC 27294.
 OS Enterobacteria phage T7.
 XX
 PN US2005100915-A1.
 XX
 PD 12-MAY-2005.
 XX
 PF 18-SEP-2003; 2003US-00665708.
 XX
 PR 17-DEC-1999; 99US-0172180P.
 PR 15-DEC-2000; 2000US-00738274.
 XX
 PA (BREN/) BRENTANO S T.
 PA (JUCK/) JUCKER M T.
 PA (DELG/) DELGADO F D.
 PA (CLEU/) CLEUZIAT P.
 PA (RODR/) RODRIGUE M.
 XX

Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
 WPI; 2005-345392/35.
 XX
 DR Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
 PT in a biological sample, comprises using in vitro nucleic acid
 PT amplification and detection of amplified products.
 XX
 PS Example 1; SEQ ID NO 9; 21pp; English.
 XX

CC The present invention relates to a method of detecting Mycobacterium
 CC species present in a biological sample. The method involves using in
 CC vitro nucleic acid amplification and detection of amplified products. The
 CC invention is useful for diagnostic detection of pathogenic bacteria such
 CC as Mycobacterium species. The present sequence is the Mycobacterium
 CC tuberculosis (ATCC 27294) 16S ribosomal RNA (16S rRNA) amplifying T7
 CC promoter PCR primer. This T7 promoter primer sequence includes a T7
 CC promoter sequence attached to the portion of the primer sequence that
 CC binds to the target or its complement.
 XX
 SQ Sequence 59 BP; 19 A; 17 C; 9 G; 14 T; 0 U; 0 Other;

Query Match 74.1%; Score 40; DB 14; Length 59;
 Best Local Similarity 93.1%; Pred. No. 4.8e-06;
 Matches 54; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA----CATGTGCAATATTCCTCCACTGC 54
 Db 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATGTGCAATATTCCTCCACTGC 58

RESULT 13
 ABK53109 ID ABK53109 standard; DNA; 54 BP.
 XX
 AC ABK53109;
 XX
 DT 29-AUG-2003 (revised)
 DT 12-AUG-2002 (first entry)
 XX
 DE HIV-1 reverse transcriptase gene specific oligonucleotide primer #12.
 XX
 KW HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;
 KW reverse transcriptase; infection; PCR.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN US2002055095-A1.
 XX
 PD 09-MAY-2002.
 XX
 PF 31-AUG-2001; 2001US-00944036.
 XX
 PR 01-SEP-2000; 2000US-0229790P.
 XX
 PA (YANG/) YANG Y Y.
 PA (BREN/) BRENTANO S T.
 PA (BABO/) BABOLA O.
 PA (TRAN/) TRAN N.
 PA (VERN/) VERNET G.
 XX
 PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
 XX
 DR WPI; 2002-462902/49.
 XX
 PT New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-
 PT 1 and probes for detecting the amplified product are specific for gag and
 PT pol regions and are useful to detect different subtypes of HIV-1.
 XX
 PS Claim 1; Page 15; 37pp; English.
 XX
 CC This invention relates to a series of nucleic acid oligomers for
 CC amplifying and detecting a nucleotide sequence of human immunodeficiency
 CC virus type 1 (HIV-1). The invention also comprises a labeled
 CC oligonucleotide that specifically hybridizes to an HIV-1 sequence derived
 CC from gag or pol sequences, having one of the sequences fully defined in
 CC the specification, and a method for detecting HIV-1 in a biological
 CC sample, comprising mixing the sample with two or more of the
 CC amplification oligomers that specifically amplify at least one HIV-1
 CC target sequence within gag and a pol sequence which is a protease or
 CC reverse transcriptase sequence, amplifying the target, and detecting the
 CC amplified product. The oligonucleotides of the invention may be used to
 CC diagnose HIV-1 infection. The presents sequence represents a PCR primer
 CC used to amplify the HIV-1 reverse transcriptase gene in the HIV detection
 CC method of the invention. (Updated on 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 54 BP; 21 A; 9 C; 9 G; 15 T; 0 U; 0 Other;

Query Match 69.6%; Score 37.6; DB 6; Length 54;
 Best Local Similarity 90.9%; Pred. No. 4.3e-05;
 Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATGTGCAATATTCCTCCACTGC 44
 Db 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATGTGCAATATTCCTCCACTGC 44

RESULT 14
 AAL45471 ID AAL45471 standard; DNA; 44 BP.
 XX
 AC AAL45471;
 XX
 DT 29-AUG-2003 (revised)
 DT 12-AUG-2002 (first entry)
 XX
 DE HIV-1 reverse transcriptase gene specific oligonucleotide primer #12.
 XX
 KW HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;
 KW reverse transcriptase; infection; PCR.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN US2002055095-A1.
 XX
 PD 09-MAY-2002.
 XX
 PF 31-AUG-2001; 2001US-00944036.
 XX
 PR 01-SEP-2000; 2000US-0229790P.
 XX
 PA (YANG/) YANG Y Y.
 PA (BREN/) BRENTANO S T.
 PA (BABO/) BABOLA O.
 PA (TRAN/) TRAN N.
 PA (VERN/) VERNET G.
 XX
 PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
 XX
 DR WPI; 2002-462902/49.
 XX
 PT New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-
 PT 1 and probes for detecting the amplified product are specific for gag and
 PT pol regions and are useful to detect different subtypes of HIV-1.
 XX
 PS Claim 1; Page 15; 37pp; English.
 XX
 CC This invention relates to a series of nucleic acid oligomers for
 CC amplifying and detecting a nucleotide sequence of human immunodeficiency
 CC virus type 1 (HIV-1). The invention also comprises a labeled
 CC oligonucleotide that specifically hybridizes to an HIV-1 sequence derived
 CC from gag or pol sequences, having one of the sequences fully defined in
 CC the specification, and a method for detecting HIV-1 in a biological
 CC sample, comprising mixing the sample with two or more of the
 CC amplification oligomers that specifically amplify at least one HIV-1
 CC target sequence within gag and a pol sequence which is a protease or
 CC reverse transcriptase sequence, amplifying the target, and detecting the
 CC amplified product. The oligonucleotides of the invention may be used to
 CC diagnose HIV-1 infection. The presents sequence represents a PCR primer
 CC used to amplify the HIV-1 reverse transcriptase gene in the HIV detection
 CC method of the invention. (Updated on 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 54 BP; 21 A; 9 C; 9 G; 15 T; 0 U; 0 Other;

Query Match 69.6%; Score 37.6; DB 6; Length 54;
 Best Local Similarity 90.9%; Pred. No. 4.3e-05;
 Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

ID AAL45471 standard; DNA; 54 BP.
AC AAL45471;
XX
XX
DT 29-AUG-2003 (revised)
DT 06-JUN-2002 (first entry)
XX
DE HIV-1 pol gene RT amplification oligomer SEQ ID NO: 9.
XX
XX HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;
XX probe; ss.
XX
XX Human immunodeficiency virus 1.
OS Enterobacteria phage T7.
XX
XX WO200220852-A1.
XX
XX 14-MAR-2002.
XX
XX 01-SEP-2000; 2000WO-US024117.
XX
XX 01-SEP-2000; 2000WO-US024117.
XX
XX (GENP-) GEN-PROBE INC.
XX (INMR) BIOMERIEUX SA.
XX
XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX WPI; 2002-292273/33.
XX
XX New nucleic acid oligomer, useful for detecting selected regions of gag
PT and pol genes of human immune deficiency virus, particularly for
PT assessing drug resistance.
XX
XX Claim 1; Page 39; 82pp; English.
XX
XX The present invention provides a number of nucleic acid oligomers which
CC can be used to amplify the gag and pol genes of human immunodeficiency
CC virus type 1 (HIV-1). These are used to detect regions of the gag and pol
CC genes, especially regions associated with drug resistance, and also for
CC identifying genetic subtypes of the virus. The present sequence is an
CC oligomer of the invention. (Updated on 29-AUG-2003 to standardise OS
CC field)
XX
XX Sequence 54 BP; 21 A; 9 C; 9 G; 15 T; 0 U; 0 Other;
SQ
Query Match 69.6%; Score 37.6; DB 6; Length 54;
Best Local Similarity 90.9%; Pred. No. 4.3e-05;
Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 GAAATTAATACGACTCACTATAGGAGAGACACATTGTGCAATAT 44
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GAAATTAATACGACTCACTATAGGAGAGACACATTGTGCAATAT 44
| | | | | | | | | | | | | | | | | | | | | |

RESULT 15
AD118918
ID AD118918 standard; DNA; 54 BP.
XX
XX AD118918;
XX
XX 22-APR-2004 (first entry)
XX
XX HIV-1 pol3 gene amplifying primer #1.
XX
XX Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.
XX
XX Human immunodeficiency virus 1.
OS
XX US2003228574-A1.
XX
XX 11-DEC-2003.
XX

PF 28-APR-2003; 2003US-00425975.
XX
XX 01-SEP-2000; 2000US-0229790P.
XX 31-AUG-2001; 2001US-00944036.
XX
XX (YANG/) YANG Y Y.
XX (BREN/) BRENTANO S T.
XX (BABO/) BABOLA O.
XX (TRAN/) TRAN N.
XX (VERN/) VERNET G.
XX
XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX WPI; 2004-060998/06.
XX
XX New nucleic acid oligomer for amplifying and detecting HIV-1 nucleotide
PT sequences and in providing information about the infective agent, e.g.
PT genetic subgroup or drug-resistance phenotype based on detectable
PT sequence information.
XX
XX Claim 1; SEQ ID NO 9; 39pp; English.
XX
XX The present invention relates to a nucleic acid oligomer for amplifying a
XX nucleotide sequence of human immune deficiency virus (HIV)-1. The
XX invention is useful in amplifying and detecting HIV-1 nucleic acid
XX sequences and in providing additional information about the infective
XX agent, such as its genetic subgroup or drug-resistance phenotype based on
XX detectable sequence information. The present sequence is HIV-1 pol3 gene
XX amplifying primer.
XX
XX Sequence 54 BP; 21 A; 9 C; 9 G; 15 T; 0 U; 0 Other;
SQ
Query Match 69.6%; Score 37.6; DB 12; Length 54;
Best Local Similarity 90.9%; Pred. No. 4.3e-05;
Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 GAAATTAATACGACTCACTATAGGAGAGACACATTGTGCAATAT 44
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GAAATTAATACGACTCACTATAGGAGAGACACATTGTGCAATAT 44
| | | | | | | | | | | | | | | | | | | | | |

RESULT 16
ABK53142
ID ABK53142 standard; DNA; 53 BP.
XX
XX ABK53142;
XX
XX 29-AUG-2003 (revised)
DT 12-AUG-2002 (first entry)
XX
XX HIV-1 reverse transcriptase gene specific oligonucleotide primer #13.
XX
XX HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;
XX reverse transcriptase; infection; PCR.
XX
XX Human immunodeficiency virus 1.
OS
XX US2002055095-A1.
XX
XX 09-MAY-2002.
XX
XX 31-AUG-2001; 2001US-00944036.
XX
XX 01-SEP-2000; 2000US-0229790P.
XX
XX (YANG/) YANG Y Y.
XX (BREN/) BRENTANO S T.
XX (BABO/) BABOLA O.
XX (TRAN/) TRAN N.
XX (VERN/) VERNET G.
XX
XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX
XX

```


DR WPI; 2002-462902/49.

XX New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-

PT 1 and probes for detecting the amplified product are specific for gag and

XX pol regions and are useful to detect different subtypes of HIV-1.

XX Claim 1; Page 26; 37pp; English.

XX This invention relates to a series of nucleic acid oligomers for

CC amplifying and detecting a nucleotide sequence of human immunodeficiency

CC virus type 1 (HIV-1). The invention also comprises a labeled

CC oligonucleotide that specifically hybridizes to an HIV-1 sequence derived

CC from gag or pol sequences, having one of the sequences fully defined in

CC the specification, and a method for detecting HIV-1 in a biological

CC sample, comprising mixing the sample with two or more of the

CC amplification oligomers that specifically amplify at least one HIV-1

CC target sequence within gag and a pol sequence which is a protease or

CC reverse transcriptase sequence, amplifying the target, and detecting the

CC amplified product. The oligonucleotides of the invention may be used to

CC diagnose HIV-1 infection. The presents sequence represents a PCR primer

CC used to amplify the HIV-1 reverse transcriptase gene in the HIV detection

CC method of the invention. (Updated on 29-AUG-2003 to standardise OS field)

XX

SQ Sequence 53 BP; 20 A; 8 C; 9 G; 16 T; 0 U; 0 Other;

Query Match 68.5%; Score 37; DB 6; Length 53;

Best Local Similarity 88.9%; Pred. No. 7.5e-05;

Matches 40; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACATTTGTGCAATATT 45

Db 1 GAAATTAATACGACTCACTATAGGAGACCACATTTGTGCAATATT 45

RESULT 17

ID AAL45504 standard; DNA; 53 BP.

XX

AC AAL45504;

XX

DT 29-AUG-2003 (revised)

DT 06-JUN-2002 (first entry)

XX

DE HIV-1 pol gene RT amplification oligomer SEQ ID NO: 42.

XX

XX HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;

KW probe; ss.

XX

OS Human immunodeficiency virus 1.

OS Enterobacteria phage T7.

XX

PN WO200220852-A1.

XX

PD 14-MAR-2002.

XX

PF 01-SEP-2000; 2000WO-US024117.

XX

PR 01-SEP-2000; 2000WO-US024117.

XX

PA (GENP-) GEN-PROBE INC.

PA (INMR) BIOMERIEUX SA.

XX

PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;

XX

DR WPI; 2002-292273/33.

XX

XX New nucleic acid oligomer, useful for detecting selected regions of gag

PT and pol genes of human immune deficiency virus, particularly for

PT assessing drug resistance.

XX

PS Claim 1; Page 61; 82pp; English.

XX

CC The present invention provides a number of nucleic acid oligomers which

/

CC can be used to amplify the gag and pol genes of human immunodeficiency

CC virus type 1 (HIV-1). These are used to detect regions of the gag and pol

CC genes, especially regions associated with drug resistance, and also for

CC identifying genetic subtypes of the virus. The present sequence is an

CC oligomer of the invention. (Updated on 29-AUG-2003 to standardise OS

CC field)

XX

SQ Sequence 53 BP; 20 A; 8 C; 9 G; 16 T; 0 U; 0 Other;

Query Match 68.5%; Score 37; DB 6; Length 53;

Best Local Similarity 88.9%; Pred. No. 7.5e-05;

Matches 40; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACATTTGTGCAATATT 45

Db 1 GAAATTAATACGACTCACTATAGGAGACCACATTTGTGCAATATT 45

RESULT 18

ID ADI18951 standard; DNA; 53 BP.

XX

AC ADI18951;

XX

DT 22-APR-2004 (first entry)

XX

DE HIV-I pol3 gene amplifying primer #4.

XX

XX Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.

KW Human immunodeficiency virus 1.

OS

XX US2003228574-A1.

PN

PD 11-DEC-2003.

XX

PF 28-APR-2003; 2003US-00425975.

XX

PR 01-SEP-2000; 2000US-0229790P.

PR 31-AUG-2001; 2001US-00944036.

XX

PA (YANG/) YANG Y Y.

PA (BREN/) BRENTANO S T.

PA (BABO/) BABOLA O.

PA (TRAN/) TRAN N.

PA (VERN/) VERNET G.

XX

PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;

XX

DR WPI; 2004-060998/06.

XX

PT New nucleic acid oligomer for amplifying and detecting HIV-1 nucleotide

PT sequences and in providing information about the infective agent, e.g.

PT genetic subgroup or drug-resistance phenotype based on detectable

PT sequence information.

XX

PS Claim 1; SEQ ID NO 42; 39pp; English.

XX

XX The present invention relates to a nucleic acid oligomer for amplifying a

CC nucleotide sequence of human immune deficiency virus (HIV)-1. The

CC invention is useful in amplifying and detecting HIV-1 nucleic acid

CC sequences and in providing additional information about the infective

CC agent, such as its genetic subgroup or drug-resistance phenotype based on

CC detectable sequence information. The present sequence is HIV-1 pol3 gene

CC amplifying primer.

XX

SQ Sequence 53 BP; 20 A; 8 C; 9 G; 16 T; 0 U; 0 Other;

Query Match 68.5%; Score 37; DB 12; Length 53;

Best Local Similarity 88.9%; Pred. No. 7.5e-05;

Matches 40; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACATTTGTGCAATATT 45

```
Db      1 GAAATTAATACGACTCACTATAGGAGGACACATCTTGATAATT 45
|||||
RESULT 19
AAD11023/c
ID  AAD11023 standard; DNA; 57 BP.
XX
AC  AAD11023;
XX
DT  24-SEP-2001 (first entry)
XX
DE  Probe #3 to detect amplified MAC 16S rRNA or DNA encoding 16S rRNA.
KW  Mycobacterium avium complex; MAC; 16S ribosomal RNA; pathogenic bacteria;
KW  in vitro amplification; MAC infection; probe; ss.
XX
OS  Mycobacterium sp.
XX
FN  WO200144511-A2.
XX
PD  21-JUN-2001.
XX
PF  15-DEC-2000; 2000WO-US033872.
XX
PR  15-DEC-1999; 99US-0171202P.
XX
PA  (GENP-) GEN-PROBE INC.
PA  (BREN/) BRENTANO S T.
PA  (LANK/) LANKFORD R L.
XX
PI  Brentano ST, Lankford RL;
XX
WPI; 2001-398171/42.
XX
PT  Detecting Mycobacterium avium complex organisms, comprises using in vitro
PT  nucleic acid amplification with amplification oligonucleotides specific
PT  for 16S ribosomal RNA or DNA encoding 16S rRNA from the bacterial
PT  species.
XX
PS  Claim 11; Page 26; 27pp; English.
XX
CC  The present invention relates to a method for detecting Mycobacterium
CC  avium complex (MAC) organisms (eg. M. avium, M. intracellulare, M.
CC  tuberculosis, M. paratuberculosis) present in a biological sample. The
CC  method comprises amplifying a 16S ribosomal RNA (rRNA) or DNA encoding
CC  16S rRNA obtained from a biological sample containing nucleic acid from a
CC  MAC species in an in vitro nucleic acid amplification mixture comprising
CC  a polymerase activity and a pair of primers to produce an amplified
CC  nucleic acid and detecting amplified nucleic acid. The method is useful
CC  for in vitro diagnostic detection of pathogenic bacteria, particularly
CC  detecting infections caused by MAC organisms, distinguished from other
CC  closely-related Mycobacterium species. The present sequence is a probe
CC  used to detect amplified MAC 16S rRNA sequence or DNA encoding 16S rRNA
XX
SQ  Sequence 57 BP; 13 A; 9 C; 16 G; 19 T; 0 U; 0 Other;

Query Match      68.5%; Score 37; DB 4; Length 57;
Best Local Similarity 91.2%; Pred. No. 7.6e-05;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy      1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTCCTCCACT 52
      57 GAAATTAATACGACTCACTATAGGAGGACACAGCCCATTTGCAATATTCCTCCACT 1
Db
|||||
RESULT 20
AAD11013
ID  AAD11013 standard; DNA; 57 BP.
XX
AC  AAD11013;
XX
DT  11-SEP-2003 (revised)
XX
DE  Probe #3 used for in vitro amplification of MAC rRNA.
KW  Mycobacterium avium complex; MAC; 16S ribosomal RNA; pathogenic bacteria;
KW  in vitro amplification; MAC infection; promoter-primer; ss.
XX
OS  Enterobacteria phage T7.
OS  Mycobacterium sp.
XX
Chimeric.
XX
Key      Location/Qualifiers
FT  promoter      1..33
FT  /*tag= a
FT  /note= "T7 promoter"
FT  misc_feature   34..57
FT  /*tag= b
FT  /note= "PCR primer from Mycobacterium sp."
XX
FN  WO200144511-A2.
XX
PD  21-JUN-2001.
XX
PF  15-DEC-2000; 2000WO-US033872.
XX
PR  15-DEC-1999; 99US-0171202P.
XX
PA  (GENP-) GEN-PROBE INC.
PA  (BREN/) BRENTANO S T.
PA  (LANK/) LANKFORD R L.
XX
PI  Brentano ST, Lankford RL;
XX
WPI; 2001-398171/42.
XX
PT  Detecting Mycobacterium avium complex organisms, comprises using in vitro
PT  nucleic acid amplification with amplification oligonucleotides specific
PT  for 16S ribosomal RNA or DNA encoding 16S rRNA from the bacterial
PT  species.
XX
PS  Claim 1; Page 12; 27pp; English.
XX
CC  The present invention relates to a method for detecting Mycobacterium
CC  avium complex (MAC) organisms (eg. M. avium, M. intracellulare, M.
CC  tuberculosis, M. paratuberculosis) present in a biological sample. The
CC  method comprises amplifying a 16S ribosomal RNA (rRNA) or DNA encoding
CC  16S rRNA obtained from a biological sample containing nucleic acid from a
CC  MAC species in an in vitro nucleic acid amplification mixture comprising
CC  a polymerase activity and a pair of primers to produce an amplified
CC  nucleic acid and detecting amplified nucleic acid. The method is useful
CC  for in vitro diagnostic detection of pathogenic bacteria, particularly
CC  detecting infections caused by MAC organisms, distinguished from other
CC  closely-related Mycobacterium species. The present sequence is a promoter
CC  -primer from Bacteriophage T7 and Mycobacterium sp. Promoter-primer is
CC  used for in vitro amplification of MAC rRNA. (Updated on 11-SEP-2003 to
CC  standardise OS field)
XX
SQ  Sequence 57 BP; 19 A; 16 C; 9 G; 13 T; 0 U; 0 Other;

Query Match      68.5%; Score 37; DB 4; Length 57;
Best Local Similarity 91.2%; Pred. No. 7.6e-05;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy      1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTCCTCCACT 52
      57 GAAATTAATACGACTCACTATAGGAGGACACAGCCCATTTGCAATATTCCTCCACT 1
Db
|||||
RESULT 21
AAD11257
ID  AAD11257 standard; DNA; 57 BP.
XX
AC  AAD11257;
XX
DT  11-SEP-2003 (revised)
XX
```


PA (CLEU/) CLEUZIAT P.
 XX (RODR/) RODRIGUE M.
 PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
 XX WPI; 2005-345392/35.
 DR
 XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
 PT in a biological sample, comprises using in vitro nucleic acid
 PT amplification and detection of amplified products.
 XX
 XX Example 1; SEQ ID NO 7; 21pp; English.
 PS
 CC The present invention relates to a method of detecting Mycobacterium
 CC species present in a biological sample. The method involves using in
 CC vitro nucleic acid amplification and detection of amplified products. The
 CC invention is useful for diagnostic detection of pathogenic bacteria such
 CC as Mycobacterium species. The present sequence is the Mycobacterium
 CC tuberculosis (ATCC 27294) 16S ribosomal RNA (16S rRNA) amplifying T7
 CC promoter PCR primer. This T7 promoter primer sequence include a T7
 CC promoter sequence attached to the portion of the primer sequence that
 CC binds to the target or its complement.
 XX
 XX Sequence 57 BP; 19 A; 16 C; 9 G; 13 T; 0 U; 0 Other;
 SQ
 Query Match 68.5%; Score 37; DB 14; Length 57;
 Best Local Similarity 91.2%; Pred. No. 7.6e-05;
 Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
 QY 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTTGCAATATTTCCCACT 52
 DB 1 GAAATTAATACGACTCACTATAGGAGACCACTTTGTGCAATATTTCCCACT 57
 RESULT 24
 ID ABK53102 standard; DNA; 37 BP.
 XX
 AC ABK53102;
 XX
 DT 29-AUG-2003 (revised)
 DT 12-AUG-2002 (first entry)
 XX
 DE T7 promoter sequence #2.
 XX
 KW HIV; human immunodeficiency virus; ss; promoter; gag; pol; protease;
 KW reverse transcriptase; infection; T7.
 XX
 OS Enterobacteria phage T7.
 XX
 PN US2002055095-A1.
 XX
 PD 09-MAY-2002.
 XX
 PF 31-AUG-2001; 2001US-00944036.
 XX
 PR 01-SEP-2000; 2000US-0229790P.
 XX
 PA (YANG/) YANG Y Y.
 PA (BREN/) BRENTANO S T.
 PA (BABO/) BABOLA O.
 PA (TRAN/) TRAN N.
 PA (VERN/) VERNET G.
 XX
 PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
 XX WPI; 2002-462902/49.
 DR
 XX New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-
 PT 1 and probes for detecting the amplified product are specific for gag and
 PT pol regions and are useful to detect different subtypes of HIV-1.
 XX
 PS Disclosure; Page 13; 37pp; English.

XX This invention relates to a series of nucleic acid oligomers for
 CC amplifying and detecting a nucleotide sequence of human immunodeficiency
 CC virus type 1 (HIV-1). The invention also comprises a labeled
 CC oligonucleotide that specifically hybridizes to an HIV-1 sequence derived
 CC from gag or pol sequences, having one of the sequences fully defined in
 CC the specification, and a method for detecting HIV-1 in a biological
 CC sample, comprising mixing the sample with two or more of the
 CC amplification oligomers that specifically amplify at least one HIV-1
 CC target sequence within gag and a pol sequence which is a protease or
 CC reverse transcriptase sequence, amplifying the target, and detecting the
 CC amplified product. The oligonucleotides of the invention may be used to
 CC diagnose HIV-1 infection. The presents sequence represents a T7 promoter
 CC sequence used to produce transcripts from amplified target sequences
 CC produced using the oligonucleotide primers of the invention. (Updated on
 CC 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 37 BP; 15 A; 7 C; 7 G; 8 T; 0 U; 0 Other;
 Query Match 66.7%; Score 36; DB 6; Length 37;
 Best Local Similarity 100.0%; Pred. No. 0.00017;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36
 DB 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36
 RESULT 25
 AAL45464
 ID AAL45464 standard; DNA; 37 BP.
 XX
 AC AAL45464;
 XX
 DT 29-AUG-2003 (revised)
 DT 06-JUN-2002 (first entry)
 XX
 DE Bacteriophage T7 promoter sequence SEQ ID NO: 2.
 XX
 KW HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;
 KW promoter; ds.
 XX
 OS Enterobacteria phage T7.
 PN WO200220852-A1.
 PD 14-MAR-2002.
 XX
 PF 01-SEP-2000; 2000WO-US024117.
 XX
 PR 01-SEP-2000; 2000WO-US024117.
 XX
 PA (GENP-) GEN-PROBE INC.
 PA (INMR) BIOMERIEUX SA.
 XX
 PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
 XX WPI; 2002-292273/33.
 DR
 XX New nucleic acid oligomer, useful for detecting selected regions of gag
 PT and pol genes of human immune deficiency virus, particularly for
 PT assessing drug resistance.
 XX
 PS Disclosure; Page 37; 82pp; English.
 XX
 CC The present invention provides a number of nucleic acid oligomers which
 CC can be used to amplify the gag and pol genes of human immunodeficiency
 CC virus type 1 (HIV-1). These are used to detect regions of the gag and pol
 CC genes, especially regions associated with drug resistance, and also for
 CC identifying genetic subtypes of the virus. The present sequence is a
 CC fragment of a bacteriophage T7 promoter described the invention. (Updated
 CC on 29-AUG-2003 to standardise OS field)
 XX


```

AC AAL45468;
XX
XX
DT 29-AUG-2003 (revised)
DT 06-JUN-2002 (first entry)
XX
XX
DE HIV-1 gag amplification oligomer SEQ ID NO: 6.
XX
XX
KW HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;
KW probe; ss.
XX
OS Human immunodeficiency virus 1.
OS Enterobacteria phage T7.
XX
XX
FH Key modified_base 46 Location/Qualifiers
FT FT /*tag= a
FT FT /mod_base= OTHER
FT FT /note= "nebularine"
XX
XX
PN WO200220852-A1.
XX
XX
PD 14-MAR-2002.
XX
XX
PF 01-SEP-2000; 2000WO-US024117.
XX
XX
PR 01-SEP-2000; 2000WO-US024117.
XX
XX
PA (GENP-) GEN-PROBE INC.
PA (INNR) BIOMERIEUX SA.
XX
XX
PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX
XX
DR WPI; 2002-292273/33.
XX
XX
PT New nucleic acid oligomer, useful for detecting selected regions of gag
PT and pol genes of human immune deficiency virus, particularly for
PT assessing drug resistance.
XX
XX
PS Claim 1; Page 38; 82pp; English.
XX
XX
CC The present invention provides a number of nucleic acid oligomers which
CC can be used to amplify the gag and pol genes of human immunodeficiency
CC virus type 1 (HIV-1). These are used to detect regions of the gag and pol
CC genes, especially regions associated with drug resistance, and also for
CC identifying genetic subtypes of the virus. The present sequence is an
CC oligomer of the invention. (Updated on 29-AUG-2003 to standardise OS
CC field)
XX
XX
SQ Sequence 54 BP; 17 A; 14 C; 9 G; 13 T; 0 U; 1 Other;

Query Match 66.7%; Score 36; DB 6; Length 54;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACACCATTTG 36
Db 1 GAAATTAATACGACTCACTATAGGAGACACCATTTG 36

RESULT 29
AD118915
ID AD118915 standard; DNA; 54 BP.
XX
XX
AC AD118915;
XX
XX
DT 22-APR-2004 (first entry)
XX
XX
DE HIV-1 gag2 gene amplifying primer #1.
XX
XX
KW Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.
XX
XX
PF Human immunodeficiency virus 1.
XX
XX

```

```

FH Key modified_base 46 Location/Qualifiers
FT FT /*tag= a
FT FT /mod_base= OTHER
FT FT /note= "Nebularine"
XX
XX
PN US2003228574-A1.
XX
XX
PD 11-DEC-2003.
XX
XX
PF 28-APR-2003; 2003US-00425975.
XX
XX
PR 01-SEP-2000; 2000US-0229790P.
PR 31-AUG-2001; 2001US-00944036.
XX
XX
PA (YANG/) YANG Y Y.
PA (BREN/) BRENTANO S T.
PA (BABO/) BABOLA O.
PA (TRAN/) TRAN N.
PA (VERN/) VERNET G.
XX
XX
PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX
XX
DR WPI; 2004-060998/06.
XX
XX
PT New nucleic acid oligomer for amplifying and detecting HIV-1 nucleotide
PT sequences and in providing information about the infective agent, e.g.
PT genetic subgroup or drug-resistance phenotype based on detectable
PT sequence information.
XX
XX
PS Claim 1; SEQ ID NO 6; 39pp; English.
XX
XX
CC The present invention relates to a nucleic acid oligomer for amplifying a
CC nucleotide sequence of human immune deficiency virus (HIV)-1. The
CC invention is useful in amplifying and detecting HIV-1 nucleic acid
CC sequences and in providing additional information about the infective
CC agent, such as its genetic subgroup or drug-resistance phenotype based on
CC detectable sequence information. The present sequence is HIV-1 gag2 gene
CC amplifying primer.
XX
XX
SQ Sequence 54 BP; 17 A; 14 C; 9 G; 13 T; 0 U; 1 Other;

Query Match 66.7%; Score 36; DB 12; Length 54;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACACCATTTG 36
Db 1 GAAATTAATACGACTCACTATAGGAGACACCATTTG 36

RESULT 30
ABK53136
ID ABK53136 standard; DNA; 53 BP.
XX
XX
AC ABK53136;
XX
XX
DT 29-AUG-2003 (revised)
DT 12-AUG-2002 (first entry)
XX
XX
DE HIV-1 Gag gene specific oligonucleotide primer #9.
XX
XX
KW HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;
KW reverse transcriptase; infection; PCR.
XX
XX
OS Human immunodeficiency virus 1.
XX
XX
PN US200205095-A1.
XX
XX
PD 09-MAY-2002.
XX
XX
PF 31-AUG-2001; 2001US-00944036.
XX
XX

```

```

PR 01-SEP-2000; 2000US-0229790P.
XX
XX (YANG/) YANG Y Y.
PA (BREN/) BRENTANO S T.
PA (BBO/) BABOLA O.
PA (TRAN/) TRAN N.
PA (VERN/) VERNET G.
XX
XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX WPI; 2002-462902/49.
DR
XX
XX New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-
PT 1 and probes for detecting the amplified product are specific for gag and
PT pol regions and are useful to detect different subtypes of HIV-1.
XX
XX Claim 1; Page 24; 37pp; English.
PS
XX
XX This invention relates to a series of nucleic acid oligomers for
CC amplifying and detecting a nucleotide sequence of human immunodeficiency
CC virus type 1 (HIV-1). The invention also comprises a labeled
CC oligonucleotide that specifically hybridizes to an HIV-1 sequence derived
CC from gag or pol sequences, having one of the sequences fully defined in
CC the specification, and a method for detecting HIV-1 in a biological
CC sample, comprising mixing the sample with two or more of the
CC amplification oligomers that specifically amplify at least one HIV-1
CC target sequence within gag and a pol sequence which is a protease or
CC reverse transcriptase sequence, amplifying the target, and detecting the
CC amplified product. The oligonucleotides of the invention may be used to
CC diagnose HIV-1 infection. The presents sequence represents a PCR primer
CC used to amplify the HIV-1 Gag gene in the HIV detection method of the
CC invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
XX Sequence 53 BP; 17 A; 14 C; 9 G; 13 T; 0 U; 0 Other;
SQ
Query Match 66.3%; Score 35.8; DB 6; Length 53;
Best Local Similarity 94.9%; Pred. No. 0.00023;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GAAATTAAATAGACTCACTATAGGAGAGACCATGTC 39
DB 1 GAAATTAAATAGACTCACTATAGGAGAGACCATGTC 39
RESULT 31
ABK53134
ID ABK53134 standard; DNA; 53 BP.
AC ABK53134;
XX
XX 29-AUG-2003 (revised)
DT 12-AUG-2002 (first entry)
XX
XX HIV-1 Gag gene specific oligonucleotide primer #7.
DE
XX HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;
KW reverse transcriptase; infection; PCR.
XX
XX Human immunodeficiency virus 1.
OS
XX
XX Key Location/Qualifiers
FH modified_base 45
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= Nebularine"
XX
XX US2002050595-A1.
PN
XX
XX 09-MAY-2002.
PD
XX
XX 31-AUG-2001; 2001US-00944036.
PF
XX
XX 01-SEP-2000; 2000US-0229790P.
PR

```

```

XX (YANG/) YANG Y Y.
PA (BREN/) BRENTANO S T.
PA (BBO/) BABOLA O.
PA (TRAN/) TRAN N.
PA (VERN/) VERNET G.
XX
XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX WPI; 2002-462902/49.
DR
XX
XX New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-
PT 1 and probes for detecting the amplified product are specific for gag and
PT pol regions and are useful to detect different subtypes of HIV-1.
XX
XX Claim 1; Page 24; 37pp; English.
PS
XX
XX This invention relates to a series of nucleic acid oligomers for
CC amplifying and detecting a nucleotide sequence of human immunodeficiency
CC virus type 1 (HIV-1). The invention also comprises a labeled
CC oligonucleotide that specifically hybridizes to an HIV-1 sequence derived
CC from gag or pol sequences, having one of the sequences fully defined in
CC the specification, and a method for detecting HIV-1 in a biological
CC sample, comprising mixing the sample with two or more of the
CC amplification oligomers that specifically amplify at least one HIV-1
CC target sequence within gag and a pol sequence which is a protease or
CC reverse transcriptase sequence, amplifying the target, and detecting the
CC amplified product. The oligonucleotides of the invention may be used to
CC diagnose HIV-1 infection. The presents sequence represents a PCR primer
CC used to amplify the HIV-1 Gag gene in the HIV detection method of the
CC invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
XX Sequence 53 BP; 17 A; 14 C; 9 G; 12 T; 0 U; 1 Other;
SQ
Query Match 66.3%; Score 35.8; DB 6; Length 53;
Best Local Similarity 94.9%; Pred. No. 0.00023;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GAAATTAAATAGACTCACTATAGGAGAGACCATGTC 39
DB 1 GAAATTAAATAGACTCACTATAGGAGAGACCATGTC 39
RESULT 32
AAL45496
ID AAL45496 standard; DNA; 53 BP.
XX
XX AAL45496;
XX
XX 29-AUG-2003 (revised)
DT 06-JUN-2002 (first entry)
XX
XX HIV-1 gag amplification oligomer SEQ ID NO: 34.
DE
XX HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;
KW probe; ss.
XX
XX Human immunodeficiency virus 1.
OS
XX Enterobacteria phage T7.
XX
XX Key Location/Qualifiers
FH modified_base 45
FT /*tag= a
FT /mod_base= OTHER
FT /note= "nebularine"
XX
XX WO200220852-A1.
PN
XX
XX 14-MAR-2002.
PD
XX
XX 01-SEP-2000; 2000WO-US024117.
PF
XX
XX 01-SEP-2000; 2000WO-US024117.
PR

```

XX (GENP-) GEN-PROBE INC.
PA (INMR) BIOMERIEUX SA.
XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX WPI; 2002-292273/33.
DR New nucleic acid oligomer, useful for detecting selected regions of gag
PT and pol genes of human immune deficiency virus, particularly for
PT assessing drug resistance.
XX Claim 1; Page 58; 82pp; English.
XX The present invention provides a number of nucleic acid oligomers which
CC can be used to amplify the gag and pol genes of human immunodeficiency
CC virus type I (HIV-1). These are used to detect regions of the gag and pol
CC genes, especially regions associated with drug resistance, and also for
CC identifying genetic subtypes of the virus. The present sequence is an
CC oligomer of the invention. (Updated on 29-AUG-2003 to standardise OS
CC field)
XX Sequence 53 BP; 17 A; 14 C; 9 G; 12 T; 0 U; 1 Other;
SQ
Query Match 66.3%; Score 35.8; DB 6; Length 53;
Best Local Similarity 94.9%; Pred. No. 0.00023;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GAAATTATACGACTCACTATAGGAGAGACCATTTGTC 39
Db 1 GAAATTATACGACTCACTATAGGAGAGACCATTTGTC 39
RESULT 33
AAL45498
ID AAL45498 standard; DNA; 53 BP.
XX
AC AAL45498;
XX 29-AUG-2003 (revised)
DT 06-JUN-2002 (first entry)
XX
DE HIV-1 gag amplification oligomer SEQ ID NO: 36.
XX
KW HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;
KW probe; ss.
XX Human immunodeficiency virus 1.
OS Enterobacteria phage T7.
XX
PN WO200220852-A1.
XX
PD 14-MAR-2002.
XX
PF 01-SEP-2000; 2000WO-US024117.
XX
PR 01-SEP-2000; 2000WO-US024117.
XX
PA (GENP-) GEN-PROBE INC.
PA (INMR) BIOMERIEUX SA.
XX
PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX WPI; 2002-292273/33.
XX
PT New nucleic acid oligomer, useful for detecting selected regions of gag
PT and pol genes of human immune deficiency virus, particularly for
PT assessing drug resistance.
XX Claim 1; Page 58; 82pp; English.
XX The present invention provides a number of nucleic acid oligomers which
CC can be used to amplify the gag and pol genes of human immunodeficiency

CC virus type I (HIV-1). These are used to detect regions of the gag and pol
CC genes, especially regions associated with drug resistance, and also for
CC identifying genetic subtypes of the virus. The present sequence is an
CC oligomer of the invention. (Updated on 29-AUG-2003 to standardise OS
CC field)
XX Sequence 53 BP; 17 A; 14 C; 9 G; 13 T; 0 U; 0 Other;
SQ
Query Match 66.3%; Score 35.8; DB 6; Length 53;
Best Local Similarity 94.9%; Pred. No. 0.00023;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GAAATTATACGACTCACTATAGGAGAGACCATTTGTC 39
Db 1 GAAATTATACGACTCACTATAGGAGAGACCATTTGTC 39
RESULT 34
AD118945
ID AD118945 standard; DNA; 53 BP.
XX
AC AD118945;
XX 22-APR-2004 (first entry)
DT
XX
DE HIV-1 gag2 gene amplifying primer #5.
XX
KW Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.
XX Human immunodeficiency virus 1.
OS
XX
PN US2003228574-A1.
XX
PD 11-DEC-2003.
XX
PF 28-APR-2003; 2003US-00425975.
XX
PR 01-SEP-2000; 2000US-0229790P.
PR 31-AUG-2001; 2001US-00944036.
XX
PA (YANG/) YANG Y Y.
PA (BREN/) BRENTANO S T.
PA (BABO/) BABOLA O.
PA (TRAN/) TRAN N.
PA (VERN/) VERNET G.
XX
PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX
DR WPI; 2004-060998/06.
XX
PT New nucleic acid oligomer for amplifying and detecting HIV-1 nucleotide
PT sequences and in providing information about the infective agent, e.g.
PT genetic subgroup or drug-resistance phenotype based on detectable
PT sequence information.
XX
PS Claim 1; SEQ ID NO 36; 39pp; English.
XX
CC The present invention relates to a nucleic acid oligomer for amplifying a
CC nucleotide sequence of human immune deficiency virus (HIV)-1. The
CC invention is useful in amplifying and detecting HIV-1 nucleic acid
CC sequences and in providing additional information about the infective
CC agent, such as its genetic subgroup or drug-resistance phenotype based on
CC detectable sequence information. The present sequence is HIV-1 gag2 gene
CC amplifying primer.
XX
SQ Sequence 53 BP; 17 A; 14 C; 9 G; 13 T; 0 U; 0 Other;
Query Match 66.3%; Score 35.8; DB 12; Length 53;
Best Local Similarity 94.9%; Pred. No. 0.00023;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GAAATTATACGACTCACTATAGGAGAGACCATTTGTC 39

PF 28-JAN-2000; 2000WO-US002270.
XX
PR 28-JAN-1999; 99US-0117640P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Harvey RC, Clark TJ;
XX
XX WPI; 2000-505986/45.
DR
XX
PT Detecting prostate-specific antigen (PSA), prostate specific membrane
PT antigen (PSMA) or human kallikrein 2 (hk2) nucleic acids in samples using
PT probe molecules, useful for the diagnosis of prostate and breast cancers.
XX
XX Claim 1; Page 14; 77pp; English.
XX
CC The present invention is concerned with the detection of nucleic acid
CC markers for prostate and breast cancer, and PCR primers and probes which
CC are able to detect and quantify these markers. Prostate specific antigen
CC (PSA), prostate-specific membrane antigen (PSMA) and glandular kallikrein
CC -2 (hk2) have all been linked to prostate and breast cancers, and the
CC primers and probes of the invention are able to detect the abnormal
CC presence of mRNA expressed by their coding sequences in tissues other
CC than the prostate. This enables the presence of cancer to be perceived
CC and aids in the detection of metastases
XX
SQ Sequence 54 BP; 17 A; 14 C; 8 G; 15 T; 0 U; 0 Other;
Query Match 65.6%; Score 35.4; DB 3; Length 54;
Best Local Similarity 79.2%; Pred. No. 0.00033;
Matches 42; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 2 AAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATCCCACTGC 54
|||||
Db 2 AAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATCCCACTGC 54
|||||
RESULT 38
ABK53110
ID ABK53110 standard; DNA; 55 BP.
XX
AC ABK53110;
XX
DT 29-AUG-2003 (revised)
DT 12-AUG-2002 (first entry)
XX
DE HIV-1 reverse transcriptase gene specific oligonucleotide primer #3.
XX
KW HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;
KW reverse transcriptase; infection; PCR.
XX
OS Human immunodeficiency virus 1.
XX
PN US2002055095-A1.
XX
PD 09-MAY-2002.
XX
PF 31-AUG-2001; 2001US-00944036.
XX
PR 01-SEP-2000; 2000US-0229790P.
XX
XX (YANG/) YANG Y Y.
PA (BREN/) BRENTANO S T.
PA (BABO/) BABOLA O.
PA (TRAN/) TRAN N.
PA (VERN/) VERNET G.
XX
PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX
DR WPI; 2002-462902/49.
XX
XX New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-
PT 1 and probes for detecting the amplified product are specific for gag and

PT pol regions and are useful to detect different subtypes of HIV-1.
XX
XX Claim 1; Page 15; 37pp; English.
XX
CC This invention relates to a series of nucleic acid oligomers for
CC amplifying and detecting a nucleotide sequence of human immunodeficiency
CC virus type 1 (HIV-1). The invention also comprises a labeled
CC oligonucleotide that specifically hybridises to an HIV-1 sequence derived
CC from gag or pol sequences, having one of the sequences fully defined in
CC the specification, and a method for detecting HIV-1 in a biological
CC sample, comprising mixing the sample with two or more of the
CC amplification oligomers that specifically amplify at least one HIV-1
CC target sequence within gag and a pol sequence which is a process or
CC reverse transcriptase sequence, amplifying the target, and detecting the
CC amplified product. The oligonucleotides of the invention may be used to
CC diagnose HIV-1 infection. The presents sequence represents a PCR primer
CC used to amplify the HIV-1 reverse transcriptase gene in the HIV detection
CC method of the invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 55 BP; 18 A; 15 C; 9 G; 13 T; 0 U; 0 Other;
Query Match 65.6%; Score 35.4; DB 6; Length 55;
Best Local Similarity 97.3%; Pred. No. 0.00033;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGGAGACCACTTGT 37
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTGT 37
|||||
RESULT 39
AAL45472
ID AAL45472 standard; DNA; 55 BP.
XX
AC AAL45472;
XX
DT 29-AUG-2003 (revised)
DT 06-JUN-2002 (first entry)
XX
DE HIV-1 pol gene RT amplification oligomer SEQ ID NO: 10.
XX
KW HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;
KW probe; ss.
XX
OS Human immunodeficiency virus 1.
OS Enterobacteria phage T7.
XX
PN WO200220852-A1.
XX
PD 14-MAR-2002.
XX
PF 01-SEP-2000; 2000WO-US024117.
XX
PR 01-SEP-2000; 2000WO-US024117.
XX
PA (GENP-) GEN-PROBE INC.
PA (INNMR) BIOMERIEUX SA.
XX
PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX
XX WPI; 2002-292273/33.
DR
XX
XX New nucleic acid oligomer, useful for detecting selected regions of gag
PT and pol genes of human immune deficiency virus, particularly for
PT assessing drug resistance.
XX
XX Claim 1; Page 40; 82pp; English.
XX
CC The present invention provides a number of nucleic acid oligomers which
CC can be used to amplify the gag and pol genes of human immunodeficiency
CC virus type 1 (HIV-1). These are used to detect regions of the gag and pol
CC genes, especially regions associated with drug resistance, and also for
CC identifying genetic subtypes of the virus. The present sequence is an

```

CC oligomer of the invention. (Updated on 29-AUG-2003 to standardise OS
CC field)
XX
SQ Sequence 55 BP; 18 A; 15 C; 9 G; 13 T; 0 U; 0 Other;

Query Match      65.6%; Score 35.4; DB 6; Length 55;
Best Local Similarity 97.3%; Pred. No. 0.00033;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTATACGACTCACTATAGGAGACCACTGT 37
   |||||
Db 1 GAAATTATACGACTCACTATAGGAGACCACTGT 37

RESULT 40
AD118919
ID AD118919 standard; DNA; 55 BP.
XX
AC AD118919;
XX
DT 22-APR-2004 (first entry)
XX
DE HIV-1 pol4 gene amplifying primer #1.
XX
KW Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.
XX
OS Human immunodeficiency virus 1.
XX
FN US2003228574-A1.
XX
PD 11-DEC-2003.
XX
PF 28-APR-2003; 2003US-00425975.
XX
PR 01-SEP-2000; 2000US-0229790P.
XX
PR 31-AUG-2001; 2001US-00944036.
XX
PA (YANG/) YANG Y Y.
PA (BREN/) BRENTANO S T.
PA (BABO/) BABOLA O.
PA (TRAN/) TRAN N.
PA (VERN/) VERNET G.
XX
PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX
WPI; 2004-060998/06.
XX
New nucleic acid oligomer for amplifying and detecting HIV-1 nucleotide
sequences and in providing information about the infective agent, e.g.
genetic subgroup or drug-resistance phenotype based on detectable
sequence information.
XX
Claim 1; SEQ ID NO 10; 39pp; English.
XX
The present invention relates to a nucleic acid oligomer for amplifying a
nucleotide sequence of human immune deficiency virus (HIV)-1. The
invention is useful in amplifying and detecting HIV-1 nucleic acid
sequences and in providing additional information about the infective
agent, such as its genetic subgroup or drug-resistance phenotype based on
detectable sequence information. The present sequence is HIV-1 pol4 gene
amplifying primer.
XX
Sequence 55 BP; 18 A; 15 C; 9 G; 13 T; 0 U; 0 Other;

Query Match      65.6%; Score 35.4; DB 12; Length 55;
Best Local Similarity 97.3%; Pred. No. 0.00033;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTATACGACTCACTATAGGAGACCACTGT 37
   |||||
Db 1 GAAATTATACGACTCACTATAGGAGACCACTGT 37

```

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RESULT 41
AAD11262
ID AAD11262 standard; DNA; 52 BP.
XX
AC AAD11262;
XX
DT 11-SEP-2003 (revised)
DT 24-SEP-2001 (first entry)
XX
XX Mycobacterium 16S rRNA amplifying T7 promoter-primer #6.
XX
XX Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
KW Mycobacterium other than tuberculosis; MOTT; PCR primer; T7 promoter; ss.
XX
XX Enterobacteria phage T7.
OS Mycobacterium sp.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT promoter 1..33
FT /*tag= a
FT /label= T7_promoter
XX
FN WO200144510-A2.
XX
PD 21-JUN-2001.
XX
PF 17-DEC-1999; 99WO-US030346.
XX
PR 17-DEC-1999; 99WO-US030346.
XX
PA (GENP-) GEN-PROBE INC.
PA (INMR ) BIOMERIEUX SA.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodriguez M;
XX
WPI; 2001-398170/42.
XX
Detecting Mycobacterium species, involves in vitro amplification of 16S
rRNA or DNA encoding RNA in nucleic acid amplification mixture using
specific primers, and detecting the amplified nucleic acid.
XX
Claim 1; Page 34; 44pp; English.
XX
The invention relates to a method of detecting Mycobacterium species,
that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
encoding 16S rRNA in an in vitro nucleic acid amplification mixture
comprising a polymerase, and at least two primers, and then detecting the
amplified nucleic acid. The method is relatively simple and useful for
detecting the presence of various Mycobacterium species in a biological
sample, and thus important for diagnosis of infections resulting from
them. The method is especially important for screening opportunistic
infections caused by M. tuberculosis or a Mycobacterium other than
tuberculosis (MOTT). The present sequence is a T7 promoter-primer used
for amplifying Mycobacterium 16S rRNA. (Updated on 11-SEP-2003 to
CC standardise OS field)
XX
SQ Sequence 52 BP; 17 A; 14 C; 11 G; 10 T; 0 U; 0 Other;

Query Match      64.8%; Score 35; DB 4; Length 52;
Best Local Similarity 80.4%; Pred. No. 0.00047;
Matches 41; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 GAAATTATACGACTCACTATAGGAGACCACTGTGCAATATATCCAC 51
   |||||
Db 1 GAAATTATACGACTCACTATAGGAGACCACTGTGCGGCC 51

RESULT 42
ABK53143
ID ABK53143 standard; DNA; 52 BP.
XX
AC ABK53143;

```

XX 29-AUG-2003 (revised)
 DT 12-AUG-2002 (first entry)
 DE HIV-1 reverse transcriptase gene specific oligonucleotide primer #14.
 DE HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;
 KW reverse transcriptase; infection; PCR.
 XX Human immunodeficiency virus 1.
 OS US2002055095-A1.
 PN 09-MAY-2002.
 XX 31-AUG-2001; 2001US-00944036.
 XX 01-SEP-2000; 2000US-0229790P.
 XX (YANG/) YANG Y Y.
 PA (BREN/) BRENTANO S T.
 PA (BABO/) BABOLA O.
 PA (TRAN/) TRAN N.
 PA (VERN/) VERNET G.
 XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
 WIPI; 2002-462902/49.
 XX New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-1 and probes for detecting the amplified product are specific for gag and pol regions and are useful to detect different subtypes of HIV-1.
 XX Claim 1; Page 26; 37pp; English.
 XX This invention relates to a series of nucleic acid oligomers for amplifying and detecting a nucleotide sequence of human immunodeficiency virus type 1 (HIV-1). The invention also comprises a labeled oligonucleotide that specifically hybridises to an HIV-1 sequence derived from gag or pol sequences, having one of the sequences fully defined in the specification, and a method for detecting HIV-1 in a biological sample, comprising mixing the sample with two or more of the amplification oligomers that specifically amplify at least one HIV-1 target sequence within gag and a pol sequence which is a protease or reverse transcriptase sequence, amplifying the target, and detecting the amplified product. The oligonucleotides of the invention may be used to diagnose HIV-1 infection. The presents sequence represents a PCR primer used to amplify the HIV-1 reverse transcriptase gene in the HIV detection method of the invention. (Updated on 29-AUG-2003 to standardise OS field)
 XX Sequence 52 BP; 16 A; 10 C; 8 G; 18 T; 0 U; 0 Other;
 Query Match 64.8%; Score 35; DB 6; Length 52;
 Best Local Similarity 100.0%; Pred. No. 0.00047;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAAATTATACGACTCACTATAGGAGACACATT 35
 DB 1 GAAATTATACGACTCACTATAGGAGACACATT 35
 RESULT 43
 AAL45505
 ID AAL45505 standard; DNA; 52 BP.
 XX AAL45505;
 XX 29-AUG-2003 (revised)
 DT 06-JUN-2002 (first entry)
 DE HIV-1 pol gene RT amplification oligomer SEQ ID NO: 43.
 KW HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;

KW probe; ss.
 XX Human immunodeficiency virus 1.
 OS Enterobacteria phage T7.
 XX WO200220852-A1.
 PN 14-MAR-2002.
 XX 01-SEP-2000; 2000WO-US024117.
 XX 01-SEP-2000; 2000WO-US024117.
 XX (GENP-) GEN-PROBE INC.
 PA (INNR) BIOMERIEUX SA.
 XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
 WIPI; 2002-292273/33.
 XX New nucleic acid oligomer, useful for detecting selected regions of gag and pol genes of human immune deficiency virus, particularly for assessing drug resistance.
 XX Claim 1; Page 61; 82pp; English.
 XX The present invention provides a number of nucleic acid oligomers which can be used to amplify the gag and pol genes of human immunodeficiency virus type 1 (HIV-1). These are used to detect regions of the gag and pol genes, especially regions associated with drug resistance, and also for identifying genetic subtypes of the virus. The present sequence is an oligomer of the invention. (Updated on 29-AUG-2003 to standardise OS field)
 XX Sequence 52 BP; 16 A; 10 C; 8 G; 18 T; 0 U; 0 Other;
 Query Match 64.8%; Score 35; DB 6; Length 52;
 Best Local Similarity 100.0%; Pred. No. 0.00047;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAAATTATACGACTCACTATAGGAGACACATT 35
 DB 1 GAAATTATACGACTCACTATAGGAGACACATT 35
 RESULT 44
 ADG88343
 ID ADG88343 standard; DNA; 52 BP.
 XX ADG88343;
 XX 11-MAR-2004 (first entry)
 XX Mycobacterium amplifying PCR primer #12.
 DE In vitro amplification; PCR; primer; ss.
 KW Mycobacterium sp.
 OS US2003165824-A1.
 PN 04-SEP-2003.
 XX 15-DEC-2000; 2000US-00738274.
 XX 17-DEC-1999; 99US-0172190P.
 XX (BREN/) BRENTANO S T.
 PA (JUCK/) JUCKER M T.
 PA (DELG/) DELGADO F D.
 PA (CLEU/) CLEUZIAT P.
 PA (RODR/) RODRIGUE M.
 XX

PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
 XX WPI; 2003-898044/82.
 XX
 XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
 PT in a biological sample comprises performing in vitro nucleic acid
 PT amplification and detection of amplified products.
 XX
 XX Claim 1; SEQ ID NO 12; 20pp; English.
 XX
 XX The present invention relates to a method of detecting Mycobacterium
 CC species present in a biological sample comprises performing an in vitro
 CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
 CC detecting the amplified Mycobacterium nucleic acid. The present sequence
 CC is Mycobacterium amplifying PCR primer.
 XX
 XX Sequence 52 BP; 17 A; 14 C; 11 G; 10 T; 0 U; 0 Other;
 SQ
 Query Match 64.8%; Score 35; DB 10; Length 52;
 Best Local Similarity 80.4%; Pred. No. 0.00047;
 Matches 41; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 Qy 1 GAAATTAATACGACTCACTATAGGAGACCATGTCGAATATTCGCCAC 51
 Db 1 GAAATTAATACGACTCACTATAGGAGACCATGTCGAATATTCGCCAC 51
 RESULT 45
 ADI18952
 ID ADI18952 standard; DNA; 52 BP.
 XX
 XX ADI18952;
 XX
 XX 22-APR-2004 (first entry)
 DT
 DE HIV-1 pol3 gene amplifying primer #5.
 XX
 XX Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.
 XX
 XX Human immunodeficiency virus 1.
 OS
 XX US2003228574-A1.
 PN
 XX 11-DEC-2003.
 PD
 XX 28-APR-2003; 2003US-00425975.
 PF
 XX 01-SEP-2000; 2000US-0229790P.
 PR
 XX 31-AUG-2001; 2001US-00944036.
 PR
 XX (YANG/) YANG Y Y.
 PA (BREN/) BRENTANO S T.
 PA (BABO/) BABOLA O.
 PA (TRAN/) TRAN N.
 PA (VERN/) VERNET G.
 XX
 XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
 PI WPI; 2004-060998/06.
 DR
 XX New nucleic acid oligomer for amplifying and detecting HIV-1 nucleotide
 XX sequences and in providing information about the infective agent, e.g.
 PT genetic subgroup or drug-resistance phenotype based on detectable
 PT sequence information.
 XX
 XX Claim 1; SEQ ID NO 43; 39pp; English.
 PS
 XX The present invention relates to a nucleic acid oligomer for amplifying a
 CC nucleotide sequence of human immune deficiency virus (HIV)-1. The
 CC invention is useful in amplifying and detecting HIV-1 nucleic acid
 CC sequences and in providing additional information about the infective
 CC agent, such as its genetic subgroup or drug-resistance phenotype based on
 CC detectable sequence information. The present sequence is HIV-1 pol3 gene

CC amplifying primer.
 XX
 XX Sequence 52 BP; 16 A; 10 C; 8 G; 18 T; 0 U; 0 Other;
 SQ
 Query Match 64.8%; Score 35; DB 12; Length 52;
 Best Local Similarity 100.0%; Pred. No. 0.00047;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GAAATTAATACGACTCACTATAGGAGACCATT 35
 Db 1 GAAATTAATACGACTCACTATAGGAGACCATT 35
 RESULT 46
 AEA08218
 ID AEA08218 standard; DNA; 52 BP.
 XX
 XX AEA08218;
 XX
 XX 14-JUL-2005 (first entry)
 DT
 XX M. tuberculosis 16S rRNA amplifying T7 promoter PCR primer, SEQ ID NO: 12.
 DE
 XX Microorganism detection; DNA amplification; 16s ribosomal RNA; 16s rRNA;
 KW PCR; primer; ss.
 KW
 XX Mycobacterium tuberculosis; ATCC 27294.
 OS
 OS Enterobacteria phage T7.
 XX
 XX US2005100915-A1.
 PN
 XX 12-MAY-2005.
 PD
 XX 18-SEP-2003; 2003US-00665708.
 PF
 XX 17-DEC-1999; 99US-0172190P.
 PR
 XX 15-DEC-2000; 2000US-00738274.
 PR
 XX (BREN/) BRENTANO S T.
 PA (JUCK/) JUCKER M T.
 PA (DELG/) DELGADO F D.
 PA (CLEU/) CLEUZIAZ P.
 PA (RODR/) RODRIGUE M.
 XX
 XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
 PI WPI; 2005-345392/35.
 DR
 XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
 PT in a biological sample, comprises using in vitro nucleic acid
 PT amplification and detection of amplified products.
 XX
 XX Example 1; SEQ ID NO 12; 21pp; English.
 PS
 XX The present invention relates to a method of detecting Mycobacterium
 CC species present in a biological sample. The method involves using in
 CC vitro nucleic acid amplification and detection of amplified products. The
 CC invention is useful for diagnostic detection of pathogenic bacteria such
 CC as Mycobacterium species. The present sequence is the Mycobacterium
 CC tuberculosis (ATCC 27294) 16S ribosomal RNA (16SrRNA) amplifying T7
 CC promoter PCR primer. This T7 promoter primer sequence include a T7
 CC promoter sequence attached to the portion of the primer sequence that
 CC binds to the target or its complement.
 XX
 XX Sequence 52 BP; 17 A; 14 C; 11 G; 10 T; 0 U; 0 Other;
 SQ
 Query Match 64.8%; Score 35; DB 14; Length 52;
 Best Local Similarity 80.4%; Pred. No. 0.00047;
 Matches 41; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 Qy 1 GAAATTAATACGACTCACTATAGGAGACCATGTCGAATATTCGCCAC 51
 Db 1 GAAATTAATACGACTCACTATAGGAGACCATGTCGAATATTCGCCAC 51

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RESULT 47
ABK53335
ID ABK53135 standard; DNA; 53 BP.
XX
AC ABK53135;
XX
XX 29-AUG-2003 (revised)
DT 12-AUG-2002 (first entry)
XX
DE HIV-1 Gag gene specific oligonucleotide primer #8.
XX
XX HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;
KW reverse transcriptase; infection; PCR.
XX
XX Human immunodeficiency virus 1.
OS
XX US2002055095-A1.
XX
XX 09-MAY-2002.
PD
XX 31-AUG-2001; 2001US-00944036.
PF
XX 01-SEP-2000; 2000US-0229790P.
PR
XX (YANG/) YANG Y Y.
PA (BREN/) BRENTANO S T.
PA (BARO/) BABOLA O.
PA (TRAN/) TRAN N.
PA (VERN/) VERNET G.
XX
XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
PI WPI; 2002-462902/49.
XX
XX New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-
PT 1 and probes for detecting the amplified product are specific for gag and
PT pol regions and are useful to detect different subtypes of HIV-1.
XX
XX Claim 1; Page 24; 37pp; English.
XX
XX This invention relates to a series of nucleic acid oligomers for
CC amplifying and detecting a nucleotide sequence of human immunodeficiency
CC virus type 1 (HIV-1). The invention also comprises a labeled
CC oligonucleotide that specifically hybridizes to an HIV-1 sequence derived
CC from gag or pol sequences, having one of the sequences fully defined in
CC the specification, and a method for detecting HIV-1 in a biological
CC sample, comprising mixing the sample with two or more of the
CC amplification oligomers that specifically amplify at least one HIV-1
CC target sequence within gag and a pol sequence which is a protease or
CC reverse transcriptase sequence, amplifying the target, and detecting the
CC amplified product. The oligonucleotides of the invention may be used to
CC diagnose HIV-1 infection. The presents sequence represents a PCR primer
CC used to amplify the HIV-1 Gag gene in the HIV detection method of the
CC invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
XX Sequence 53 BP; 17 A; 11 C; 12 G; 13 T; 0 U; 0 Other;
SQ
Query Match 64.4%; Score 34.8; DB 6; Length 53;
Best Local Similarity 84.8%; Pred. No. 0.00057;
Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 GAAATTATACCACTCACTATAGGAGACCACCATTTGCAATATTC 46
Db 1 GAAATTATACCACTCACTATAGGAGACCACCATTTGCTCCTTC 46
RESULT 48
AAL45497
ID AAL45497 standard; DNA; 53 BP.
XX
XX AAL45497;
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XX 29-AUG-2003 (revised)
DT 06-JUN-2002 (first entry)
XX
DE HIV-1 gag amplification oligomer SEQ ID NO: 35.
XX
XX HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;
KW probe; ss.
XX
XX Human immunodeficiency virus 1.
OS Enterobacteria phage T7.
XX
XX WO200220852-A1.
XX
XX 14-MAR-2002.
XX
XX 01-SEP-2000; 2000WO-US024117.
PF
XX 01-SEP-2000; 2000WO-US024117.
PR (GENP-) GEN-PROBE INC.
PA (INMR ) BIOMERIEUX SA.
XX
XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
PI WPI; 2002-292273/33.
XX
XX New nucleic acid oligomer, useful for detecting selected regions of gag
PT and pol genes of human immune deficiency virus, particularly for
PT assessing drug resistance.
XX
XX Claim 1; Page 58; 82pp; English.
XX
XX The present invention provides a number of nucleic acid oligomers which
CC can be used to amplify the gag and pol genes of human immunodeficiency
CC virus type 1 (HIV-1). These are used to detect regions of the gag and pol
CC genes, especially regions associated with drug resistance, and also for
CC identifying genetic subtypes of the virus. The present sequence is an
CC oligomer of the invention. (Updated on 29-AUG-2003 to standardise OS
CC field)
XX
XX Sequence 53 BP; 17 A; 11 C; 12 G; 13 T; 0 U; 0 Other;
SQ
Query Match 64.4%; Score 34.8; DB 6; Length 53;
Best Local Similarity 84.8%; Pred. No. 0.00057;
Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 GAAATTATACCACTCACTATAGGAGACCACCATTTGCAATATTC 46
Db 1 GAAATTATACCACTCACTATAGGAGACCACCATTTGCTCCTTC 46
RESULT 49
AD118944
ID AD118944 standard; DNA; 53 BP.
XX
XX AD118944;
XX
XX 22-APR-2004 (first entry)
DT
XX HIV-I gag1 gene amplifying primer #5.
DE
XX Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.
KW
XX Human immunodeficiency virus 1.
OS
XX US2003228574-A1.
XX
XX 11-DEC-2003.
PD
XX 28-APR-2003; 2003US-00425975.
PF
XX 01-SEP-2000; 2000US-0229790P.
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PR 31-AUG-2001; 2001US-00944036.
XX (YANG/) YANG Y Y.
PA (BREN/) BRENTANO S T.
PA (BABO/) BABOLA O.
PA (TRAN/) TRAN N.
PA (VERN/) VERNET G.
XX
PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX WPI; 2004-060998/06.
XX
XX New nucleic acid oligomer for amplifying and detecting HIV-1 nucleotide
PT sequences and in providing information about the infective agent, e.g.
PT genetic subgroup or drug-resistance phenotype based on detectable
PT sequence information.
XX
XX Claim 1; SEQ ID NO 35; 39pp; English.
XX
XX The present invention relates to a nucleic acid oligomer for amplifying a
CC nucleotide sequence of human immune deficiency virus (HIV)-1. The
CC invention is useful in amplifying and detecting HIV-1 nucleic acid
CC sequences and in providing additional information about the infective
CC agent, such as its genetic subgroup or drug-resistance phenotype based on
CC detectable sequence information. The present sequence is HIV-1 gag1 gene
CC amplifying primer.
XX
XX Sequence 53 BP; 17 A; 11 C; 12 G; 13 T; 0 U; 0 Other;
SQ
Query Match 64.4%; Score 34.8; DB 12; Length 53;
Best Local Similarity 84.8%; Pred. No. 0.00057;
Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTGTCGAATATTC 46
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTGTCGAATATTC 46
RESULT 50
ABKS3133
ID ABK53133 standard; DNA; 54 BP.
XX
XX ABK53133;
XX
XX 29-AUG-2003 (revised)
DT 12-AUG-2002 (first entry)
XX
XX HIV-1 Gag gene specific oligonucleotide primer #6.
XX
XX HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;
KW reverse transcriptase; infection; PCR.
XX
XX Human immunodeficiency virus 1.
XX
XX US200205095-A1.
XX
XX 09-MAY-2002.
XX
XX 31-AUG-2001; 2001US-00944036.
XX
XX 01-SEP-2000; 2000US-0229790P.
XX
XX (YANG/) YANG Y Y.
PA (BREN/) BRENTANO S T.
PA (BABO/) BABOLA O.
PA (TRAN/) TRAN N.
PA (VERN/) VERNET G.
XX
XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX WPI; 2002-462902/49.
XX
XX New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-
PR
31-AUG-2001; 2001US-00944036.
XX (YANG/) YANG Y Y.
PA (BREN/) BRENTANO S T.
PA (BABO/) BABOLA O.
PA (TRAN/) TRAN N.
PA (VERN/) VERNET G.
XX
PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX WPI; 2002-462902/49.
XX
XX New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-

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PT 1 and probes for detecting the amplified product are specific for gag and
PT pol regions and are useful to detect different subtypes of HIV-1.
XX
XX Claim 1; Page 24; 37pp; English.
XX
XX This invention relates to a series of nucleic acid oligomers for
CC amplifying and detecting a nucleotide sequence of human immunodeficiency
CC virus type 1 (HIV-1). The invention also comprises a labeled
CC oligonucleotide that specifically hybridizes to an HIV-1 sequence derived
CC from gag or pol sequences, having one of the sequences fully defined in
CC the specification, and a method for detecting HIV-1 in a biological
CC sample, comprising mixing the sample with two or more of the
CC amplification oligomers that specifically amplify at least one HIV-1
CC target sequence within gag and a pol sequence which is a protease or
CC reverse transcriptase sequence, amplifying the target, and detecting the
CC amplified product. The oligonucleotides of the invention may be used to
CC diagnose HIV-1 infection. The presents sequence represents a PCR primer
CC used to amplify the HIV-1 Gag gene in the HIV detection method of the
CC invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
XX Sequence 54 BP; 17 A; 12 C; 11 G; 14 T; 0 U; 0 Other;
SQ
Query Match 63.7%; Score 34.4; DB 6; Length 54;
Best Local Similarity 97.2%; Pred. No. 0.00083;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTG 36
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTG 36
RESULT 51
AAL45495
ID AAL45495 standard; DNA; 54 BP.
XX
XX AAL45495;
XX
XX 29-AUG-2003 (revised)
DT 06-JUN-2002 (first entry)
XX
XX HIV-1 gag amplification oligomer SEQ ID NO: 33.
XX
XX HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;
KW probe; ss.
XX
XX Human immunodeficiency virus 1.
OS Enterobacteria phage T7.
XX
XX WO200220852-A1.
XX
XX 14-MAR-2002.
XX
XX 01-SEP-2000; 2000WO-US024117.
XX
XX 01-SEP-2000; 2000WO-US024117.
PA (GENP-) GEN-PROBE INC.
PA (INWR ) BIOMERIEUX SA.
XX
XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX WPI; 2002-292273/33.
XX
XX New nucleic acid oligomer, useful for detecting selected regions of gag
PT and pol genes of human immune deficiency virus, particularly for
PT assessing drug resistance.
XX
XX Claim 1; Page 57; 82pp; English.
XX
XX The present invention provides a number of nucleic acid oligomers which
CC can be used to amplify the gag and pol genes of human immunodeficiency
CC virus type 1 (HIV-1). These are used to detect regions of the gag and pol
CC genes, especially regions associated with drug resistance, and also for

```

CC identifying genetic subtypes of the virus. The present sequence is an
CC oligomer of the invention. (Updated on 29-AUG-2003 to standardise OS
CC field)

XX SQ Sequence 54 BP; 17 A; 12 C; 11 G; 14 T; 0 U; 0 Other;
Query Match 63.7%; Score 34.4; DB 6; Length 54;
Best Local Similarity 97.2%; Pred. No. 0.00083;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GAAATTAATACGACTCACTATAGGAGACACCATTTG 36
Db 1 GAAATTAATACGACTCACTATAGGAGACACCATTTG 36

RESULT 52
AD118942
ID AD118942 standard; DNA; 54 BP.
XX AC
XX AD118942;
XX 22-APR-2004 (first entry)
XX HIV-I gagl gene amplifying primer #4.
DE Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.
XX KW
XX OS
XX Human immunodeficiency virus 1.
XX PN
XX US2003228574-A1.
XX 11-DEC-2003.
XX 28-APR-2003; 2003US-00425975..
XX 01-SEP-2000; 2000US-0229790P.
XX 31-AUG-2001; 2001US-00944036.
XX (YANG//) YANG Y Y.
XX (BREN//) BRENTANO S T.
XX (BABO//) BABOLA O.
XX (TRAN//) TRAN N.
XX (VERN//) VERNET G.
XX Yang YV, Brentano ST, Babola O, Tran N, Vernet G;
XX WPI; 2004-060998/06.

XX New nucleic acid oligomer for amplifying and detecting HIV-1 nucleotide
XX sequences and in providing information about the infective agent, e.g.
XX genetic subgroup or drug-resistance phenotype based on detectable
XX sequence information.

PS Claim 1; SEQ ID NO 33; 39pp; English.

XX The present invention relates to a nucleic acid oligomer for amplifying a
XX nucleotide sequence of human immune deficiency virus (HIV)-1. The
XX invention is useful in amplifying and detecting HIV-1 nucleic acid
XX sequences and in providing additional information about the infective
XX agent, such as its genetic subgroup or drug-resistance phenotype based on
XX detectable sequence information. The present sequence is HIV-I gagl gene
XX amplifying primer.

XX SQ Sequence 54 BP; 17 A; 12 C; 11 G; 14 T; 0 U; 0 Other;

Query Match 63.7%; Score 34.4; DB 12; Length 54;
Best Local Similarity 97.2%; Pred. No. 0.00083;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GAAATTAATACGACTCACTATAGGAGACACCATTTG 36
Db 1 GAAATTAATACGACTCACTATAGGAGACACCATTTG 36

RESULT 53
AAD51759
ID AAD51759 standard; DNA; 62 BP.

XX AC
XX AAD51759;
XX 16-APR-2003 (first entry)

XX Yeast intergenic region (YIR) 8 amplifying forward PCR primer #2.
DE Yeast intergenic region; YIR; gene expression analysis; yeast; PCR;
XX KW
XX primer; ss.
XX OS
XX Saccharomyces cerevisiae.

XX WO200290516-A2.

XX 14-NOV-2002.

XX 07-MAY-2002; 2002WO-US014575.

XX 07-MAY-2001; 2001US-0289202P.

XX 15-AUG-2001; 2001US-0312420P.

XX (AMSH) AMERSHAM BIOSCIENCES CORP.

XX Samartzidou H, Turner L, Daniel S, Houts T;

XX WPI; 2003-120541/11.

XX Producing at least one control useful as negative controls or calibrators
XX in a gene expression analysis system, comprises selecting inter- or
XX intragenic region of genomic DNA from a known sequence to be amplified
XX and cloned into a vector.

XX Disclosure; Page 15; 47pp; English.

XX The invention relates to a method for producing at least one control
XX useful as negative controls or calibrators in a gene expression analysis
XX system, which involves selecting inter- or intragenic region of genomic
XX DNA from a known sequence to be amplified and cloned into a vector. The
XX method is useful for producing controls useful in gene expression
XX analysis systems and which can be tested to ensure lack of hybridisation
XX with mRNA from sources other than the control DNA itself. The controls
XX are useful as negative controls or calibrators in a gene expression
XX analysis system or in a two-colour gene expression analysis system. The
XX present sequence is a PCR primer used for amplifying yeast intergenic
XX region (YIR). This sequence is used to illustrate the method of the
XX invention

XX SQ Sequence 62 BP; 23 A; 13 C; 14 G; 12 T; 0 U; 0 Other;

Query Match 63.7%; Score 34.4; DB 8; Length 62;
Best Local Similarity 97.2%; Pred. No. 0.00086;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GAAATTAATACGACTCACTATAGGAGACACCATTTG 36
Db 15 GAAATTAATACGACTCACTATAGGAGACACCATTTG 50

RESULT 54

ABK53138
ID ABK53138 standard; DNA; 53 BP.

XX AC
XX ABK53138;
XX 29-AUG-2003 (revised)

XX 12-AUG-2002 (first entry)

XX HIV-1 protease gene specific oligonucleotide primer #5.
XX DE
XX

KW HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;
 KW reverse transcriptase; infection; PCR.
 OS Human immunodeficiency virus 1.
 XX US2002055095-A1.
 XX 09-MAY-2002.
 XX 31-AUG-2001; 2001US-00944036.
 XX 01-SEP-2000; 2000US-0229790P.
 XX (YANG/) YANG Y Y.
 PA (BREN/) BRENTANO S T.
 PA (BABO/) BABOLA O.
 PA (TRAN/) TRAN N.
 PA (VERN/) VERNET G.
 XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
 WPI; 2002-462902/49.
 XX New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-
 PT 1 and probes for detecting the amplified product are specific for gag and
 PT pol regions and are useful to detect different subtypes of HIV-1.
 XX Claim 1; Page 25; 37pp; English.
 PS This invention relates to a series of nucleic acid oligomers for
 CC amplifying and detecting a nucleotide sequence of human immunodeficiency
 CC virus type 1 (HIV-1). The invention also comprises a labeled
 CC oligonucleotide that specifically hybridises to an HIV-1 sequence derived
 CC from gag or pol sequences, having one of the sequences fully defined in
 CC the specification, and a method for detecting HIV-1 in a biological
 CC sample, comprising mixing the sample with two or more of the
 CC amplification oligomers that specifically amplify at least one HIV-1
 CC target sequence within gag and a pol sequence which is a protease or
 CC reverse transcriptase sequence, amplifying the target, and detecting the
 CC amplified product. The oligonucleotides of the invention may be used to
 CC diagnose HIV-1 infection. The presents sequence represents a PCR primer
 CC used to amplify the HIV-1 protease gene in the HIV detection method of
 CC the invention. (Updated on 29-AUG-2003 to standardise OS field)
 XX Sequence 53 BP; 18 A; 14 C; 8 G; 13 T; 0 U; 0 Other;
 SQ Query Match 63.0%; Score 34; DB 6; Length 53;
 Best Local Similarity 88.1%; Pred. No. 0.0012;
 Matches 37; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 GAAATTAAATACGACTACTATAGGAGACCACTTGTCAT 42
 |||||
 Db 1 GAAATTAAATACGACTACTATAGGAGACCACTTGTCAT 42
 |||||
 RESULT 55
 AAL45500
 ID AAL45500 standard; DNA; 53 BP.
 XX AAL45500;
 AC AAL45500;
 XX 29-AUG-2003 (revised)
 DT 06-JUN-2002 (first entry)
 XX HIV-1 pol gene protease amplification oligomer SEQ ID NO: 38.
 DE HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;
 XX probe; ss.
 KW Human immunodeficiency virus 1.
 XX Enterobacteria phage T7.
 OS WO200220852-A1.
 XX

XX 14-MAR-2002.
 PD 01-SEP-2000; 2000WO-US024117.
 XX 01-SEP-2000; 2000WO-US024117.
 PR (GENP-) GEN-PROBE INC.
 XX (INMR) BIOMERIEUX SA.
 PA Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
 WPI; 2002-292273/33.
 DR New nucleic acid oligomer, useful for detecting selected regions of gag
 XX and pol genes of human immune deficiency virus, particularly for
 PT assessing drug resistance.
 PT Claim 1; Page 59; 82pp; English.
 PS The present invention provides a number of nucleic acid oligomers which
 CC can be used to amplify the gag and pol genes of human immunodeficiency
 CC virus type 1 (HIV-1). These are used to detect regions of the gag and pol
 CC genes, especially regions associated with drug resistance, and also for
 CC identifying genetic subtypes of the virus. The present sequence is an
 CC oligomer of the invention. (Updated on 29-AUG-2003 to standardise OS
 CC field)
 XX Sequence 53 BP; 18 A; 14 C; 8 G; 13 T; 0 U; 0 Other;
 SQ Query Match 63.0%; Score 34; DB 6; Length 53;
 Best Local Similarity 88.1%; Pred. No. 0.0012;
 Matches 37; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 GAAATTAAATACGACTACTATAGGAGACCACTTGTCAT 42
 |||||
 Db 1 GAAATTAAATACGACTACTATAGGAGACCACTTGTCAT 42
 |||||
 RESULT 56
 ADI18947
 ID ADI18947 standard; DNA; 53 BP.
 XX ADI18947;
 AC ADI18947;
 XX 22-APR-2004 (first entry)
 DT HIV-I pol gene amplifying primer #5.
 DE Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.
 XX Human immunodeficiency virus 1.
 OS US2003228574-A1.
 XX 11-DEC-2003.
 PD 28-APR-2003; 2003US-00425975.
 XX 01-SEP-2000; 2000US-0229790P.
 PR 31-AUG-2001; 2001US-00944036.
 XX (YANG/) YANG Y Y.
 PA (BREN/) BRENTANO S T.
 PA (BABO/) BABOLA O.
 PA (TRAN/) TRAN N.
 PA (VERN/) VERNET G.
 XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
 WPI; 2004-060998/06.
 DR New nucleic acid oligomer for amplifying and detecting HIV-1 nucleotide
 XX

PT sequences and in providing information about the infective agent, e.g.
PT genetic subgroup or drug-resistance phenotype based on detectable
PT sequence information.
PS Claim 1; SEQ ID NO 38; 39pp; English.
XX
XX The present invention relates to a nucleic acid oligomer for amplifying a
CC nucleotide sequence of human immune deficiency virus (HIV)-1. The
CC invention is useful in amplifying and detecting HIV-1 nucleic acid
CC sequences and in providing additional information about the infective
CC agent, such as its genetic subgroup or drug-resistance phenotype based on
CC detectable sequence information. The present sequence is HIV-1 pol gene
CC amplifying primer.
XX
XX Sequence 53 BP; 18 A; 14 C; 8 G; 13 T; 0 U; 0 Other;
SQ
Query Match 63.0%; Score 34; DB 12; Length 53;
Best Local Similarity 88.1%; Pred. No. 0.0012;
Matches 37; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGGAGACCACTTGCAAT 42
DB 1 GAAATTAATACGACTCACTATAGGAGACCACTTCATT 42
RESULT 57
AAAA76065
ID AAA76065 standard; DNA; 54 BP.
XX
AC AAA76065;
XX
DT 25-JAN-2001 (first entry)
XX
DE Human prostate specific antigen PCR primer SEQ ID NO: 27.
XX
XX Prostate specific antigen; PSA; prostate-specific membrane antigen; PSMA;
KW glandular kallikrein-2; hK2; prostate cancer; breast cancer; probe;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
XX WO200044940-A2.
PN
XX
PD 03-AUG-2000.
XX
PF 28-JAN-2000; 2000WO-US002270.
XX
PR 28-JAN-1999; 99US-0117640P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Harvey RC, Clark TJ;
XX
XX WPI; 2000-505986/45.
DR
XX
XX Detecting prostate-specific antigen (PSA), prostate specific membrane
PT antigen (PSMA) or human kallikrein 2 (hK2) nucleic acids in samples using
PT probe molecules, useful for the diagnosis of prostate and breast cancers.
XX
PS Claim 1; Page 12; 77pp; English.
XX
XX The present invention is concerned with the detection of nucleic acid
CC markers for prostate and breast cancer, and PCR primers and probes which
CC are able to detect and quantify these markers. Prostate specific antigen
CC (PSA), prostate-specific membrane antigen (PSMA) and glandular kallikrein
CC -2 (hK2) have all been linked to prostate and breast cancers, and the
CC primers and probes of the invention are able to detect the abnormal
CC presence of mRNA expressed by their coding sequences in tissues other
CC than the prostate. This enables the presence of cancer to be perceived
CC and aids in the detection of metastases
XX
XX Sequence 54 BP; 19 A; 12 C; 13 G; 10 T; 0 U; 0 Other;
SQ

Query Match 63.0%; Score 34; DB 3; Length 54;
Best Local Similarity 80.0%; Pred. No. 0.0012;
Matches 40; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 2 AAATTAATACGACTCACTATAGGAGACCACTTGCAATATTCACAC 51
DB 2 AAATTAATACGACTCACTATAGGAGACCACTTGCAATATTCACAC 51
RESULT 58
ABKS3145
ID ABKS3145 standard; DNA; 55 BP.
XX
AC ABKS3145;
XX
DT 29-AUG-2003 (revised)
DT 12-AUG-2002 (first entry)
XX
DE HIV-1 reverse transcriptase gene specific oligonucleotide primer #16.
XX
KW HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;
KW reverse transcriptase; infection; PCR.
XX
OS Human immunodeficiency virus 1.
XX
XX US200205095-A1.
PN
XX
PD 09-MAY-2002.
XX
PF 31-AUG-2001; 2001US-00944036.
XX
PR 01-SEP-2000; 2000US-0229790P.
XX
PA (YANG/) YANG Y Y.
PA (BREN/) BRENTANO S T.
PA (BABO/) BABOLA O.
PA (TRAN/) TRAN N.
PA (VERN/) VERNET G.
XX
PI Yang YV, Brentano ST, Babola O, Tran N, Vernet G;
XX
XX WPI; 2002-462902/49.
DR
XX
XX New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-
PT 1 and probes for detecting the amplified product are specific for gag and
PT pol regions and are useful to detect different subtypes of HIV-1.
XX
PS Claim 1; Page 26; 37pp; English.
XX
XX This invention relates to a series of nucleic acid oligomers for
CC amplifying and detecting a nucleotide sequence of human immunodeficiency
CC virus type 1 (HIV-1). The invention also comprises a labeled
CC oligonucleotide that specifically hybridizes to an HIV-1 sequence derived
CC from gag or pol sequences, having one of the sequences fully defined in
CC the specification, and a method for detecting HIV-1 in a biological
CC sample, comprising mixing the sample with two or more of the
CC amplification oligomers that specifically amplify at least one HIV-1
CC target sequence within gag and a pol sequence which is a protease or
CC reverse transcriptase sequence, amplifying the target, and detecting the
CC amplified product. The oligonucleotides of the invention may be used to
CC diagnose HIV-1 infection. The presents sequence represents a PCR primer
CC used to amplify the HIV-1 reverse transcriptase gene in the HIV detection
CC method of the invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 55 BP; 17 A; 16 C; 9 G; 13 T; 0 U; 0 Other;
Query Match 63.0%; Score 34; DB 6; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGGAGACCACTAT 34
DB 1 GAAATTAATACGACTCACTATAGGAGACCACTAT 34

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RESULT 59
AAL45507
ID AAL45507 standard; DNA; 55 BP.
XX
AC AAL45507;
XX
XX 29-AUG-2003 (revised)
DT 06-JUN-2002 (first entry)
XX
XX HIV-1 pol gene RT amplification oligomer SEQ ID NO: 45.
XX
XX HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;
KW probe; ss.
XX
XX Human immunodeficiency virus 1.
OS Enterobacteria phage T7.
XX
XX WO200220852-A1.
XX
PD 14-MAR-2002.
XX
XX 01-SEP-2000; 2000WO-US024117.
XX
XX 01-SEP-2000; 2000WO-US024117.
XX
PA (GENP-) GEN-PROBE INC.
PA (INNR) BIOMERIEUX SA.
XX
PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX WPI; 2002-292273/33.
XX
XX New nucleic acid oligomer, useful for detecting selected regions of gag
PT and pol genes of human immune deficiency virus, particularly for
PT assessing drug resistance.
XX
XX Claim 1; Page 62; 82pp; English.
XX
XX The present invention provides a number of nucleic acid oligomers which
CC can be used to amplify the gag and pol genes of human immunodeficiency
CC virus type 1 (HIV-1). These are used to detect regions of the gag and pol
CC genes, especially regions associated with drug resistance, and also for
CC identifying genetic subtypes of the virus. The present sequence is an
CC oligomer of the invention. (Updated on 29-AUG-2003 to standardise OS
CC field)
XX
XX Sequence 55 BP; 17 A; 16 C; 9 G; 13 T; 0 U; 0 Other;
SQ
Query Match 63.0%; Score 34; DB 6; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GAAATTATACGACTCACTATAGGAGACCAT 34
QY |||||||
DB 1 GAAATTATACGACTCACTATAGGAGACCAT 34
|||||||

RESULT 60
ADI18954
ID ADI18954 standard; DNA; 55 BP.
XX
XX ADI18954;
XX
XX 22-APR-2004 (first entry)
DT
DE HIV-I pol4 gene amplifying primer #5.
XX
XX Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.
KW Human immunodeficiency virus 1.
XX
XX

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PN US2003228574-A1.
XX
XX 11-DEC-2003.
XX
XX 28-APR-2003; 2003US-00425975.
XX
XX 01-SEP-2000; 2000US-0229790P.
PR 31-AUG-2001; 2001US-00944036.
XX
XX (YANG/) YANG Y Y.
PA (BREN/) BRENTANO S T.
PA (BABO/) BABOLA O.
PA (TRAN/) TRAN N.
PA (VERN/) VERNET G.
XX
XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
PI WPI; 2004-060998/06.
XX
XX New nucleic acid oligomer for amplifying and detecting HIV-1 nucleotide
PT sequences and in providing information about the infective agent, e.g.
PT genetic subgroup or drug-resistance phenotype based on detectable
PT sequence information.
XX
XX Claim 1; SEQ ID NO 45; 39pp; English.
XX
XX The present invention relates to a nucleic acid oligomer for amplifying a
CC nucleotide sequence of human immune deficiency virus (HIV)-1. The
CC invention is useful in amplifying and detecting HIV-1 nucleic acid
CC sequences and in providing additional information about the infective
CC agent, such as its genetic subgroup or drug-resistance phenotype based on
CC detectable sequence information. The present sequence is HIV-1 pol4 gene
CC amplifying primer.
XX
XX Sequence 55 BP; 17 A; 16 C; 9 G; 13 T; 0 U; 0 Other;
SQ
Query Match 63.0%; Score 34; DB 12; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GAAATTATACGACTCACTATAGGAGACCAT 34
QY |||||||
DB 1 GAAATTATACGACTCACTATAGGAGACCAT 34
|||||||

RESULT 61
AAD11022/c
ID AAD11022 standard; DNA; 61 BP.
XX
XX AAD11022;
XX
XX 24-SEP-2001 (first entry)
DT
DE Probe #2 to detect amplified MAC 16S rRNA or DNA encoding 16S rRNA.
XX
XX Mycobacterium avium complex; MAC; 16S ribosomal RNA; pathogenic bacteria;
KW in vitro amplification; MAC infection; probe; ss.
XX
XX Mycobacterium sp.
OS
XX WO200144511-A2.
XX
XX 21-JUN-2001.
PD
XX 15-DEC-2000; 2000WO-US033872.
XX
XX 15-DEC-1999; 99US-0171202P.
XX
XX (GENP-) GEN-PROBE INC.
PA (BREN/) BRENTANO S T.
PA (LANK/) LANKFORD R L.
XX
XX Brentano ST, Lankford RL;
PI

```

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XX WPI; 2001-398171/42.
XX
XX Detecting Mycobacterium avium complex organisms, comprises using in vitro
PT nucleic acid amplification with amplification oligonucleotides specific
PT for 16S ribosomal RNA or DNA encoding 16S rRNA from the bacterial
PT species.
XX
XX Claim 11; Page 26; 27pp; English.
XX
XX The present invention relates to a method for detecting Mycobacterium
CC avium complex (MAC) organisms (eg. M. avium, M. intracellulare, M.
CC tuberculosis, M. paratuberculosis) present in a biological sample. The
CC method comprises amplifying a 16S ribosomal RNA (rRNA) or DNA encoding
CC 16S rRNA obtained from a biological sample containing nucleic acid from a
CC MAC species in an in vitro nucleic acid amplification mixture comprising
CC a polymerase activity and a pair of primers to produce an amplified
CC nucleic acid and detecting amplified nucleic acid. The method is useful
CC for in vitro diagnostic detection of pathogenic bacteria, particularly
CC detecting infections caused by MAC organisms, distinguished from other
CC closely-related Mycobacterium species. The present sequence is a probe
CC used to detect amplified MAC 16S rRNA sequence or DNA encoding 16S rRNA
XX
XX Sequence 61 BP; 13 A; 15 C; 16 G; 17 T; 0 U; 0 Other;
SQ
Query Match 63.0%; Score 34; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGGAGACCAT 34
DB 61 GAAATTAATACGACTCACTATAGGAGACCAT 28
RESULT 62
AADI1012
ID AADI1012 standard; DNA; 61 BP.
XX
XX AADI1012;
XX
XX 11-SEP-2003 (revised)
DT 24-SEP-2001 (first entry)
XX
XX Promoter-primer #2 used for in vitro amplification of MAC rRNA.
XX
XX Mycobacterium avium complex; MAC; 16S ribosomal RNA; pathogenic bacteria;
KW in vitro amplification; MAC infection; promoter-primer; ss.
XX
XX Enterobacteria phage T7.
OS Mycobacterium sp.
OS Chimeric.
XX
XX Key Location/Qualifiers
FH promoter 1..33
FT /*tag= a
FT /note= "T7 promoter"
FT misc_feature 34..61
FT /*tag= b
FT /note= "PCR primer from Mycobacterium sp."
XX
XX WO200144511-A2.
XX
XX 21-JUN-2001.
XX
XX 15-DEC-2000; 2000WO-US033872.
XX
XX 15-DEC-1999; 99US-0171202P.
XX
XX (GENP-) GEN-PROBE INC.
PA (BREN/) BRENTANO S T.
PA (LANK/) LANKFORD R L.
XX
XX Brentano ST, Lankford RL;
PI

```

```

XX WPI; 2001-398171/42.
XX
XX Detecting Mycobacterium avium complex organisms, comprises using in vitro
PT nucleic acid amplification with amplification oligonucleotides specific
PT for 16S ribosomal RNA or DNA encoding 16S rRNA from the bacterial
PT species.
XX
XX Claim 1; Page 14; 27pp; English.
XX
XX The present invention relates to a method for detecting Mycobacterium
CC avium complex (MAC) organisms (eg. M. avium, M. intracellulare, M.
CC tuberculosis, M. paratuberculosis) present in a biological sample. The
CC method comprises amplifying a 16S ribosomal RNA (rRNA) or DNA encoding
CC 16S rRNA obtained from a biological sample containing nucleic acid from a
CC MAC species in an in vitro nucleic acid amplification mixture comprising
CC a polymerase activity and a pair of primers to produce an amplified
CC nucleic acid and detecting amplified nucleic acid. The method is useful
CC for in vitro diagnostic detection of pathogenic bacteria, particularly
CC detecting infections caused by MAC organisms, distinguished from other
CC closely-related Mycobacterium species. The present sequence is a promoter
CC primer from Bacteriophage T7 and Mycobacterium sp. Promoter-primer is
CC used for in vitro amplification of MAC rRNA. (Updated on 11-SEP-2003 to
XX standardise OS field)
XX
XX Sequence 61 BP; 17 A; 16 C; 15 G; 13 T; 0 U; 0 Other;
SQ
Query Match 63.0%; Score 34; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGGAGACCAT 34
DB 1 GAAATTAATACGACTCACTATAGGAGACCAT 34
RESULT 63
AAA76204
ID AAA76204 standard; DNA; 52 BP.
XX
XX AAA76204;
XX
XX 25-JAN-2001 (first entry)
DT
XX
XX Human prostate specific antigen PCR primer SEQ ID NO: 33.
XX
XX Prostate specific antigen; PSA; prostate-specific membrane antigen; PSMA;
KW glandular kallikrein-2; HK2; prostate cancer; breast cancer; probe;
KW PCR primer; ss.
XX
XX Homo sapiens.
OS
XX WO200044940-A2.
XX
XX 03-AUG-2000.
XX
XX 28-JAN-2000; 2000WO-US002270.
XX
XX 28-JAN-1999; 99US-0117640P.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Harvey RC, Clark TJ;
PI
XX
XX WPI; 2000-505986/45.
XX
XX Detecting prostate-specific antigen (PSA), prostate specific membrane
PT antigen (PSMA) or human kallikrein 2 (HK2) nucleic acids in samples using
PT probe molecules, useful for the diagnosis of prostate and breast cancers.
XX
XX Claim 1; Page 13; 77pp; English.
XX
XX The present invention is concerned with the detection of nucleic acid
CC

```

CC markers for prostate and breast cancer, and PCR primers and probes which
 CC are able to detect and quantify these markers. Prostate specific antigen
 CC (PSA), prostate-specific membrane antigen (PSMA) and glandular kallikrein
 CC -2 (hk2) have all been linked to prostate and breast cancers, and the
 CC primers and probes of the invention are able to detect the abnormal
 CC presence of mRNA expressed by their coding sequences in tissues other
 CC than the prostate. This enables the presence of cancer to be perceived
 CC and aids in the detection of metastases

XX SQ Sequence 52 BP; 16 A; 11 C; 12 G; 13 T; 0 U; 0 Other;

Query Match 62.6%; Score 33.8; DB 3; Length 52;

Best Local Similarity 94.6%; Pred. No. 0.0014;
 Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAATTAATACGACTCACTATAGGGAGACCATTTGTG 38
 |||||
 Db 2 AAATTAATACGACTCACTATAGGGAGACCATTTGTG 38
 |||||

RESULT 64

ABK93895
 ID ABK93895 standard; DNA; 58 BP.

XX AC ABK93895;

XX DT 29-AUG-2003 (revised)

XX DT 26-AUG-2002 (first entry)

XX DE Human immunodeficiency virus type 2 detection probe #19.

XX KW Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B virus; HBV;
 XX KW hepatitis C virus; HCV; probe; ss.

XX OS Human immunodeficiency virus 2.

XX PN WO200234951-A2.

XX PD 02-MAY-2002.

XX PF 22-OCT-2001; 2001WO-US045396.

XX PR 23-OCT-2000; 2000US-0242620P.

XX PR 30-MAR-2001; 2001US-0280058P.

XX FA (GENP-) GEN-PROBE INC.

XX FI Yang YX, Burrell TA;

XX DR WPI; 2002-489953/52.

XX PT Detecting human immunodeficiency virus-2 nucleic acids in a sample, by
 PT amplifying nucleic acids with oligonucleotides and detecting nucleic
 PT acid, or hybridizing nucleic acid with a probe and detecting probe:target
 PT duplex.

XX PS Claim 11; Page 25; 58pp; English.

XX CC The invention relates to a method of detecting human immunodeficiency
 CC virus-2 nucleic acids (NA) in a biological sample, by contacting NAs with
 CC 1st and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide
 CC base sequence, and detecting the amplified NA; or providing a
 CC hybridisation probe and detectable label, hybridising HIV-2 NA with the
 CC probe to form probe:target duplex, and detecting the duplex. The method
 CC is useful for detecting the presence of HIV-2 NAs in a lysate or a blood
 CC product such as plasma or serum, and also for detecting subtypes A, B, C
 CC and D of HIV-2. The method is useful for amplifying and detecting the NA
 CC in blood serum and also as components of multiplex amplification
 CC reactions that synthesise amplicons corresponding to polynucleotides of
 CC unrelated viruses, e.g. HIV-1, hepatitis B virus (HBV) and hepatitis C
 CC virus (HCV). ABK93897-ABK93910 represent HIV-2 detection probes of the
 CC invention. (Updated on 29-AUG-2003 to standardise OS field)

SQ Sequence 58 BP; 17 A; 17 C; 13 G; 11 T; 0 U; 0 Other;

Query Match 61.5%; Score 33.2; DB 6; Length 58;

Best Local Similarity 92.1%; Pred. No. 0.0026;
 Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGGAGACCATTTGTG 38
 |||||
 Db 1 GAAATTAATACGACTCACTATAGGGAGACCATTTGTG 38
 |||||

RESULT 65

ADZ15190
 ID ADZ15190 standard; DNA; 1246 BP.

XX AC ADZ15190;

XX DT 16-JUN-2005 (first entry)

XX DE Human glutamine synthetase (GS) DNA fragment from expression vector.
 XX KW cell culture; artificial organ; liver disease; hepatotropic;
 XX KW gastrointestinal disease; ds; glutamine synthetase;
 XX KW glutamate-ammonia ligase.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN JP2003274963-A.

XX PD 30-SEP-2003.

XX PF 22-MAR-2002; 2002JP-00081344.

XX PR 22-MAR-2002; 2002JP-00081344.

XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX PA (KOKU-) KOKURITSU SEIKU IRYO CENT SOCHO.

XX DR WPI; 2003-869433/81.

XX PT New cell line transformed by a gene encoding an enzyme involved in drug
 PT metabolism and by gene encoding an enzyme involved in ammonia metabolism,
 PT useful in liver function supporting equipment for assessing liver
 PT function.

XX PS Example 3; Page 11; 22pp; Japanese.

XX CC The invention relates to a novel cell line (HepG2) transformed by a gene
 CC encoding an enzyme involved in drug metabolism, such as cytochrome P450
 CC 3A4 (CYP3A4) and a gene encoding an enzyme involved in ammonia
 CC metabolism, such as glutamine synthetase. The cell line of the invention
 CC provides a hybrid artificial liver and facilitates cell procurement, and
 CC thus may be useful in liver function studies. The current sequence is
 CC that of the human glutamine synthetase (GS) DNA fragment of the invention
 CC which was isolated from an expression vector.

XX SQ Sequence 1246 BP; 324 A; 325 C; 323 G; 274 T; 0 U; 0 Other;

Query Match 61.5%; Score 33.2; DB 11; Length 1246;

Best Local Similarity 75.9%; Pred. No. 0.0049;
 Matches 41; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGGAGACCATTTGTGCAATATTCCTCCCTGC 54
 |||||

Db 39 GAAATTAATACGACTCACTATAGGGAGACCATTTGTGCAATATTCCTCCCTGC 92
 |||||

RESULT 66

AAAD11615

ID AAAD11615 standard; DNA; 5731 BP.

XX AC AAAD11615;

XX 24-SEP-2001 (first entry)
XX Six finger ZFP (2C7)-Sin3 interaction domain (SID) DNA.
DE Zinc finger protein; ZFP; gene expression; metabolic pathway regulator;
KW modulation; plant technology; agriculture; Sin3 interaction domain; SID;
KW six finger ZFP; 2C7; ds.
XX Unidentified.
XX WO200152620-A2.
XX 26-JUL-2001.
XX 19-JAN-2001; 2001WO-US001817.
XX 21-JAN-2000; 2000US-0177468P.
XX 21-JUL-2000; 2000US-00620897.
XX (SCRI) SCRIPPS RES INST.
XX (SYGN) SYNGENTA AGRIC DISCOVERY INC.
XX Barbas CF, Stege JT, Guan X, Dalmia B;
XX WPI; 2001-465325/50.
XX New zinc finger proteins, useful for modulating or regulating gene
XX expression and metabolic pathways in plants, e.g. for treating in the
XX plant cells a disorder that is associated with abnormal expression of the
XX target gene.
XX Disclosure; Page 153-156; 156pp; English.
XX The patent discloses methods and compositions to modulate the expression
XX of a target gene in plant cells. The method involves providing plant
XX cells with a zinc finger protein (ZFP) which is capable of specifically
XX binding to a target nucleotide sequence or its complementary strand
XX within a target gene and allowing the ZFP binding to the target
XX nucleotide sequence, where the expression of the target gene in the plant
XX cells is modulated. The ZFP and fusions of the ZFP proteins are useful
XX for modulating or regulating gene expression and metabolic pathways in
XX plants. The ZFP, fusion proteins and methods are useful in plant and
XX agricultural technology. The method is useful particularly for treating a
XX disorder in the plant cells, where the disorder is associated with
XX abnormal expression of the target gene. The present sequence is six
XX finger ZFP (2C7)-Sin3 interaction domain (SID) DNA
XX Sequence 5731 BP; 1340 A; 1515 C; 1463 G; 1413 T; 0 U; 0 Other;
Query Match 61.5%; Score 33.2; DB 4; Length 5731;
Best Local Similarity 75.9%; Pred. No. 0.0068;
Matches 41; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCACTATAGGAGACCACATTGTGCAATATTCCTCCACTGC 54
Db 858 GAAATTAATACGACTCACTATAGGAGACCACCAAGCTGCTAGCATGGCGCTGC 911
RESULT 67
AAD11020
ID AAD11020 standard; DNA; 33 BP.
XX AAD11020;
AC AAD11020;
XX 11-SEP-2003 (revised)
DT 24-SEP-2001 (first entry)
XX Bacteriophage T7 promoter used to amplify MAC rRNA along with a primer.
XX Mycobacterium avium complex; MAC; 16S ribosomal RNA; pathogenic bacteria;
KW in vitro amplification; MAC infection; promoter; ds.
XX

OS Enterobacteria phage T7.
XX WO200144511-A2.
XX 21-JUN-2001.
XX 15-DEC-2000; 2000WO-US033872.
XX 15-DEC-1999; 99US-0171202P.
XX (GENP-) GEN-PROBE INC.
XX (BREN/) BRENTANO S T.
XX (LANK/) LANKFORD R L.
XX Brentano ST, Lankford RL;
XX WPI; 2001-398171/42.
XX Detecting Mycobacterium avium complex organisms, comprises using in vitro
XX nucleic acid amplification with amplification oligonucleotides specific
XX for 16S ribosomal RNA or DNA encoding 16S rRNA from the bacterial
XX species.
XX Disclosure; Page 26; 27pp; English.
XX The present invention relates to a method for detecting Mycobacterium
XX avium complex (MAC) organisms (eg. M. avium, M. intracellulare, M.
XX tuberculosis, M. paratuberculosis) present in a biological sample. The
XX method comprises amplifying a 16S ribosomal RNA (rRNA) or DNA encoding
XX 16S rRNA obtained from a biological sample containing nucleic acid from a
XX MAC species in an in vitro nucleic acid amplification mixture comprising
XX a polymerase activity and a pair of primers to produce an amplified
XX nucleic acid and detecting amplified nucleic acid. The method is useful
XX for in vitro diagnostic detection of pathogenic bacteria, particularly
XX detecting infections caused by MAC organisms, distinguished from other
XX closely-related Mycobacterium species. The present sequence is
XX Bacteriophage T7 promoter. This promoter along with a primer is used for
XX in vitro amplification of MAC rRNA. (Updated on 11-SEP-2003 to
XX standardise OS field)
XX Sequence 33 BP; 14 A; 7 C; 6 G; 6 T; 0 U; 0 Other;
Query Match 61.1%; Score 33; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
RESULT 68
AAD11286
ID AAD11286 standard; DNA; 33 BP.
XX AAD11286;
AC AAD11286;
XX 11-SEP-2003 (revised)
DT 24-SEP-2001 (first entry)
XX Bacteriophage T7 promoter.
XX Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
KW Mycobacterium other than tuberculosis; MOTT; T7 promoter; ds.
XX Enterobacteria phage T7.
XX WO200144510-A2.
XX 21-JUN-2001.
XX 17-DEC-1999; 99WO-US030346.
XX

CC 1st and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide
 CC base sequence, and detecting the amplified NA; or providing a
 CC hybridisation probe and detectable label, hybridising HIV-2 NA with the
 CC probe to form probe:target duplex, and detecting the duplex. The method
 CC is useful for detecting the presence of HIV-2 NAs in a lysate or a blood
 CC product, such as plasma or serum, and also for detecting subtypes A, B, C
 CC and D of HIV-2. The method is useful for amplifying and detecting the NA
 CC in blood serum and also as components of multiplex amplification
 CC reactions that synthesise amplicons corresponding to polynucleotides of
 CC unrelated viruses, e.g. HIV-1, hepatitis B virus (HBV) and hepatitis C
 CC virus (HCV). ABK93877-ABK93910 represent HIV-2 detection probes of the
 CC invention. (Updated on 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 33 BP; 14 A; 7 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 61.1%; Score 33; DB 6; Length 33;
 Best Local Similarity 100.0%; Pred. No. 0.0027;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
 Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 71
 AAL45466
 ID AAL45466 standard; DNA; 33 BP.
 XX
 AC AAL45466;
 XX
 DT 29-AUG-2003 (revised)
 DT 06-JUN-2002 (first entry)
 XX
 DE Bacteriophage T7 promoter sequence SEQ ID NO: 4.
 XX
 KW HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;
 KW promoter; ds.
 XX
 OS Enterobacteria phage T7.
 XX
 PN WO200220852-A1.
 XX
 PD 14-MAR-2002.
 XX
 PF 01-SEP-2000; 2000WO-US024117.
 XX
 PR 01-SEP-2000; 2000WO-US024117.
 XX
 PA (GENP-) GEN-PROBE INC.
 PA (INNR) BIOMERIEUX SA.
 XX
 PI Yang YV, Brentano ST, Babola O, Tran N, Vernet G;
 XX
 DR WPI; 2002-292273/33.
 XX
 PT New nucleic acid oligomer, useful for detecting selected regions of gag
 PT and pol genes of human immune deficiency virus, particularly for
 PT assessing drug resistance.
 XX
 PS Disclosure; Page 37; 82pp; English.
 XX
 CC The present invention provides a number of nucleic acid oligomers which
 CC can be used to amplify the gag and pol genes of human immunodeficiency
 CC virus type I (HIV-1). These are used to detect regions of the gag and pol
 CC genes, especially regions associated with drug resistance, and also for
 CC identifying genetic subtypes of the virus. The present sequence is a
 CC fragment of a bacteriophage T7 promoter described in the invention.
 CC (Updated on 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 33 BP; 14 A; 7 C; 6 G; 6 T; 0 U; 0 Other;
 Query Match 61.1%; Score 33; DB 6; Length 33;
 Best Local Similarity 100.0%; Pred. No. 0.0027;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
 Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
 RESULT 72
 ADG88367
 ID ADG88367 standard; DNA; 33 BP.
 XX
 AC ADG88367;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE T7 promoter DNA.
 XX
 KW In vitro amplification; ds.
 XX
 OS Enterobacteria phage T7.
 XX
 PN US2003165824-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 15-DEC-2000; 2000US-00738274.
 XX
 PR 17-DEC-1999; 99US-0172190P.
 XX
 PA (BREN/) BRENTANO S T.
 PA (JUCK/) JUCKER M T.
 PA (DELG/) DELGADO F D.
 PA (CLEU/) CLEUZIAT P.
 PA (RODR/) RODRIGUE M.
 XX
 PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
 XX
 DR WPI; 2003-898044/82.
 XX
 PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
 PT in a biological sample comprises performing in vitro nucleic acid
 PT amplification and detection of amplified products.
 XX
 PS Disclosure; SEQ ID NO 36; 20pp; English.
 XX
 CC The present invention relates to a method of detecting Mycobacterium
 CC species present in a biological sample comprises performing an in vitro
 CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
 CC detecting the amplified Mycobacterium nucleic acid. The present sequence
 CC is T7 promoter DNA.
 XX
 SQ Sequence 33 BP; 14 A; 7 C; 6 G; 6 T; 0 U; 0 Other;
 Query Match 61.1%; Score 33; DB 10; Length 33;
 Best Local Similarity 100.0%; Pred. No. 0.0027;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
 Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
 RESULT 73
 ADI18913
 ID ADI18913 standard; DNA; 33 BP.
 XX
 AC ADI18913;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE T7 promoter-primer #4.
 XX
 KW Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.


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XX OS Enterobacteria phage T7.
XX PA US2003228574-A1.
XX PN 11-DEC-2003.
XX PD
XX PF 28-APR-2003; 2003US-00425975.
XX PR 01-SEP-2000; 2000US-0229790P.
XX PT 31-AUG-2001; 2001US-00944036.
XX PS (YANG/) YANG Y Y.
XX CC (BREN/) BRENTANO S T.
XX CC (BABO/) BABOLA O.
XX CC (TRAN/) TRAN N.
XX CC (VERN/) VERNET G.
XX PI Yang YV, Brentano ST, Babola O, Tran N, Vernet G;
XX WIPI; 2004-060998/06.
XX PT New nucleic acid oligomer for amplifying and detecting HIV-1 nucleotide
XX sequences and in providing information about the infective agent, e.g.
XX genetic subgroup or drug-resistance phenotype based on detectable
XX sequence information.
XX PS Disclosure; SEQ ID NO 4; 39pp; English.
XX CC The present invention relates to a nucleic acid oligomer for amplifying a
XX nucleotide sequence of human immune deficiency virus (HIV)-1. The
XX invention is useful in amplifying and detecting HIV-1 nucleic acid
XX sequences and in providing additional information about the infective
XX agent, such as its genetic subgroup or drug-resistance phenotype based on
XX detectable sequence information. The present sequence is T7 promoter-
XX primer.
XX SQ Sequence 33 BP; 14 A; 7 C; 6 G; 6 T; 0 U; 0 Other;
Query Match 61.1%; Score 33; DB 12; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
RESULT 74
AEA08242
ID AEA08242 standard; DNA; 33 BP.
XX AC
XX AE AEA08242;
XX DT 14-JUL-2005 (first entry)
XX DE Bacteriophage T7 promoter DNA, SEQ ID NO: 36.
XX KW Microorganism detection; DNA amplification; promoter; ds.
XX OS Enterobacteria phage T7.
XX PN US2005100915-A1.
XX PD 12-MAY-2005.
XX PF 18-SEP-2003; 2003US-00665708.
XX PR 17-DEC-1999; 99US-0172190P.
XX PT 15-DEC-2000; 2000US-00738274.
XX PA (BREN/) BRENTANO S T.
XX PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAI P.
PA (RODR/) RODRIGUE M.
XX PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WIPI; 2005-345392/35.
XX PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX in a biological sample, comprises using in vitro nucleic acid
XX amplification and detection of amplified products.
XX PS Disclosure; SEQ ID NO 36; 21pp; English.
XX CC The present invention relates to a method of detecting Mycobacterium
XX species present in a biological sample. The method involves using in
XX vitro nucleic acid amplification and detection of amplified products. The
XX invention is useful for diagnostic detection of pathogenic bacteria such
XX as Mycobacterium species. The present sequence is the Bacteriophage T7
XX promoter DNA.
XX SQ Sequence 33 BP; 14 A; 7 C; 6 G; 6 T; 0 U; 0 Other;
Query Match 61.1%; Score 33; DB 14; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
RESULT 75
ADM11857
ID ADM11857 standard; DNA; 39 BP.
XX AC ADM11857;
XX DT 01-JUL-2004 (first entry)
XX DE Peptide library RT-PCR primer.
XX KW ss: membrane interacting peptide; food putrefaction; infectious disease;
XX cancer; apoptosis; antibiotic; glioblastoma; leukaemia;
XX autoimmune disorder; viral infection; inflammation;
XX graft versus host disease; PCR; primer; RT-PCR;
XX reverse transcriptase PCR.
XX OS Synthetic.
XX PN US2004072992-A1.
XX PD 15-APR-2004.
XX PF 29-AUG-2003; 2003US-00651563.
XX PR 30-AUG-2002; 2002JP-00253169.
XX PT 29-JAN-2003; 2003JP-00021198.
XX PA (MACH/) MACHIDA S.
XX PA (TOKU/) TOKUYASU K.
XX PA (MATS/) MATSUNAGA S.
XX PA (SAKA/) SAKAKIBARA Y.
XX PA (KOB0/) KOBORI M.
XX PA (WENZ/) WEN Z.
XX PI Machida S, Tokuyasu K, Matsunaga S, Sakakibara Y, Kobori M;
XX WIPI; 2004-328618/30.
XX PT New peptide acting on a membrane of a microorganism, for preventing
XX putrefaction of food or industrial products and treating an infectious

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PT disease, cancer, autoimmune disorders, inflammation and graft versus host
 XX disease.

PS Example 6; SEQ ID NO 9; 58pp; English.

XX The invention relates to a peptide capable of specifically acting on a
 CC membrane of a microorganism or an animal cell having an abnormality. The
 CC peptide conforms to the formula given in claim 1 of the specification.
 CC Exemplary sequences appear as ADMI1859-ADMI1965 (SEQ ID 110-113 and 119
 CC are not indexed as being too short). Also included are a library
 CC comprising nucleic acid sequences (each nucleic acid sequence comprising
 CC (i) a first cassette comprising a base sequence encoding a first peptide,
 CC (ii) a second cassette comprising a base sequence encoding a second
 CC peptide, the base sequence having the same reading frame as that of the
 CC base sequence encoding the first peptide, where the second peptide and
 CC comprises a site allowing flexible movement of the first peptide and
 CC (iii) a third cassette comprising a base sequence essentially required
 CC for transcription and translation of the first and second cassette (e.g.
 CC a T7 promoter), the third cassette being operatively linked to the first
 CC and second cassette, where the number of the nucleic acid sequences in
 CC the library whose first cassettes are different from another is at least
 CC two), a vector comprising the library, a method for screening for a
 CC nucleic acid encoding a peptide capable of acting on biological membrane,
 CC a pharmaceutical composition for killing a microorganism (or preventing
 CC putrefaction of food or industrial products, for treating an infectious
 CC disease caused by a microorganism or a cancer and for suppressing
 CC apoptosis), comprising the peptide, an antibiotic comprising the peptide,
 CC a pharmaceutical delivery substance for delivering a drug to a site
 CC infected with a microorganism (or to a cancer lesion site or to a site
 CC undergoing apoptosis) comprising the peptide and a kit, for screening for
 CC a nucleic acid encoding a peptide capable of acting on a biological
 CC membrane. The peptides and compositions are useful in killing a
 CC microorganism, preventing putrefaction of food or industrial products,
 CC treating an infectious disease caused by a microorganism or a cancer,
 CC e.g. bladder, stomach, breast, lung, prostate, large intestine, uterine,
 CC ovarian or kidney cancer, glioblastoma, leukaemia, autoimmune disorders,
 CC viral infections, inflammation and graft versus host disease and in
 CC suppressing apoptosis. The present sequence is an RT-PCR (reverse
 CC transcriptase PCR) primer used to recover mRNA expressing a membrane
 CC interacting peptide of the invention.

XX Sequence 39 BP; 15 A; 9 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 61.1%; Score 33; DB 12; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTATACGACTCACTATAGGAGACCACA 33

DB 3 GAAATTATACGACTCACTATAGGAGACCACA 35

RESULT 76

AAV70242

ID AAV70242 standard; DNA; 41 BP.

XX

AC AAV70242;

XX 04-FEB-1999 (first entry)

DE Polysome display library construction PCR primer T7B.

XX scFv antibody; identification; in vitro translation; PCR primer;
 KW antisease oligonucleotide; tag-coding sequence; ssrA-RNA; polysome; ss.
 XX Synthetic.

OS W09848008-A1.

PN 29-OCT-1998.

XX

PD 23-APR-1998;

XX 98WO-EF002420.

XX

PR 23-APR-1997; 97EP-00106753.

XX (PLUE/) PLUECKTHUN A.

XX Plueckthun A, Hanes J;

PI WPI; 1998-609984/51.

XX Method of identifying polypeptide binding target molecules - uses an in

XX vitro translation system with formation of polysomes.

XX Example 8; Page 27; 47pp; English.

XX A method has been developed of identifying a nucleic acid encoding a
 CC (poly)peptide that interacts with a target molecule. The method
 CC comprises: (i) translating a population of mRNA molecules lacking stop
 CC codons, in the correct reading frame in an in vitro translation system,
 CC where the system either comprises antisense oligonucleotides
 CC complementary to the tag-coding sequence of ssrA-RNA or is free of ssrA-
 CC RNA so that formation of polysomes is allowed; (ii) contacting the formed
 CC polysomes with the target molecules so that the nascent (poly)peptide
 CC encoded by the RNA and produced by the polysome, binds the target
 CC molecule; (iii) separating polysomes where the nascent (poly)peptide
 CC produced by the polysome is bound to the target molecule from those
 CC polysomes not displaying novel (poly)peptides; and (iv) identifying the
 CC nucleic acid sequence encoding the (poly)peptide binding the target
 CC molecule. Optionally prior to the formation of polysomes, DNA molecules
 CC devoid of stop codons are transcribed in the presence of a reducing
 CC agent, either beta-mercaptoethanol or DTT, to produce the corresponding
 CC RNA molecules, and the reducing agent is then removed from the RNA
 CC molecules. The method is used to identify polypeptides that bind target
 CC molecules. The present sequence represents a PCR primer used in an
 CC example from the present invention for construction of a polysome display
 CC library

XX Sequence 41 BP; 17 A; 9 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 61.1%; Score 33; DB 2; Length 41;

Best Local Similarity 100.0%; Pred. No. 0.0028;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTATACGACTCACTATAGGAGACCACA 33

DB 5 GAAATTATACGACTCACTATAGGAGACCACA 37

RESULT 77

ACC70757

ID ACC70757 standard; DNA; 41 BP.

XX

AC ACC70757;

XX 20-NOV-2003 (first entry)

XX Green fluorescent protein, GFP, PCR primer Md0 SS, SEQ ID 3.

XX PCR; primer; green fluorescent protein; GFP; ss.

XX Synthetic.

XX EPI316616-A1.

XX 04-JUN-2003.

XX 26-NOV-2002; 2002EP-00026225.

XX 30-NOV-2001; 2001DE-01058904.

XX (HOFF) ROCHE DIAGNOSTICS GMBH.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Nemetz C, Buchberger B, Watzele M, Mutter W, Roeder A, Wessner S;

XX

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DR WPI; 2003-543650/52.
XX
PT Producing linear DNA fragments for the in vitro expression of proteins,
PT comprises amplifying a linear DNA fragment containing control elements
PT and a protein-coding gene having two ends with complementary regions to
PT the linear DNA fragment.
XX
XX Example 1; Page 6; 26pp; English.
XX
CC The present invention relates to a method for producing linear DNA
CC fragments for the in vitro expression of proteins. The method comprises
CC amplifying a linear DNA fragment, which contains control elements and a
CC protein-coding gene having two ends with complementary regions to the two
CC ends of the linear DNA fragment, using a primer pair that binds upstream
CC and downstream of the expression control region on the linear DNA
CC fragment. The method is useful for producing a linear DNA fragment for
CC the in vitro expression of proteins. The linear DNA fragment is
CC particularly useful for the in vitro expression of a protein using a
CC lysate from bacterial strains or eukaryotic cells. The present sequence
CC is a PCR primer, which was used in an example from the invention
XX
SQ Sequence 41 BP; 15 A; 9 C; 8 G; 9 T; 0 U; 0 Other;
Query Match 61.1%; Score 33; DB 9; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
DB 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
RESULT 78
ADW95371
ID ADW95371 standard; DNA; 41 BP.
AC ADW95371;
XX
XX 07-APR-2005 (first entry)
XX
XX PCR primer full T7 forward used to add T7 promoter.
XX
XX protease; T7 promoter; protein display; PCR; primer; ss.
XX
XX Synthetic.
XX
XX WO2005007886-A2.
XX
XX 27-JAN-2005.
XX
XX 12-JUL-2004; 2004WO-GB003055.
XX
XX 12-JUL-2003; 2003GB-00016314.
XX
XX (UYBE-) UNIV QUEENS BELFAST.
XX
XX Scott C, Walker B;
XX
XX WPI; 2005-122776/13.
XX
XX Displaying/selecting protease molecule, by incubating mRNA to enable its
XX translation to form complexes of ribosome, mRNA and encoded nascent
XX peptide, contacting complexes with protease binding ligand, selecting
XX complexes bound to ligand.
XX
XX Example 2; Page 41; 72pp; English.
XX
XX The specification describes a method for displaying and selecting
XX protease molecules. The method comprises incubating mRNA molecules
XX encoding a peptide under conditions suitable for translation of mRNA
XX molecules to form complexes comprising ribosome, mRNA and encoded nascent
XX peptide displayed on ribosome; contacting complexes with a protease
XX binding ligand; and selecting complexes which specifically bind protease
XX
CC binding ligand. The method is useful for displaying and selecting a
CC protease molecule; identifying one or more protease from a tissue sample;
CC identifying a protease with particular substrate specificity; identifying
CC protease binding ligand; displaying, characterizing and/or identifying
CC protease and modulators of protease activity; identifying new proteases
CC from library of peptides; and characterizing one or more tissues or
CC groups of tissues with respect to protease activity. The present PCR
CC primer was used to add the T7 promoter to mRNA constructs for display of
CC cathepsin S.
XX
SQ Sequence 41 BP; 17 A; 9 C; 8 G; 7 T; 0 U; 0 Other;
Query Match 61.1%; Score 33; DB 14; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
DB 5 GAAATTAATACGACTCACTATAGGAGACCACA 37
RESULT 79
AEE96336
ID AEE96336 standard; DNA; 42 BP.
AC AEE96336;
XX
XX 23-FEB-2006 (first entry)
XX
XX T7 universal primer forward.
XX
XX ss; primer; toxin; DNA library; DNA detection; Mcal617;
XX restriction endonuclease.
XX
XX Enterobacteria phage T7.
XX
XX WO2005121946-A2.
XX
XX 22-DEC-2005.
XX
XX 01-JUN-2005; 2005WO-US019241.
XX
XX 02-JUN-2004; 2004US-0576196P.
XX
XX (NEWE ) NEW ENGLAND BIOLABS INC.
XX
XX Roberts RJ;
XX
XX WPI; 2006-067158/07.
XX
XX Identifying an open reading frame encoding toxic protein, involves
XX detecting gap in map of shotgun clones from shotgun library aligned on
XX target DNA sequence, corresponding to numerical deficiency in start sites
XX of shotgun clones.
XX
XX Example 1; SEQ ID NO 3; 34pp; English.
XX
XX This invention describes a novel method for identifying an open reading
XX frame encoding a toxic protein, which involves obtaining an in silico map
XX of several shotgun clones from a shotgun library aligned on target DNA
XX sequence, detecting a gap in the map corresponding to numerical
XX deficiency at the start sites of shotgun clones in a region such that
XX there is a statistically underrepresented number of clones spanning the
XX ORF, and determining whether the product of the ORF is a toxic protein.
XX The target DNA fragment is a genome chosen from a bacterial genome,
XX archaeal genome and viral genome. The toxic gene is mapped to an ORF
XX adjacent to a methylase. The step of identifying the gene expressing the
XX toxic protein from the ORF further involves expressing the ORF in vivo or
XX by in vitro translation. The method is useful for identifying ORF's
XX encoding toxic proteins e.g. restriction endonucleases and enables
XX efficient characterization of toxic genes. This sequence represents a T7
XX universal primer used with AEE96337 to identify the Methylococcus
XX capsulatus Mcal617 restriction endonuclease using the method of the
```

CC invention.

XX Sequence 42 BP; 15 A; 10 C; 8 G; 9 T; 0 U; 0 Other;

Query Match 61.1%; Score 33; DB 15; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAAATACGACTCACTATAGGAGACCACA 33

DB 1 GAAATTAAATACGACTCACTATAGGAGACCACA 33

RESULT 80

ABL53868

ID ABL53868 standard; DNA; 49 BP.

XX ABL53868;

XX 29-AUG-2003 (revised)

DT 24-JUN-2002 (first entry)

XX Phase T7 promoter.

XX Phase T7; promoter; phase display; library; ss.

XX Enterobacteria phage T7.

XX Key Location/Qualifiers

FT misc_feature

FT /*tag= a

FT /note= "site of initiation of transcription"

XX WO200183734-A2.

XX 08-NOV-2001.

XX 03-MAY-2001; 2001WO-EP005016.

XX 03-MAY-2000; 2000GB-00010543.

XX (BIOI-) BIOINVENT INT AB.

XX Nilsson N;

XX WPI; 2002-062123/08.

XX Expression vector library, especially a phage display library comprises several nucleic acid sequences whose expression is under regulatory control of T7 promoter and encode antibodies or their fragments.

PS Claim 4; Page 43; 54pp; English.

XX The present sequence is a T7 promoter sequence preferred for use in claimed expression vector libraries of the invention. These expression vector libraries, preferably phage display libraries, comprise nucleic acid sequences whose expression is under the regulatory control of a T7 promoter, and which encode antibodies or antibody fragments. The strong repression of the T7 promoter increases the possibility of finding larger variability in the pool of antibody fragments due to the low frequency of deletion of undesirable, to the bacterial host, gene fragments. The high efficiency of T7 RNA polymerase allows induction, by infection, at late stages of the cell cycle, increasing the number of host cells and limiting unwanted effects on the bacterial cells. (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 49 BP; 22 A; 8 C; 10 G; 9 T; 0 U; 0 Other;

Query Match 61.1%; Score 33; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAAATACGACTCACTATAGGAGACCACA 33

DB 1 GAAATTAAATACGACTCACTATAGGAGACCACA 33

RESULT 81

AAAX25962

ID AAAX25962 standard; DNA; 50 BP.

XX AAAX25962;

XX 08-JUN-1999 (first entry)

DT Capture domain primer T7loop.

XX Capture domain; screening; gene library; selection; phenotype; isolation; cell survival; microorganism; bacterium; bacteriophage; liposome; primer; PCR; amplification; ss.

XX Synthetic.

XX WO9911777-A1.

XX 11-MAR-1999.

XX 03-SEP-1998; 98WO-GB002649.

XX 03-SEP-1997; 97GB-00018552.

XX 18-SEP-1997; 97GB-00019834.

XX 24-SEP-1997; 97GB-00020184.

XX 29-SEP-1997; 97GB-00020522.

XX 29-SEP-1997; 97GB-00020523.

XX 29-SEP-1997; 97GB-00020524.

XX 29-SEP-1997; 97GB-00020525.

XX 30-DEC-1997; 97US-0070037P.

XX 30-DEC-1997; 97US-0070050P.

XX 30-DEC-1997; 97US-0070062P.

XX 30-DEC-1997; 97US-0070063P.

XX 22-JAN-1998; 98GB-00001255.

XX 25-FEB-1998; 98GB-00003828.

XX 14-APR-1998; 98GB-00007760.

XX 23-MAY-1998; 98GB-00011130.

XX (BIOV-) BIOVATION LTD.

XX Carr FJ, Carter G, Hamilton A, Adair F, Williams S;

XX WPI; 1999-205184/17.

XX Screening proteins or polypeptides by generating a gene library and synthesizing proteins - useful for direct selection of a biological phenotype.

XX Example 10; Page 69; 118pp; English.

XX This sequence corresponds to a PCR primer used to amplify a capture domain sequence used in a method of screening proteins or polypeptides, involving the generation of a gene library and the synthesis of proteins. The methods permit direct selection of a biological phenotype, involving contacting displayed proteins or polypeptides with target cells to enable binding to the cell. The resulting alteration in the target cell permits isolation of the cell and recovery of genes encoding the displayed protein or polypeptide. Binding also results in the production or cessation of production of molecules from the target cell, which also permits the recovery of genes encoding the displayed protein or polypeptide. Molecules produced are needed for cell survival when the cell is a microorganism (especially a bacteria or bacteriophage). Release of a molecule is needed for release of other molecules from liposomes. Alteration also results in appearance or disappearance of a cell surface marker on a cell

XX Sequence 50 BP; 20 A; 10 C; 9 G; 11 T; 0 U; 0 Other;

Query Match

61.1%; Score 33; DB 2; Length 50;

Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
| | | | | | | | | | | | | | | | | | | | | |
Db 15 GAAATTAATACGACTCACTATAGGAGACCACA 47

RESULT 82

AAx85760
ID AAX85760 standard; DNA; 51 BP.

XX
AC AAX85760;

XX
DT 07-SEP-1999 (first entry)

XX PCR primer used to amplify a polysome library.

XX Polysome library; nascent peptide display; PCR primer;
KW affinity interaction screening; multiple binding specificity;
KW single chain antibody; ss.

XX Synthetic.

XX US5922545-A.

XX
PN 13-JUL-1999.

XX
DT 29-JUL-1997; 97US-00902623.

XX
PR 29-OCT-1993; 93US-00144775.

XX
PR 02-SEP-1994; 94US-00300262.

XX
PR 25-OCT-1994; 94WO-US012206.

XX
PR 17-JAN-1996; 96US-00586176.

XX (APFY-) AFFYMAX TECHNOLOGIES NV.

XX
PI Mattheakis LC, Dower WJ;

XX
DR WPI; 1999-417975/35.

XX In vitro peptide and antibody display libraries for identifying multiple
PT binding specificities of single chain antibodies.

XX Example 1; Col 46; 50pp; English.

XX The specification describes a method for generating libraries of
CC polysomes displaying nascent peptides suitable for affinity interaction
CC screening. The method can be used to identify multiple binding
CC specificities of single chain antibodies, and comprises contacting
CC antigens with a polysome library displaying nascent peptides having a
CC single chain antibody segment, separating polysomes bound to the antigen
CC species from polysomes not bound to the antigen species, and synthesizing
CC cDNA from the separated bound polysomes to identify single chain
CC antibodies which bind to at least one of the antigen species present. The
CC method for generating libraries of polysomes displaying nascent peptides
CC is useful for affinity interaction screening. PCR primers AAX85760-61
CC were used in the course of the invention

XX Sequence 51 BP; 16 A; 14 C; 8 G; 13 T; 0 U; 0 Other;

Query Match 61.1%; Score 33; DB 2; Length 51;

Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
| | | | | | | | | | | | | | | | | | | | | |
Db 6 GAAATTAATACGACTCACTATAGGAGACCACA 38

RESULT 83

ABK53141
ID ABK53141 standard; DNA; 51 BP.

XX
AC ABK53141;

XX
DT 29-AUG-2003 (revised)
DT 12-AUG-2002 (first entry)

XX HIV-1 reverse transcriptase gene specific oligonucleotide primer #12.

XX HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;
KW reverse transcriptase; infection; PCR.

XX Human immunodeficiency virus 1.

XX US200205095-A1.

XX
PD 09-MAY-2002.

XX
PF 31-AUG-2001; 2001US-00944036.

XX
PR 01-SEP-2000; 2000US-0229790P.

XX (YANG/) YANG Y Y.

XX (BREN/) BRENTANO S T.

XX (BABO/) BABOLA O.

XX (TRAN/) TRAN N.

XX (VERN/) VERNET G.

XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;

XX WPI; 2002-462902/49.

XX New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-
PT 1 and probes for detecting the amplified product are specific for gag and
PT pol regions and are useful to detect different subtypes of HIV-1.

XX Claim 1; Page 26; 37pp; English.

XX This invention relates to a series of nucleic acid oligomers for
CC amplifying and detecting a nucleotide sequence of human immunodeficiency
CC virus type 1 (HIV-1). The invention also comprises a labeled
CC oligonucleotide that specifically hybridizes to an HIV-1 sequence derived
CC from gag or pol sequences, having one of the sequences fully defined in
CC the specification, and a method for detecting HIV-1 in a biological
CC sample, comprising mixing the sample with two or more of the
CC amplification oligomers that specifically amplify at least one HIV-1
CC target sequence within gag and a pol sequence which is a protease or
CC reverse transcriptase sequence, amplifying the target, and detecting the
CC amplified product. The oligonucleotides of the invention may be used to
CC diagnose HIV-1 infection. The presents sequence represents a PCR primer
CC used to amplify the HIV-1 reverse transcriptase gene in the HIV detection
CC method of the invention. (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 51 BP; 17 A; 12 C; 9 G; 13 T; 0 U; 0 Other;

Query Match 61.1%; Score 33; DB 6; Length 51;

Best Local Similarity 100.0%; Pred. No. 0.003;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 84

AAL45503
ID AAL45503 standard; DNA; 51 BP.

XX
AC AAL45503;

XX
DT 29-AUG-2003 (revised)

XX
DT 06-JUN-2002 (first entry)

XX HIV-1 pol gene RT amplification oligomer SEQ ID NO: 41.

XX HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;
 KW probe; ss.
 XX OS Human immunodeficiency virus 1.
 OS Enterobacteria phage T7.
 XX WO200220852-A1.
 PN 14-MAR-2002.
 XX 01-SEP-2000; 2000WO-US024117.
 XX 01-SEP-2000; 2000WO-US024117.
 XX (GENP-) GEN-PROBE INC.
 PA (INNR) BIOMERIEUX SA.
 XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
 PI WPI; 2002-292273/33.
 DR New nucleic acid oligomer, useful for detecting selected regions of gag
 PT and pol genes of human immune deficiency virus, particularly for
 PT assessing drug resistance.
 XX Claim 1; Page 60; 82pp; English.
 XX The present invention provides a number of nucleic acid oligomers which
 CC can be used to amplify the gag and pol genes of human immunodeficiency
 CC virus type 1 (HIV-1). These are used to detect regions of the gag and pol
 CC genes, especially regions associated with drug resistance, and also for
 CC identifying genetic subtypes of the virus. The present sequence is an
 CC oligomer of the invention. (Updated on 29-AUG-2003 to standardise OS
 CC field)
 XX Sequence 51 BP; 17 A; 12 C; 9 G; 13 T; 0 U; 0 Other;
 SQ Query Match 61.1%; Score 33; DB 6; Length 51;
 Best Local Similarity 100.0%; Pred. No. 0.003;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GAAATTAATACGACTCTACTATAGGAGACCACA 33
 Db 1 GAAATTAATACGACTCTACTATAGGAGACCACA 33
 RESULT 85
 ADI18950
 ID ADI18950 standard; DNA; 51 BP.
 XX AC ADI18950;
 XX 22-APR-2004 (first entry)
 DE HIV-1 pol2 gene amplifying primer #6.
 XX Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.
 OS Human immunodeficiency virus 1.
 XX US2003228574-A1.
 PN 11-DEC-2003.
 PD 28-APR-2003; 2003US-00425975.
 XX 01-SEP-2000; 2000US-0229790P.
 PR 31-AUG-2001; 2001US-00944036.
 XX (YANG/) YANG Y Y.
 PA (BREN/) BRENTANO S T.
 PA (BABO/) BABOLA O.

PA (TRAN/) TRAN N.
 PA (VERN/) VERNET G.
 XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
 DR WPI; 2004-060998/06.
 XX New nucleic acid oligomer for amplifying and detecting HIV-1 nucleotide
 PT sequences and in providing information about the infective agent, e.g.
 PT genetic subgroup or drug-resistance phenotype based on detectable
 PT sequence information.
 XX Claim 1; SEQ ID NO 41; 39pp; English.
 XX The present invention relates to a nucleic acid oligomer for amplifying a
 CC nucleotide sequence of human immune deficiency virus (HIV)-1. The
 CC invention is useful in amplifying and detecting HIV-1 nucleic acid
 CC sequences and in providing additional information about the infective
 CC agent, such as its genetic subgroup or drug-resistance phenotype based on
 CC detectable sequence information. The present sequence is HIV-1 pol2 gene
 CC amplifying primer.
 XX Sequence 51 BP; 17 A; 12 C; 9 G; 13 T; 0 U; 0 Other;
 SQ Query Match 61.1%; Score 33; DB 12; Length 51;
 Best Local Similarity 100.0%; Pred. No. 0.003;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GAAATTAATACGACTCTACTATAGGAGACCACA 33
 Db 1 GAAATTAATACGACTCTACTATAGGAGACCACA 33
 RESULT 86
 AAA29795
 ID AAA29795 standard; DNA; 52 BP.
 XX AC AAA29795;
 XX 06-AUG-2003 (revised)
 DT 17-AUG-2000 (first entry)
 XX Plant plastid expressing human BPI gene construction oligonucleotide #3.
 DE Plant; transgenic; therapeutically active protein; plastid genome;
 KW vacuole; allergen; vaccine; antiinflammatory; immunosuppressant; allergy;
 KW autoimmune disease; transplant rejection; ss.
 XX Homo sapiens.
 OS Viridiplantae.
 OS Synthetic.
 XX WO200020612-A2.
 PN 13-APR-2000.
 PD 05-OCT-1999; 99WO-EP007414.
 XX 07-OCT-1998; 98US-00167362.
 PR 07-OCT-1998; 98US-00168231.
 XX (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX Heifetz PB, Goff SA, Tuttle AB, Griot-Wenk ME;
 DR WPI; 2000-328938/28.
 XX Novel transgenic plants expressing therapeutically active proteins form
 PT their plastid genome, useful for producing allergens for vaccines.
 XX Example 30; Page 58; 99pp; English.

CC The present invention describes plants (I) comprising a DNA molecule (II)
 CC encoding a protein that is therapeutically active when administered to a
 CC host, in its plastid genome. The transgenic plants are used to express
 CC therapeutically active proteins, such as antigens, allergens, and
 CC autoantigens. The therapeutically active proteins are used to treat or
 CC prevent diseases, e.g. allergies, autoimmune diseases or transplant
 CC rejection. The invention allows the production of large and inexpensive
 CC supplies of protein-based medications. The plants are able to express
 CC large amounts of proteins in a cost effective manner, and, as the
 CC proteins are packaged in plastids, they can be isolated easily. The
 CC present sequence represents an oligonucleotide used in the construction
 CC of plant plastids which express the human BPI gene, which is used in an
 CC example from the present invention. (Updated on 06-AUG-2003 to correct OS
 CC field.)
 XX

SQ Sequence 52 BP; 16 A; 16 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 61.1%; Score 33; DB 3; Length 52;
 Best Local Similarity 100.0%; Pred. No. 0.003;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
 |||||
 Db 10 GAAATTAATACGACTCACTATAGGAGACCACA 42

RESULT 87

AAAD21601
 ID AAAD21601 standard; DNA; 52 BP.

XX

AC AAAD21601;

XX 28-JAN-2002 (first entry)

XX

DE Phage RNA polymerase-human BPI chimeric gene constructing T73a_U oligo.

XX Transgenic plant; antibacterial; immunosuppressive; virucide; therapy;
 KW antiparasitic; allergy; autoimmune disease; immune response; PCR primer;
 KW transplantation; ss.

OS Unidentified.

XX WO200177353-A2.

XX 18-OCT-2001.

XX 03-APR-2001; 2001WO-EP003788.

XX 05-APR-2000; 2000US-00543619.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Helfetz PB, Goff SA, Tuttle AB, Griot-Wenk ME;

XX WPI; 2001-657175/75.

XX Novel plant useful for treating or preventing allergy, comprising a DNA
 PT molecule encoding a mature ragweed pollen allergen in its plastid genome
 PT and capable of expressing the pollen allergen.

XX Example 30; Page 59; 99pp; English.

XX The invention relates to a transgenic plant comprising in its plastid
 CC genome a DNA molecule encoding a mature ragweed pollen allergen, which is
 CC capable of expressing the pollen allergen. The plant or plant matter
 CC derived from the transgenic plant such as tobacco, tomato, soybean, rice
 CC or maize is useful for treating or preventing an allergy. The plant is
 CC also useful as a pharmaceutical and as a medical food. The plant is
 CC useful for suppressing and reducing undesired immune response, and
 CC production of an antigen for determination of immunological activity. The
 CC plant is useful for treating and preventing bacterial, parasitic and
 CC viral diseases, allergies, autoimmune diseases and transplantations. The
 CC present sequence is an oligonucleotide used for constructing a chimeric

CC gene containing human BPI gene under control of a promoter element
 CC responsive to the bacteriophage T7 RNA polymerase

SQ Sequence 52 BP; 16 A; 16 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 61.1%; Score 33; DB 5; Length 52;
 Best Local Similarity 100.0%; Pred. No. 0.003;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
 |||||
 Db 10 GAAATTAATACGACTCACTATAGGAGACCACA 42

RESULT 88

ABK53139
 ID ABK53139 standard; DNA; 52 BP.

XX

AC ABK53139;

XX 29-AUG-2003 (revised)

DT 12-AUG-2002 (first entry)

XX

DE HIV-1 reverse transcriptase gene specific oligonucleotide primer #10.

XX HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;

KW reverse transcriptase; infection; PCR.

XX Human immunodeficiency virus 1.

OS US2002055095-A1.

XX 09-MAY-2002.

XX 31-AUG-2001; 2001US-00944036.

XX 01-SEP-2000; 2000US-0229790P.

XX (YANG/) YANG Y. Y.

XX (BREN/) BRENTANO S. T.

XX (BABO/) BABOLA O.

XX (TRAN/) TRAN N.

XX (VERN/) VERNET G.

XX

PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;

XX WPI; 2002-462902/49.

XX

XX New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-
 PT 1 and probes for detecting the amplified product are specific for gag and
 PT pol regions and are useful to detect different subtypes of HIV-1.

XX Claim 1; Page 25; 37pp; English.

XX This invention relates to a series of nucleic acid oligomers for
 CC amplifying and detecting a nucleotide sequence of human immunodeficiency
 CC virus type 1 (HIV-1). The invention also comprises a labeled
 CC oligonucleotide that specifically hybridizes to an HIV-1 sequence derived
 CC from gag or pol sequences, having one of the sequences fully defined in
 CC the specification, and a method for detecting HIV-1 in a biological
 CC sample, comprising mixing the sample with two or more of the
 CC amplification oligomers that specifically amplify at least one HIV-1
 CC target sequence within gag and a pol sequence which is a protease or
 CC reverse transcriptase sequence, amplifying the target, and detecting the
 CC amplified product. The oligonucleotides of the invention may be used to
 CC diagnose HIV-1 infection. The presents sequence represents a PCR primer
 CC used to amplify the HIV-1 reverse transcriptase gene in the HIV detection
 CC method of the invention. (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 52 BP; 17 A; 13 C; 9 G; 13 T; 0 U; 0 Other;

Query Match 61.1%; Score 33; DB 6; Length 52;
 Best Local Similarity 100.0%; Pred. No. 0.003;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTATACGACTCACTATAGGAGACCACA 33
 Db 1 GAAATTATACGACTCACTATAGGAGACCACA 33

RESULT 89
 AAL45501
 ID AAL45501 standard; DNA; 52 BP.
 XX
 AC AAL45501;
 XX
 XX
 DT 29-AUG-2003 (revised)
 DT 06-JUN-2002 (first entry)
 XX
 DE HIV-1 pol gene RT amplification oligomer SEQ ID NO: 39.
 XX
 XX HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;
 KW probe; ss.
 XX
 OS Human immunodeficiency virus 1.
 OS Enterobacteria phage T7.
 XX
 XX WO200220852-A1.
 XX
 PD 14-MAR-2002.
 XX
 PF 01-SEP-2000; 2000WO-US024117.
 XX
 PR 01-SEP-2000; 2000WO-US024117.
 XX
 PA (GENP-) GEN-PROBE INC.
 PA (INNR-) BIOMERIEUX SA.
 XX
 XX Yang YX, Brentano ST, Babola O, Tran N, Vernet G;
 XX WPI; 2002-292273/33.
 XX
 XX New nucleic acid oligomer, useful for detecting selected regions of gag
 PT and pol genes of human immune deficiency virus, particularly for
 PT assessing drug resistance.
 XX
 PS Claim 1; Page 60; 82pp; English.
 XX
 CC The present invention provides a number of nucleic acid oligomers which
 CC can be used to amplify the gag and pol genes of human immunodeficiency
 CC virus type 1 (HIV-1). These are used to detect regions of the gag and pol
 CC genes, especially regions associated with drug resistance, and also for
 CC identifying genetic subtypes of the virus. The present sequence is an
 CC oligomer of the invention. (Updated on 29-AUG-2003 to standardise OS
 CC field)

Qy 1 GAAATTATACGACTCACTATAGGAGACCACA 33
 Db 1 GAAATTATACGACTCACTATAGGAGACCACA 33

RESULT 90
 ADI18948
 ID ADI18948 standard; DNA; 52 BP.
 XX
 AC ADI18948;
 XX
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE HIV-1 pol2 gene amplifying primer #4.

XX Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.
 KW
 XX Human immunodeficiency virus 1.
 OS
 XX US2003228574-A1.
 PN
 XX 11-DEC-2003.
 PD
 XX 28-APR-2003; 2003US-00425975.
 PF
 XX 01-SEP-2000; 2000US-0229790P.
 PR 31-AUG-2001; 2001US-00944036.
 XX
 XX (YANG/) YANG Y X.
 PA (BREN/) BRENTANO S T.
 PA (BABO/) BABOLA O.
 PA (TRAN/) TRAN N.
 PA (VERN/) VERNET G.
 XX
 PI Yang YX, Brentano ST, Babola O, Tran N, Vernet G;
 XX WPI; 2004-060998/06.
 DR
 XX New nucleic acid oligomer for amplifying and detecting HIV-1 nucleotide
 PT sequences and in providing information about the infective agent, e.g.
 PT genetic subgroup or drug-resistance phenotype based on detectable
 PT sequence information.
 XX
 PS Claim 1; SEQ ID NO 39; 39pp; English.
 XX
 CC The present invention relates to a nucleic acid oligomer for amplifying a
 CC nucleotide sequence of human immune deficiency virus (HIV)-1. The
 CC invention is useful in amplifying and detecting HIV-1 nucleic acid
 CC sequences and in providing additional information about the infective
 CC agent, such as its genetic subgroup or drug-resistance phenotype based on
 CC detectable sequence information. The present sequence is HIV-1 pol2 gene
 CC amplifying primer.
 XX
 SQ Sequence 52 BP; 17 A; 13 C; 9 G; 13 T; 0 U; 0 Other;
 Query Match 61.1%; Score 33; DB 12; Length 52;
 Best Local Similarity 100.0%; Pred. No. 0.003;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTATACGACTCACTATAGGAGACCACA 33
 Db 1 GAAATTATACGACTCACTATAGGAGACCACA 33

RESULT 91
 ABK53137
 ID ABK53137 standard; DNA; 53 BP.
 XX
 AC ABK53137;
 XX
 DT 29-AUG-2003 (revised)
 DT 12-AUG-2002 (first entry)
 XX
 DE HIV-1 protease gene specific oligonucleotide primer #4.
 XX
 XX HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;
 KW reverse transcriptase; infection; PCR.
 XX
 OS Human immunodeficiency virus 1.
 OS
 XX US200205095-A1.
 PN
 XX 09-MAY-2002.
 PD
 XX 31-AUG-2001; 2001US-00944036.
 PF
 XX 01-SEP-2000; 2000US-0229790P.

XX (YANG/) YANG Y Y.
PA (BREN/) BRENTANO S T.
PA (BABO/) BABOLA O.
PA (TRAN/) TRAN N.
PA (VERN/) VERNET G.
PI Yang YV, Brentano ST, Babola O, Tran N, Vernet G;
XX
XX WPI; 2002-462902/49.
DR
XX New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-
PT 1 and probes for detecting the amplified product are specific for gag and
PT pol regions and are useful to detect different subtypes of HIV-1.
XX
PS Claim 1; Page 25; 37pp; English.
XX
XX This invention relates to a series of nucleic acid oligomers for
CC amplifying and detecting a nucleotide sequence of human immunodeficiency
CC virus type 1 (HIV-1). The invention also comprises a labeled
CC oligonucleotide that specifically hybridises to an HIV-1 sequence derived
CC from gag or pol sequences, having one of the sequences fully defined in
CC the specification, and a method for detecting HIV-1 in a biological
CC sample, comprising mixing the sample with two or more of the
CC amplification oligomers that specifically amplify at least one HIV-1
CC target sequence within gag and a pol sequence which is a protease or
CC reverse transcriptase sequence, amplifying the target, and detecting the
CC amplified product. The oligonucleotides of the invention may be used to
CC diagnose HIV-1 infection. The presents sequence represents a PCR primer
CC used to amplify the HIV-1 protease gene in the HIV detection method of
CC the invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
XX Sequence 53 BP; 17 A; 14 C; 9 G; 13 T; 0 U; 0 Other;
SQ
Query Match 61.1%; Score 33; DB 6; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
RESULT 92
AAL45499
ID AAL45499 standard; DNA; 53 BP.
XX
XX AAL45499;
AC
DT 29-AUG-2003 (revised)
DT 06-JUN-2002 (first entry)
XX
DE HIV-1 pol gene protease amplification oligomer SEQ ID NO: 37.
XX
XX HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;
KW probe; ss.
XX
XX Human immunodeficiency virus 1.
OS
OS Enterobacteria phage T7.
XX
XX WO200220852-A1.
XX
XX 14-MAR-2002.
PD
PF 01-SEP-2000; 2000WO-US024117.
XX
XX 01-SEP-2000; 2000WO-US024117.
PR
XX (GENP-) GEN-PROBE INC.
PA (INMR) BIOMERIEUX SA.
XX
XX Yang YV, Brentano ST, Babola O, Tran N, Vernet G;
PI
XX

DR WPI; 2002-292273/33.
XX
XX New nucleic acid oligomer, useful for detecting selected regions of gag
PT and pol genes of human immune deficiency virus, particularly for
PT assessing drug resistance.
XX
PS Claim 1; Page 59; 82pp; English.
XX
XX The present invention provides a number of nucleic acid oligomers which
CC can be used to amplify the gag and pol genes of human immunodeficiency
CC virus type 1 (HIV-1). These are used to detect regions of the gag and pol
CC genes, especially regions associated with drug resistance, and also for
CC identifying genetic subtypes of the virus. The present sequence is an
CC oligomer of the invention. (Updated on 29-AUG-2003 to standardise OS
CC field)
XX
XX Sequence 53 BP; 17 A; 14 C; 9 G; 13 T; 0 U; 0 Other;
SQ
Query Match 61.1%; Score 33; DB 6; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
RESULT 93
ADI18946
ID ADI18946 standard; DNA; 53 BP.
XX
XX ADI18946;
AC
XX
DT 22-APR-2004 (first entry)
DE
DE HIV-1 pol gene amplifying primer #4.
XX
XX Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.
KW
XX Human immunodeficiency virus 1.
OS
XX US2003228574-A1.
XX
XX 11-DEC-2003.
PD
PF 28-APR-2003; 2003US-00425975.
XX
XX 01-SEP-2000; 2000US-0229790P.
PR 31-AUG-2001; 2001US-00944036.
XX
XX (YANG/) YANG Y Y.
PA (BREN/) BRENTANO S T.
PA (BABO/) BABOLA O.
PA (TRAN/) TRAN N.
PA (VERN/) VERNET G.
XX
XX Yang YV, Brentano ST, Babola O, Tran N, Vernet G;
XX
XX WPI; 2004-060998/06.
DR
XX New nucleic acid oligomer for amplifying and detecting HIV-1 nucleotide
PT sequences and in providing information about the infective agent, e.g.
PT genetic subgroup or drug-resistance phenotype based on detectable
PT sequence information.
XX
XX Claim 1; SEQ ID NO 37; 39pp; English.
PS
XX The present invention relates to a nucleic acid oligomer for amplifying a
CC nucleotide sequence of human immune deficiency virus (HIV)-1. The
CC invention is useful in amplifying and detecting HIV-1 nucleic acid
CC sequences and in providing additional information about the infective
CC agent, such as its genetic subgroup or drug-resistance phenotype based on
CC detectable sequence information. The present sequence is HIV-1 pol gene

```

CC amplifying primer.
XX
SQ Sequence 53 BP; 17 A; 14 C; 9 G; 13 T; 0 U; 0 Other;
  Query Match      61.1%; Score 33; DB 12; Length 53;
  Best Local Similarity 100.0%; Pred. No. 0.003;
  Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
   |||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 94
AAQ50482
ID AAQ50482 standard; DNA; 55 BP.
XX
AC AAQ50482;
XX
DT 25-MAR-2003 (revised)
DT 20-MAY-1994 (first entry)
XX
DE Promoter-primer.
XX
KW Mycobacterium tuberculosis; 16S rRNA; promoter-primer; hybridisation;
KW amplification; RNA polymerase; reverse transcriptase; probe;
KW helper probe; ss.
XX
OS Synthetic.
XX
PN WO9322461-Al.
XX
PD 11-NOV-1993.
XX
PF 29-APR-1993; 93WO-US004015.
XX
PR 06-MAY-1992; 92US-00879686.
XX
PA (GENP-) GEN PROBE INC.
XX
PI Kacian DL, Mcallister DL, McDonough SH, Dattagupta N;
XX
DR WPI; 1993-368818/46.
XX
PT Nucleic acid sequence amplification method - utilises RNA polymerase and
PT reverse transcriptase under stable conditions.
XX
PS Claim 56; Page 34; 51pp; English.
XX
CC Promoter-primers with a sequence complementary to the 16S rRNA of
CC Mycobacterium tuberculosis (AAQ50482) were synthesised, either modified
CC with cordycepin or unmodified. These promoter-primers were used to
CC amplify Mycobacterium tuberculosis rRNA. The reaction was assayed with
CC probes (AAQ50483) and helper probes (AAQ50484-85). A mixt. of modified
CC and unmodified promoter primer worked better than completely modified
CC promoter primer. (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 55 BP; 20 A; 18 C; 9 G; 8 T; 0 U; 0 Other;
  Query Match      61.1%; Score 33; DB 2; Length 55;
  Best Local Similarity 100.0%; Pred. No. 0.003;
  Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
   |||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 96
AAQ89910
ID AAQ89910 standard; DNA; 55 BP.
XX
AC AAQ89910;
XX
DT 18-DEC-2000 (first entry)
XX
DE Primer #1 used to generate M.avium rRNA amplicon.
XX
KW Oligonucleotide; probe; nucleic acid detection; ss.
XX
OS Mycobacterium avium.
XX
PN WO200047777-Al.
XX
PD 17-AUG-2000.
XX
PF 11-FEB-2000; 2000WO-US003525.
XX
PR 12-FEB-1999; 99US-0120019P.
XX
PA (GENP-) GEN-PROBE INC.

```

AAQ85669;

25-MAR-2003 (revised)
04-OCT-1995 (first entry)

Promoter primer for Mycobacterium avium rRNA.

Mycobacterium avium; promoter primer; ss.

Synthetic.

WO9506755-Al.

09-MAR-1995.

01-SEP-1994; 94WO-US009902.

03-SEP-1993; 93US-00116984.

(GENP-) GEN-PROBE INC.

Hammond PW;

WPI; 1995-115467/15.

Hybridisation probes for detection and quantification of Mycobacterium avium complex organism - comprise nucleic acid sequences derived from M. avium ribosomal RNA, and distinguish M. avium from other Mycobacterium species.

Example; Page 27; 43pp; English.

rRNA from a clinical isolate of an organism biochemically classified as Mycobacterium avium complex (MAC) but not reactive with AccProbe M. avium or M. intracellulare species- specific probes, was amplified by incubating at 42 degrees C for two hours in 100 microl of a soln. contg. 0.15 microm of a promoter-primer (AAQ85669), and 0.15 microm of a primer (AAQ85970). (Updated on 25-MAR-2003 to correct PN field.)

Sequence 55 BP; 20 A; 18 C; 9 G; 8 T; 0 U; 0 Other;

Query Match 61.1%; Score 33; DB 2; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||

DB 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||

RESULT 96
AAQ89910
ID AAQ89910 standard; DNA; 55 BP.
XX
AC AAQ89910;
XX
DT 18-DEC-2000 (first entry)
XX
DE Primer #1 used to generate M.avium rRNA amplicon.
XX
KW Oligonucleotide; probe; nucleic acid detection; ss.
XX
OS Mycobacterium avium.
XX
PN WO200047777-Al.
XX
PD 17-AUG-2000.
XX
PF 11-FEB-2000; 2000WO-US003525.
XX
PR 12-FEB-1999; 99US-0120019P.
XX
PA (GENP-) GEN-PROBE INC.

```
XX
PI Brentano ST, Mcdonough SH, Nelson NC;
XX
DR WPI; 2000-524543/47.
XX
PT Protective compositions for stabilizing signaling labels on
PT oligonucleotide probes used in nucleic acid amplification reactions.
XX
PS Example 4; Page 29; 6lpp; English.
XX
CC The present invention relates to oligonucleotide probes for detecting the
CC presence of nucleic acids in samples. The method involves compositions
CC made up of detection probe, containing a label susceptible to chemical or
CC enzymatic alteration, and a protection probe. The protection probe
CC protects the label from alteration and/or enhances nucleic acid
CC amplification. The present sequence is a primer used to generate a
CC Mycobacterium avium rRNA amplicon used in an example of the invention
XX
SQ Sequence 55 BP; 20 A; 18 C; 9 G; 8 T; 0 U; 0 Other;
XX
Query Match 61.1%; Score 33; DB 3; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
DB 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
XX
RESULT 97
ABK53144
ID ABK53144 standard; DNA; 55 BP.
XX
AC ABK53144;
XX
DT 29-AUG-2003 (revised)
DT 12-AUG-2002 (first entry)
XX
DE HIV-1 reverse transcriptase gene specific oligonucleotide primer #15.
XX
KW HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;
KW reverse transcriptase; infection; PCR.
XX
OS Human immunodeficiency virus 1.
XX
PN US2002055095-A1.
XX
PD 09-MAY-2002.
XX
PF 31-AUG-2001; 2001US-00944036.
XX
PR 01-SEP-2000; 2000US-0229790P.
XX
PA (YANG/) YANG Y Y.
PA (BREN/) BRENTANO S T.
PA (BBO/) BABOLA O.
PA (TRAN/) TRAN N.
PA (VERN/) VERNET G.
XX
PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX
DR WPI; 2002-462902/49.
XX
PT New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-
PT 1 and probes for detecting the amplified product are specific for gag and
PT pol regions and are useful to detect different subtypes of HIV-1.
XX
PS Claim 1; Page 26; 37pp; English.
XX
CC This invention relates to a series of nucleic acid oligomers for
CC amplifying and detecting a nucleotide sequence of human immunodeficiency
CC virus type 1 (HIV-1). The invention also comprises a labeled
CC oligonucleotide that specifically hybridises to an HIV-1 sequence derived
XX
from gag or pol sequences, having one of the sequences fully defined in
XX the specification, and a method for detecting HIV-1 in a biological
XX sample, comprising mixing the sample with two or more of the
XX amplification oligomers that specifically amplify at least one HIV-1
XX target sequence within gag and a pol sequence which is a protease or
XX reverse transcriptase sequence, amplifying the target, and detecting the
XX amplified product. The oligonucleotides of the invention may be used to
XX diagnose HIV-1 infection. The presents sequence represents a PCR primer
XX used to amplify the HIV-1 reverse transcriptase gene in the HIV detection
XX method of the invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 55 BP; 18 A; 16 C; 9 G; 12 T; 0 U; 0 Other;
XX
Query Match 61.1%; Score 33; DB 6; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
DB 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
XX
RESULT 98
AAL45506
ID AAL45506 standard; DNA; 55 BP.
XX
AC AAL45506;
XX
DT 29-AUG-2003 (revised)
DT 06-JUN-2002 (first entry)
XX
DE HIV-1 pol gene RT amplification oligomer SEQ ID NO: 44.
XX
KW HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;
KW probe; ss.
XX
OS Human immunodeficiency virus 1.
OS Enterobacteria phage T7.
XX
PN WO200220852-A1.
XX
PD 14-MAR-2002.
XX
PF 01-SEP-2000; 2000WO-US024117.
XX
PR 01-SEP-2000; 2000WO-US024117.
XX
PA (GENP-) GEN-PROBE INC.
PA (INNR ) BIOMERIEUX SA.
XX
PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX
DR WPI; 2002-292273/33.
XX
PT New nucleic acid oligomer, useful for detecting selected regions of gag
PT and pol genes of human immune deficiency virus, particularly for
PT assessing drug resistance.
XX
PS Claim 1; Page 61; 82pp; English.
XX
CC The present invention provides a number of nucleic acid oligomers which
CC can be used to amplify the gag and pol genes of human immunodeficiency
CC virus type 1 (HIV-1). These are used to detect regions of the gag and pol
CC genes, especially regions associated with drug resistance, and also for
CC identifying genetic subtypes of the virus. The present sequence is an
CC oligomer of the invention. (Updated on 29-AUG-2003 to standardise OS
CC field)
XX
SQ Sequence 55 BP; 18 A; 16 C; 9 G; 12 T; 0 U; 0 Other;
XX
Query Match 61.1%; Score 33; DB 6; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
 Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 99
 ADI18953
 ID ADI18953 standard; DNA; 55 BP.
 XX
 AC ADI18953;
 DT 22-APR-2004 (first entry)
 XX
 DE HIV-1 pol4 gene amplifying primer #4.
 XX
 KW Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN US2003228574-A1.
 XX
 PD 11-DEC-2003.
 XX
 PF 28-APR-2003; 2003US-00425975.
 XX
 PR 01-SEP-2000; 2000US-0229790P.
 PR 31-AUG-2001; 2001US-00944036.
 XX
 PA (YANG/) YANG Y. Y.
 PA (BREN/) BRENTANO S. T.
 PA (BABO/) BABOLA O.
 PA (TRAN/) TRAN N.
 PA (VERN/) VERNET G.
 XX
 PI Yang Y., Brentano S., Babola O., Tran N., Vernet G;
 XX
 DR WPI; 2004-060998/06.
 XX
 PT New nucleic acid oligomer for amplifying and detecting HIV-1 nucleotide
 PT sequences and in providing information about the infective agent, e.g.
 PT genetic subgroup or drug-resistance phenotype based on detectable
 PT sequence information.
 XX
 PS Claim 1; SEQ ID NO 44; 39pp; English.
 XX
 CC The present invention relates to a nucleic acid oligomer for amplifying a
 CC nucleotide sequence of human immune deficiency virus (HIV)-1. The
 CC invention is useful in amplifying and detecting HIV-1 nucleic acid
 CC sequences and in providing additional information about the infective
 CC agent, such as its genetic subgroup or drug-resistance phenotype based on
 CC detectable sequence information. The present sequence is HIV-1 pol4 gene
 CC amplifying primer.
 XX
 SQ Sequence 55 BP; 18 A; 16 C; 9 G; 12 T; 0 U; 0 Other;
 CC
 CC Query Match 61.1%; Score 33; DB 12; Length 55;
 CC Best Local Similarity 100.0%; Pred. No. 0.003;
 CC Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
 Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 100
 AAA29796/c
 ID AAA29796 standard; DNA; 56 BP.
 XX
 AC AAA29796;
 XX
 DT 06-AUG-2003 (revised)
 DT 17-AUG-2000 (first entry)

XX Plant plasmid expressing human BPI gene construction oligonucleotide #4.
 DE Plant; transgenic; therapeutically active protein; plasmid genome;
 XX vacuole; allergen; vaccine; antiinflammatory; immunosuppressant; allergy;
 KW autoimmune disease; transplant rejection; ss.
 XX
 OS Homo sapiens.
 OS Viridiplantae.
 OS Synthetic.
 XX
 PN WO200020612-A2.
 XX
 PD 13-APR-2000.
 XX
 PF 05-OCT-1999; 99WO-EP007414.
 XX
 PR 07-OCT-1998; 98US-00167362.
 PR 07-OCT-1998; 98US-00168231.
 XX
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX
 PI Helfetz PB, Goff SA, Tuttle AB, Griot-Wenk ME;
 XX
 DR WPI; 2000-328938/28.
 XX
 PT Novel transgenic plants expressing therapeutically active proteins form
 PT their plasmid genome, useful for producing allergens for vaccines.
 XX
 PS Example 30; Page 58; 99pp; English.
 XX
 CC The present invention describes plants (I) comprising a DNA molecule (II)
 CC encoding a protein that is therapeutically active when administered to a
 CC host, in its plasmid genome. The transgenic plants are used to express
 CC therapeutically active proteins, such as antigens, allergens, and
 CC autoantigens. The therapeutically active proteins are used to treat or
 CC prevent diseases, e.g. allergies, autoimmune diseases or transplant
 CC rejection. The invention allows the production of large and inexpensive
 CC supplies of protein-based medications. The plants are able to express
 CC large amounts of proteins in a cost effective manner, and, as the
 CC proteins are packaged in plasmids, they can be isolated easily. The
 CC present sequence represents an oligonucleotide used in the construction
 CC of plant plasmids which express the human BPI gene, which is used in an
 CC example from the present invention. (Updated on 06-AUG-2003 to correct OS
 CC field.)
 XX
 SQ Sequence 56 BP; 12 A; 10 C; 17 G; 17 T; 0 U; 0 Other;
 CC
 CC Query Match 61.1%; Score 33; DB 3; Length 56;
 CC Best Local Similarity 100.0%; Pred. No. 0.003;
 CC Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
 Db 47 GAAATTAATACGACTCACTATAGGAGACCACA 15

Search completed: May 19, 2006, 04:19:07
 Job time : 642.615 secs

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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 02:24:46 ; Search time 3611.49 Seconds
(without alignments)
836.120 Million cell updates/sec

Title: US-10-665-708-11
Perfect score: 54
Sequence: 1 gaataataacgactacta.....tgcgaattatcccaactgc 54

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_hcc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	33.2	61.5	701	7	BE749125
C 2	32	59.3	864	8	CV775907
C 3	31.8	58.9	203	2	BF974085
C 4	31	57.4	188	2	BG475075
C 5	30.8	57.0	681	14	AG002474
C 6	30.8	57.0	687	14	AG002475
C 7	30.8	57.0	688	14	AG002477
C 8	30.4	56.3	815	7	BE278087
C 9	30.2	55.9	143	3	BQ102727
C 10	30.2	55.9	267	3	BQ102748
C 11	30.2	55.9	310	3	BQ102753
C 12	30.2	55.9	329	3	BQ102710
C 13	30.2	55.9	348	3	BQ102721
C 14	30.2	55.9	389	3	BQ102690
C 15	30.2	55.9	393	3	BQ102723
C 16	30.2	55.9	395	3	BQ102707
C 17	30.2	55.9	401	3	BQ102746
C 18	30.2	55.9	427	3	BQ102731
C 19	30.2	55.9	452	3	BQ102670

93	27.8	51.5	737	14	AG409074	Mus muscu	AG409074	Mus muscu	c 166	26.8	49.6	710	9	DN998835	TC107024
94	27.8	51.5	742	14	AG409684	Mus muscu	AG409684	Mus muscu	c 167	26.8	49.6	726	12	CG401341	CG401341 ZMMBB5023
95	27.8	51.5	743	14	AG357071	Mus muscu	AG357071	Mus muscu	c 168	26.8	49.6	733	14	AG410319	AG410319 Mus muscu
96	27.8	51.5	767	14	AG377287	Mus muscu	AG377287	Mus muscu	169	26.8	49.6	733	14	AG447313	AG447313 Mus muscu
c 97	27.6	51.1	874	14	CT010966	KBH118G0	CT010966	KBH118G0	170	26.8	49.6	734	14	AG399888	AG399888 Mus muscu
c 98	27.6	51.1	897	13	CW946685	TCB29.4.A	CW946685	TCB29.4.A	171	26.8	49.6	734	14	AG412507	AG412507 Mus muscu
c 99	27.4	50.7	317	11	BH501537	BOHS275TF	BH501537	BOHS275TF	172	26.8	49.6	735	14	AG366167	AG366167 Mus muscu
100	27.4	50.7	317	11	BH523081	BOGJM68TF	BH523081	BOGJM68TF	173	26.8	49.6	737	14	AG406199	AG406199 Mus muscu
101	27.4	50.7	325	11	BH595583	BOHGG16TF	BH595583	BOHGG16TF	174	26.8	49.6	737	14	AG422762	AG422762 Mus muscu
c 102	27.4	50.7	509	11	BH394191	AG-ND-147	BH394191	AG-ND-147	175	26.8	49.6	737	14	AG365736	AG365736 Mus muscu
c 103	27.4	50.7	560	12	CG968661	BOIFL85TR	CG968661	BOIFL85TR	176	26.8	49.6	754	14	AG378413	AG378413 Mus muscu
c 104	27.4	50.7	571	12	CG964269	BOIFEN76TR	CG964269	BOIFEN76TR	177	26.8	49.6	755	14	AG358595	AG358595 Mus muscu
c 105	27.4	50.7	582	11	BH381251	AG-ND-146	BH381251	AG-ND-146	178	26.8	49.6	758	14	AG382943	AG382943 Mus muscu
c 106	27.4	50.7	585	12	CG947693	BOIEQA1TR	CG947693	BOIEQA1TR	179	26.8	49.6	770	14	AG357529	AG357529 Mus muscu
c 107	27.4	50.7	592	12	CG961654	BOIDB28TR	CG961654	BOIDB28TR	c 180	26.8	49.6	882	13	CW942653	CW942653 TCB24.2.A
c 108	27.4	50.7	604	12	CG952121	BOIFB18TR	CG952121	BOIFB18TR	c 181	26.8	49.6	882	13	CW771324	CW771324 FGAS06571
c 109	27.4	50.7	610	12	CG948768	BOIDG32TR	CG948768	BOIDG32TR	c 182	26.8	49.6	952	13	CW938071	CW938071 TCB17.4.B
c 110	27.4	50.7	612	12	CG947463	BOIGK06TR	CG947463	BOIGK06TR	c 183	26.8	49.6	962	13	CW953281	CW953281 TCB39.2.C
c 111	27.4	50.7	612	13	CL703442	SP_B5000	CL703442	SP_B5000	c 184	26.8	49.6	1217	12	CL025113	CL025113 CH216-21C
c 112	27.4	50.7	617	12	CG967304	BOIFK41TR	CG967304	BOIFK41TR	c 185	26.6	49.3	116	8	CV605216	CV605216 L_AH-aaal
c 113	27.4	50.7	619	11	BH394119	AG-ND-160	BH394119	AG-ND-160	c 186	26.6	49.3	116	8	CV605332	CV605332 L_AH-aaal
c 114	27.4	50.7	621	12	CG968451	BOIFB27TR	CG968451	BOIFB27TR	c 187	26.6	49.3	423	11	AZ301311	AZ301311 UP_315-19
c 115	27.4	50.7	642	12	CG944751	BOIFB01TR	CG944751	BOIFB01TR	c 188	26.6	49.3	464	11	AZ301337	AZ301337 UP_294-4G
c 116	27.4	50.7	642	12	CG946396	BOICQ54TR	CG946396	BOICQ54TR	c 189	26.6	49.3	491	11	AQ139170	AQ139170 HS_3080.B
c 117	27.4	50.7	644	12	CG949404	BOIGZ19TR	CG949404	BOIGZ19TR	c 190	26.6	49.3	528	5	CD609671	CD609671 55110515H
c 118	27.4	50.7	644	12	CG951454	BOIEA52TR	CG951454	BOIEA52TR	c 191	26.6	49.3	528	5	CD609679	CD609679 55110555H
c 119	27.4	50.7	649	12	CG928886	BOIGN54TR	CG928886	BOIGN54TR	c 192	26.6	49.3	695	14	AG366198	AG366198 Mus muscu
c 120	27.4	50.7	651	12	CG961061	BOICX68TR	CG961061	BOICX68TR	c 193	26.6	49.3	701	14	AG385370	AG385370 Mus muscu
c 121	27.4	50.7	657	5	CD625576	55147834H	CD625576	55147834H	c 194	26.6	49.3	702	14	AG398017	AG398017 Mus muscu
c 122	27.4	50.7	684	12	CG945503	BOIDK74TR	CG945503	BOIDK74TR	c 195	26.6	49.3	720	14	AG397487	AG397487 Mus muscu
c 123	27.4	50.7	687	12	CG948738	BOIFI28TR	CG948738	BOIFI28TR	c 196	26.6	49.3	720	14	AG434424	AG434424 Mus muscu
c 124	27.4	50.7	688	12	CG944195	BOIBL59TR	CG944195	BOIBL59TR	c 197	26.6	49.3	733	14	AG424477	AG424477 Mus muscu
c 125	27.4	50.7	693	12	CG944485	BOIHL39TR	CG944485	BOIHL39TR	c 198	26.6	49.3	733	14	AG427858	AG427858 Mus muscu
c 126	27.4	50.7	705	12	CG951566	BOIEJ65TR	CG951566	BOIEJ65TR	c 199	26.6	49.3	740	14	AG398077	AG398077 Mus muscu
c 127	27.4	50.7	705	12	CG958824	BOIBM11TR	CG958824	BOIBM11TR	c 200	26.6	49.3	744	14	AG539556	AG539556 Mus muscu
c 128	27.4	50.7	718	12	CG954347	BOIBW60TR	CG954347	BOIBW60TR	c 201	26.6	49.3	751	14	AG376751	AG376751 Mus muscu
c 129	27.4	50.7	719	12	CG968802	BOICJ62TR	CG968802	BOICJ62TR	c 202	26.6	49.3	754	14	AG360113	AG360113 Mus muscu
c 130	27.4	50.7	727	12	CG969001	BOICR93TR	CG969001	BOICR93TR	c 203	26.6	49.3	764	14	AG392794	AG392794 Mus muscu
c 131	27.4	50.7	735	12	CG958105	BOIGX30TR	CG958105	BOIGX30TR	c 204	26.6	49.3	764	14	AG591873	AG591873 Mus muscu
c 132	27.4	50.7	735	12	CG961701	BOIDQ39TR	CG961701	BOIDQ39TR	c 205	26.6	49.3	768	5	CD632807	CD632807 55148215H
c 133	27.4	50.7	741	13	CG641742	OA_ABA017	CG641742	OA_ABA017	c 206	26.6	49.3	775	14	AG603308	AG603308 Mus muscu
c 134	27.4	50.7	806	11	BH381710	AG-ND-150	BH381710	AG-ND-150	c 207	26.6	49.3	799	14	AG292790	AG292790 Mus muscu
c 135	27.4	50.7	811	14	AG406886	Mus muscu	AG406886	Mus muscu	c 208	26.6	49.3	828	14	AG292507	AG292507 Mus muscu
c 136	27.4	50.7	830	12	CG953502	BOIGT40TR	CG953502	BOIGT40TR	c 209	26.6	49.3	839	13	CW939353	CW939353 TCB19.3.G
c 137	27.4	50.7	830	12	CG968053	BOICE19TR	CG968053	BOICE19TR	c 210	26.6	48.9	268	12	CC948310	CC948310 BOIHE34TR
c 138	27.4	50.7	859	12	CG958532	BOIFG34TR	CG958532	BOIFG34TR	c 211	26.4	48.9	278	12	CC944849	CC944849 BOIHM72TR
c 139	27.4	50.7	868	13	CW939269	TCB19.3.D	CW939269	TCB19.3.D	c 212	26.4	48.9	279	12	CC945126	CC945126 BOIHM57TR
c 140	27.4	50.7	926	13	CW942725	TCB24.2.D	CW942725	TCB24.2.D	c 213	26.4	48.9	287	12	CC944569	CC944569 BOIDK73TR
c 141	27.2	50.4	279	10	DR974592	CHUT006G0	DR974592	CHUT006G0	c 214	26.4	48.9	291	12	CC953980	CC953980 BOICZ11TR
c 142	27.2	50.4	409	5	CD637299	55140618J	CD637299	55140618J	c 215	26.4	48.9	292	12	CC964479	CC964479 BOIDC94TR
c 143	27.2	50.4	516	13	DU277966	109844808	DU277966	109844808	c 216	26.4	48.9	292	12	CC964865	CC964865 BOIDC94TR
c 144	27.2	50.4	724	14	AG369244	Mus muscu	AG369244	Mus muscu	c 217	26.4	48.9	292	12	CC966120	CC966120 BOIC236TR
c 145	27.2	50.4	727	14	AG277281	Mus muscu	AG277281	Mus muscu	c 218	26.4	48.9	294	12	CC963072	CC963072 BOIGV85TR
c 146	27.2	50.4	748	14	AG605379	Mus muscu	AG605379	Mus muscu	c 219	26.4	48.9	298	11	BH705477	BH705477 BOMLD11TF
c 147	27.2	50.4	751	14	AG392816	Mus muscu	AG392816	Mus muscu	c 220	26.4	48.9	299	12	CC964673	CC964673 BOIFQ34TR
c 148	27.2	50.4	761	14	AG426744	Mus muscu	AG426744	Mus muscu	c 221	26.4	48.9	337	12	CC948300	CC948300 BOIHE34TF
c 149	27.2	50.4	773	14	AG378000	Mus muscu	AG378000	Mus muscu	c 222	26.4	48.9	340	12	CC946725	CC946725 BOIHM57TF
c 150	27.2	50.4	811	14	AG378000	Mus muscu	AG378000	Mus muscu	c 223	26.4	48.9	341	12	CC949245	CC949245 BOIHM72TF
c 151	27.2	50.4	917	13	CW942801	TCB24.2.G	CW942801	TCB24.2.G	c 224	26.4	48.9	341	12	CC963910	CC963910 BOIGP84TF
c 152	27.2	50.4	140	9	D42398	D42398	D42398	D42398	c 225	26.4	48.9	341	12	CC963910	CC963910 BOIGP84TF
c 153	27.2	50.4	158	9	D42400	D42400	D42400	D42400	c 226	26.4	48.9	346	12	CC947981	CC947981 BOIFE48TF
c 154	27.2	50.4	234	9	D42230	D42230	D42230	D42230	c 227	26.4	48.9	350	12	CC964858	CC964858 BOIDC32TF
c 155	27.2	50.4	274	9	D42362	D42362	D42362	D42362	c 228	26.4	48.9	351	12	CC966108	CC966108 BOIC236TF
c 156	27.2	50.4	281	9	D42335	D42335	D42335	D42335	c 229	26.4	48.9	354	12	CC964561	CC964561 BOIDK73TF
c 157	27.2	50.4	336	9	D42342	D42342	D42342	D42342	c 230	26.4	48.9	367	12	CC964475	CC964475 BOIDC94TF
c 158	27.2	50.4	397	8	CV583227	L_AJ-aaal	CV583227	L_AJ-aaal	c 231	26.4	48.9	368	12	CC949181	CC949181 BOICR29TF
c 159	27.2	50.4	397	11	Q5185139	HS_3022.B	Q5185139	HS_3022.B	c 232	26.4	48.9	369	12	CC959582	CC959582 BOIFU74TF
c 160	27.2	50.4	488	8	AG165139	Mus muscu	AG165139	Mus muscu	c 233	26.4	48.9	371	12	CC967226	CC967226 BOIBS28TF
c 161	27.2	50.4	725	14	AG391229	Mus muscu	AG391229	Mus muscu	c 234	26.4	48.9	371	12	CC963061	CC963061 BOIGV85TF
c 162	27.2	50.4	795	14	AG416065	Mus muscu	AG416065	Mus muscu	c 235	26.4	48.9	373	12	CC953969	CC953969 BOICZ11TF
c 163	26.8	49.6	163	8	CN655972	LCM003J.C	CN655972	LCM003J.C	c 236	26.4	48.9	373	12	CC967455	CC967455 BOLET15TF
c 164	26.8	49.6	601	12	CG401357	ZMMBB5023	CG401357	ZMMBB5023	c 237	26.4	48.9	375	12	CC944054	CC944054 BOIBS39TF
c 165	26.8	49.6	759	12	CG401365	ZMMBB5023	CG401365	ZMMBB5023	c 238	26.4	48.9	386	1	AA514191	AA514191 HFUEST-74

RESULT 1	LOCUS	DEFINITION	ACCESSION
----------	-------	------------	-----------

1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033

Email: fgas_estseqs.usask.ca

This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [95,663].

Plate: WEF085 row: K column: 23.

Location/Qualifiers

FEATURES

source

1..864

/organism="Triticum aestivum"

/mol_type="mRNA"

/db_xref="taxon:4565"

/clone_lib="Triticum aestivum FGAS: Library 2 Gate 3"
/note="Organ: Crown and leaf; Vector: pCMV.SPORT6; Aerial
parts (crown and leaf) of wheat cultivar Norstar from
control and long exposure times to low temperature. 4 mRNA
populations were combined before constructing the library;
7 days non-acclimated plants and 1, 23, and 53 days
cold-acclimated at 4C. Non-acclimated and cold-acclimated
plants were grown in vermiculite This is the only library
that was done according to the Invitrogen manual, and
therefore, a percentage of clones will not have the 3
prime end because of NotI digestion within the cDNA."

ORIGIN

Query Match 59.3%; Score 32; DB 8; Length 864;

Best Local Similarity 87.5%; Pred. No. 0.29;

Matches 35; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 4 ATTAATACGACTCTACTATAGGAGACCAATGTGCAATA 43

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Db 821 AATAATACGACTCTACTATAGGGGACCCTTTGTACAAGA 782

RESULT 3

BF974085/c

LOCUS

DEFINITION 602240343F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4328843 5',

mRNA sequence.

ACCESSION BF974085

VERSION BF974085.1 GI:12341300

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 203)

NIH-MGC http://mgc.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1189 row: f column: 12

High quality sequence start: 59

High quality sequence stop: 155.

Location/Qualifiers

1..203

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4328843"

/tissue_type="leiomyosarcoma cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_46"

/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:

GGCACGAG(G). Size-selected >500bp for average insert size

1.8kb. Library constructed by Ling Hong in the laboratory

of Gerald M. Rubin (University of California, Berkeley)

using ZAP-cDNA synthesis kit (Stratagene) and Superscript

II RT (Life Technologies). Note: this is a NIH_MGC

Library."

ORIGIN

Query Match 58.9%; Score 31.8; DB 2; Length 203;

Best Local Similarity 94.3%; Pred. No. 0.29;

Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GAAATTAATACGACTCTACTATAGGAGACCAATT 35

|||||

Db 131 GAAATTAATACGACTCTACTATAGGAGACCAATT 97

RESULT 4

BG475075/c

LOCUS

DEFINITION 602491094F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4620071 5',

mRNA sequence.

ACCESSION BG475075

VERSION BG475075.1 GI:13407352

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 188)

NIH-MGC http://mgc.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/BCRD/Drp

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1380 row: 1 column: 24

High quality sequence stop: 100.

Location/Qualifiers

1..188

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4620071"

/tissue_type="melanotic melanoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_20"

/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 57.4%; Score 31; DB 2; Length 188;

Best Local Similarity 100.0%; Pred. No. 0.57;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GAAATTAATACGACTCACTATAGGAGACCA 31
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Db 67 GAAATTAATACGACTCACTATAGGAGACCA 37

RESULT 5
AG002474/c
LOCUS      Homo sapiens genomic DNA, 681 bp      DNA      linear      GSS 16-FEB-2005
DEFINITION Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic
survey sequence.
ACCESSION  AG002474
VERSION     AG002474.2  GI:55786605
KEYWORDS   GSS.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1
AUTHORS    Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE      Homo sapiens genomic DNA, chromosome 21q
JOURNAL    Published Only in Database (1997)
REFERENCE   2
AUTHORS    Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE      Direct Submission
JOURNAL    Submitted (21-NOV-1997) Mashira Hattori, RIKEN Genomic Sciences
Center, RIKEN Yokohama Institute, Yokohama Research Promotion
Division; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa,
230-0045, Japan (E-mail:hattori@gsc.riken.jp, Tel:81-45-503-9111,
Fax:81-45-503-9113)
COMMENT    On Nov 16, 2004 this sequence version replaced gi:2641771.
FEATURES   Location/Qualifiers
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                        /mol_type="genomic DNA"
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                        /chromosome="21"
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                        /clone="Q82F5A16"

ORIGIN
Query Match      57.0%; Score 30.8; DB 14; Length 681;
Best Local Similarity 76.0%; Pred. No. 0.82;
Matches 38; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCAATTGTGCAATATTCCTCCA 50
   |||||
Db 218 GAAATTAATACGACTCACTATAGGAGACCAAGCTTAGGATCTTGACA 169

RESULT 6
AG002475/c
LOCUS      Homo sapiens genomic DNA, 687 bp      DNA      linear      GSS 16-FEB-2005
DEFINITION Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic
survey sequence.
ACCESSION  AG002475
VERSION     AG002475.2  GI:55786606
KEYWORDS   GSS.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1
AUTHORS    Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE      Homo sapiens genomic DNA, chromosome 21q
JOURNAL    Published Only in Database (1997)
REFERENCE   2
AUTHORS    Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE      Direct Submission
JOURNAL    Submitted (21-NOV-1997) Mashira Hattori, RIKEN Genomic Sciences
Center, RIKEN Yokohama Institute, Yokohama Research Promotion
Division; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa,
230-0045, Japan (E-mail:hattori@gsc.riken.jp, Tel:81-45-503-9111,
Fax:81-45-503-9113)
COMMENT    On Nov 16, 2004 this sequence version replaced gi:2641771.
FEATURES   Location/Qualifiers
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                        /clone="Q82F5A16"

ORIGIN
Query Match      57.0%; Score 30.8; DB 14; Length 681;
Best Local Similarity 76.0%; Pred. No. 0.82;
Matches 38; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCAATTGTGCAATATTCCTCCA 50
   |||||
Db 218 GAAATTAATACGACTCACTATAGGAGACCAAGCTTAGGATCTTGACA 169

RESULT 6
AG002475/c
LOCUS      Homo sapiens genomic DNA, 687 bp      DNA      linear      GSS 16-FEB-2005
DEFINITION Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic
survey sequence.
ACCESSION  AG002475
VERSION     AG002475.2  GI:55786606
KEYWORDS   GSS.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1
AUTHORS    Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE      Homo sapiens genomic DNA, chromosome 21q
JOURNAL    Published Only in Database (1997)
REFERENCE   2
AUTHORS    Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE      Direct Submission
JOURNAL    Submitted (21-NOV-1997) Mashira Hattori, RIKEN Genomic Sciences
Center, RIKEN Yokohama Institute, Yokohama Research Promotion
Division; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa,
230-0045, Japan (E-mail:hattori@gsc.riken.jp, Tel:81-45-503-9111,
Fax:81-45-503-9113)
COMMENT    On Nov 16, 2004 this sequence version replaced gi:2641772.
FEATURES   Location/Qualifiers
            source          1..687
                        /organism="Homo sapiens"
                        /mol_type="genomic DNA"
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                        /chromosome="21"
                        /map="21q22.1"
                        /clone="Q82F5A16"

ORIGIN
Query Match      57.0%; Score 30.8; DB 14; Length 687;
Best Local Similarity 76.0%; Pred. No. 0.82;
Matches 38; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCAATTGTGCAATATTCCTCCA 50
   |||||
Db 216 GAAATTAATACGACTCACTATAGGAGACCAAGCTTAGGATCTTGACA 167

RESULT 7
AG002477/c
LOCUS      Homo sapiens genomic DNA, 688 bp      DNA      linear      GSS 16-FEB-2005
DEFINITION Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic
survey sequence.
ACCESSION  AG002477
VERSION     AG002477.1  GI:2641774
KEYWORDS   GSS.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1
AUTHORS    Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE      Homo sapiens genomic DNA, chromosome 21q
JOURNAL    Published Only in Database (1997)
REFERENCE   2
AUTHORS    Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE      Direct Submission
JOURNAL    Submitted (21-NOV-1997) Masahira Hattori, RIKEN Genomic Sciences
Center, RIKEN Yokohama Institute, Yokohama Research Promotion
Division; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa,
230-0045, Japan (E-mail:hattori@gsc.riken.jp, Tel:81-45-503-9111,
Fax:81-45-503-9113)
FEATURES   Location/Qualifiers
            source          1..688
                        /organism="Homo sapiens"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9606"
                        /chromosome="21"
                        /map="21q22.1"
                        /clone="Q82F5A16"

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Query Match      57.0%; Score 30.8; DB 14; Length 688;
Best Local Similarity 76.0%; Pred. No. 0.82;
Matches 38; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCAATTGTGCAATATTCCTCCA 50
   |||||
Db 217 GAAATTAATACGACTCACTATAGGAGACCAAGCTTAGGATCTTGACA 168

RESULT 8
BE278087/c
LOCUS      BE278087
DEFINITION 601179624F1 NIH MGC_21 Homo sapiens cDNA clone IMAGE:3546485 5',
mRNA sequence.
ACCESSION  BE278087

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Qy 1 GAAATTAATACGACTCACTATAGGAGACCA 31
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Db 67 GAAATTAATACGACTCACTATAGGAGACCA 37

RESULT 5
AG002474/c
LOCUS      Homo sapiens genomic DNA, 681 bp      DNA      linear      GSS 16-FEB-2005
DEFINITION Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic
survey sequence.
ACCESSION  AG002474
VERSION     AG002474.2 GI:55786605
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE   1
AUTHORS     Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE       Homo sapiens genomic DNA, chromosome 21q
JOURNAL     Published Only in Database (1997)
REFERENCE   2 (bases 1 to 681)
AUTHORS     Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE       Direct Submission
JOURNAL     Submitted (21-NOV-1997) Mashira Hattori, RIKEN Genomic Sciences
            Center, RIKEN Yokohama Institute, Yokohama Research Promotion
            Division; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa,
            230-0045, Japan (E-mail:hattori@gsc.riken.jp, Tel:81-45-503-9111,
            Fax:81-45-503-9113)
COMMENT     On Nov 16, 2004 this sequence version replaced gi:2641771.
FEATURES    Location/Qualifiers
             source          1..681
                        /organism="Homo sapiens"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9606"
                        /chromosome="21"
                        /map="21q22.1"
                        /clone="Q82F5A16"

ORIGIN
Query Match      57.0%; Score 30.8; DB 14; Length 681;
Best Local Similarity 76.0%; Pred. No. 0.82;
Matches 38; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCAATTCGCAATATTCCTCCCA 50
   |||||
Db 218 GAAATTAATACGACTCACTATAGGAGACCAAGCTTAGGATCTTGACA 169

RESULT 6
AG002475/c
LOCUS      Homo sapiens genomic DNA, 687 bp      DNA      linear      GSS 16-FEB-2005
DEFINITION Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic
survey sequence.
ACCESSION  AG002475
VERSION     AG002475.2 GI:55786606
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE   1
AUTHORS     Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE       Homo sapiens genomic DNA, chromosome 21q
JOURNAL     Published Only in Database (1997)
REFERENCE   2 (bases 1 to 687)
AUTHORS     Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE       Direct Submission
JOURNAL     Submitted (21-NOV-1997) Mashira Hattori, RIKEN Genomic Sciences
            Center, RIKEN Yokohama Institute, Yokohama Research Promotion
            Division; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa,
            230-0045, Japan (E-mail:hattori@gsc.riken.jp, Tel:81-45-503-9111,
            Fax:81-45-503-9113)
COMMENT     On Nov 16, 2004 this sequence version replaced gi:2641771.
FEATURES    Location/Qualifiers
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                        /chromosome="21"
                        /map="21q22.1"
                        /clone="Q82F5A16"

ORIGIN
Query Match      57.0%; Score 30.8; DB 14; Length 687;
Best Local Similarity 76.0%; Pred. No. 0.82;
Matches 38; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCAATTCGCAATATTCCTCCCA 50
   |||||
Db 218 GAAATTAATACGACTCACTATAGGAGACCAAGCTTAGGATCTTGACA 169

RESULT 7
AG002477/c
LOCUS      Homo sapiens genomic DNA, 688 bp      DNA      linear      GSS 16-FEB-2005
DEFINITION Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic
survey sequence.
ACCESSION  AG002477
VERSION     AG002477.1 GI:2641774
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE   1
AUTHORS     Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE       Homo sapiens genomic DNA, chromosome 21q
JOURNAL     Published Only in Database (1997)
REFERENCE   2 (bases 1 to 688)
AUTHORS     Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE       Direct Submission
JOURNAL     Submitted (21-NOV-1997) Masahira Hattori, RIKEN Genomic Sciences
            Center, RIKEN Yokohama Institute, Yokohama Research Promotion
            Division; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa,
            230-0045, Japan (E-mail:hattori@gsc.riken.jp, Tel:81-45-503-9111,
            Fax:81-45-503-9113)
COMMENT     On Nov 16, 2004 this sequence version replaced gi:2641772.
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                        /mol_type="genomic DNA"
                        /db_xref="taxon:9606"
                        /chromosome="21"
                        /map="21q22.1"
                        /clone="Q82F5A16"

ORIGIN
Query Match      57.0%; Score 30.8; DB 14; Length 688;
Best Local Similarity 76.0%; Pred. No. 0.82;
Matches 38; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCAATTCGCAATATTCCTCCCA 50
   |||||
Db 217 GAAATTAATACGACTCACTATAGGAGACCAAGCTTAGGATCTTGACA 168

RESULT 8
BE278087/c
LOCUS      Homo sapiens genomic DNA, 685 bp      mRNA      linear      EST 13-JUL-2000
DEFINITION Homo sapiens genomic DNA, clone IMAGE:3546485 5',
mRNA sequence.
ACCESSION  BE278087

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VERSION BE278087.1 GI:9153063
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM244 row: P column: 06
High quality sequence stop: 99.
FEATURES
source
1..815
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3546485"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 21"
/note="Organ: placenta; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN
Query Match 56.3%; Score 30.4; DB 7; Length 815;
Best Local Similarity 96.9%; Pred. No. 1.2;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCAC 32
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Db 63 GAAATTAATACGACTCACTATAGGAGACCAC 32

RESULT 9
BQ102727/c
LOCUS BQ102727 143 bp mRNA linear EST 12-APR-2002
DEFINITION UGC0111 Drosophila 8-12 hr embryonic cDNA library Drosophila
melanogaster cDNA 5', mRNA sequence.
ACCESSION BQ102727
VERSION BQ102727.1 GI:20144210
KEYWORDS EST.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 143)
REFERENCE Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B.,
AUTHORS Metherall,J.E. and Letsou,A.
TITLE An automated screen for spatially restricted transcripts in
Drosophila embryogenesis
JOURNAL Genome Res. (2002) In press
COMMENT Department of Human Genetics
Eccles Institute of Human Genetics, University of Utah
15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA
Tel: 801 581-4422

Qy 1 GAAATTAATACGACTCACTATAGGAGACCAC 32
|||||
Db 63 GAAATTAATACGACTCACTATAGGAGACCAC 32

RESULT 9
BQ102727/c
LOCUS BQ102727 143 bp mRNA linear EST 12-APR-2002
DEFINITION UGC0111 Drosophila 8-12 hr embryonic cDNA library Drosophila
melanogaster cDNA 5', mRNA sequence.
ACCESSION BQ102727
VERSION BQ102727.1 GI:20144210
KEYWORDS EST.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 143)
REFERENCE Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B.,
AUTHORS Metherall,J.E. and Letsou,A.
TITLE An automated screen for spatially restricted transcripts in
Drosophila embryogenesis
JOURNAL Genome Res. (2002) In press
COMMENT Department of Human Genetics
Eccles Institute of Human Genetics, University of Utah
15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA
Tel: 801 581-4422

us-10-665-708-11.rst
Fax: 801 581-7796
Email: aletsou@genetics.utah.edu
Seq primer: SP6.
Location/Qualifiers
1..143
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/dev_stage="embryonic 8-12 hr post-fertilization"
/clone_lib="Drosophila 8-12 hr embryonic cDNA library"
/note="Vector: plasmid pNB; see Brown, N.H. and Kafatos,
F.C. (1988) Functional cDNA libraries from Drosophila
embryos. J. Mol Biol. 203, 425-37."
ORIGIN
Query Match 55.9%; Score 30.2; DB 3; Length 143;
Best Local Similarity 91.4%; Pred. No. 1.1;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACATT 35
|||||
Db 48 GAAATTAATACGACTCACTATAGGAGACCGGAAT 14

RESULT 10
BQ102748/c
LOCUS BQ102748 267 bp mRNA linear EST 12-APR-2002
DEFINITION UGC0132 Drosophila 8-12 hr embryonic cDNA library Drosophila
melanogaster cDNA 5', mRNA sequence.
ACCESSION BQ102748
VERSION BQ102748.1 GI:20144231
KEYWORDS EST.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 267)
REFERENCE Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B.,
AUTHORS Metherall,J.E. and Letsou,A.
TITLE An automated screen for spatially restricted transcripts in
Drosophila embryogenesis
JOURNAL Genome Res. (2002) In press
COMMENT Department of Human Genetics
Eccles Institute of Human Genetics, University of Utah
15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA
Tel: 801 581-4422
Fax: 801 581-7796
Email: aletsou@genetics.utah.edu
Seq primer: SP6.
Location/Qualifiers
1..267
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/mol_type="mRNA"
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/dev_stage="embryonic 8-12 hr post-fertilization"
/clone_lib="Drosophila 8-12 hr embryonic cDNA library"
/note="Vector: plasmid pNB; see Brown, N.H. and Kafatos,
F.C. (1988) Functional cDNA libraries from Drosophila
embryos. J. Mol Biol. 203, 425-37."
ORIGIN
Query Match 55.9%; Score 30.2; DB 3; Length 267;
Best Local Similarity 91.4%; Pred. No. 1.2;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACATT 35
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Db 57 GAAATTAATACGACTCACTATAGGAGACCGGAAT 23

RESULT 11

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BQ102753/c
LOCUS          BQ102753      310 bp      mRNA      linear      EST 12-APR-2002
DEFINITION     UUGC0137 Drosophila 8-12 hr embryonic cDNA library Drosophila
ACCESSION      BQ102753
VERSION        BQ102753.1  GI:20144236
KEYWORDS       EST.
ORGANISM       Drosophila melanogaster (fruit fly)
SOURCE         Drosophila melanogaster
  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
  Ephydroidea; Drosophilidae; Drosophila.
  1 (bases 1 to 310)
REFERENCE      Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B.,
AUTHORS        Metherall,J.E. and Letsou,A.
TITLE          An automated screen for spatially restricted transcripts in
JOURNAL        Drosophila embryogenesis
COMMENT        Genome Res. (2002) In press
               Contact: Letsou, A.
               Department of Human Genetics
               Eccles Institute of Human Genetics, University of Utah
               15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA
               Tel: 801 581-4422
               Fax: 801 581-7796
               Email: aletsou@genetics.utah.edu
Seq primer: SP6.
Location/Qualifiers
  1..310
   /organism="Drosophila melanogaster"
   /mol_type="mRNA"
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   /dev_stage="embryonic 8-12 hr post-fertilization"
   /clone_lib="Drosophila 8-12 hr embryonic cDNA library"
   /note="Vector: plasmid pNB; see Brown, N.H. and Kafatos,
F.C. (1988) Functional cDNA libraries from Drosophila
embryos. J. Mol Biol. 203, 425-37."

ORIGIN
Query Match          55.9%; Score 30.2; DB 3; Length 310;
Best Local Similarity 91.4%; Pred. No. 1.2;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACTT 35
    |||||||
Db 43 GAAATTAATACGACTCACTATAGGAGACCGGAAT 9

RESULT 12
BQ102710/c
LOCUS          BQ102710      329 bp      mRNA      linear      EST 12-APR-2002
DEFINITION     UUGC0094 Drosophila 8-12 hr embryonic cDNA library Drosophila
ACCESSION      BQ102710
VERSION        BQ102710.1  GI:20144193
KEYWORDS       EST.
ORGANISM       Drosophila melanogaster (fruit fly)
SOURCE         Drosophila melanogaster
  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
  Ephydroidea; Drosophilidae; Drosophila.
  1 (bases 1 to 329)
REFERENCE      Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B.,
AUTHORS        Metherall,J.E. and Letsou,A.
TITLE          An automated screen for spatially restricted transcripts in
JOURNAL        Drosophila embryogenesis
COMMENT        Genome Res. (2002) In press
               Contact: Letsou, A.
               Department of Human Genetics
               Eccles Institute of Human Genetics, University of Utah
               15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA
               Tel: 801 581-4422
               Fax: 801 581-7796
               Email: aletsou@genetics.utah.edu

ORIGIN
Query Match          55.9%; Score 30.2; DB 3; Length 310;
Best Local Similarity 91.4%; Pred. No. 1.2;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACTT 35
    |||||||
Db 43 GAAATTAATACGACTCACTATAGGAGACCGGAAT 9

RESULT 13
BQ102721/c
LOCUS          BQ102721      348 bp      mRNA      linear      EST 12-APR-2002
DEFINITION     UUGC0105 Drosophila 8-12 hr embryonic cDNA library Drosophila
ACCESSION      BQ102721
VERSION        BQ102721.1  GI:20144204
KEYWORDS       EST.
ORGANISM       Drosophila melanogaster (fruit fly)
SOURCE         Drosophila melanogaster
  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
  Ephydroidea; Drosophilidae; Drosophila.
  1 (bases 1 to 348)
REFERENCE      Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B.,
AUTHORS        Metherall,J.E. and Letsou,A.
TITLE          An automated screen for spatially restricted transcripts in
JOURNAL        Drosophila embryogenesis
COMMENT        Genome Res. (2002) In press
               Contact: Letsou, A.
               Department of Human Genetics
               Eccles Institute of Human Genetics, University of Utah
               15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA
               Tel: 801 581-4422
               Fax: 801 581-7796
               Email: aletsou@genetics.utah.edu
Seq primer: SP6.
Location/Qualifiers
  1..348
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   /mol_type="mRNA"
   /db_xref="taxon:7227"
   /dev_stage="embryonic 8-12 hr post-fertilization"
   /clone_lib="Drosophila 8-12 hr embryonic cDNA library"
   /note="Vector: plasmid pNB; see Brown, N.H. and Kafatos,
F.C. (1988) Functional cDNA libraries from Drosophila
embryos. J. Mol Biol. 203, 425-37."

ORIGIN
Query Match          55.9%; Score 30.2; DB 3; Length 348;
Best Local Similarity 91.4%; Pred. No. 1.3;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACTT 35
    |||||||
Db 48 GAAATTAATACGACTCACTATAGGAGACCGGAAT 14

RESULT 14
BQ102690/c
LOCUS          BQ102690      389 bp      mRNA      linear      EST 12-APR-2002

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DEFINITION UUGC0071 Drosophila 8-12 hr embryonic cDNA library Drosophila melanogaster cDNA 5', mRNA sequence.

ACCESSION BQ102690
VERSION BQ102690.1
KEYWORDS GI:20144173
SOURCE EST.

ORGANISM Drosophila melanogaster (fruit fly)

DESCRIPTION Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 389)

REFERENCE 1. (bases 1 to 389)
AUTHORS Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B., Metherall,J.E. and Letsou,A.

TITLE An automated screen for spatially restricted transcripts in Drosophila embryogenesis

JOURNAL Genome Res. (2002) In press

COMMENT Contact: Letsou, A.

Department of Human Genetics

Eccles Institute of Human Genetics, University of Utah

15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA

Tel: 801 581-4422

Fax: 801 581-7796

Email: aletsou@genetics.utah.edu

Seq primer: SP6.

FEATURES Location/Qualifiers

source
1..389
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/dev_stage="embryonic 8-12 hr post-fertilization"
/clone_lib="Drosophila 8-12 hr embryonic cDNA library"
/note="Vector: plasmid pNB; see Brown, N.H. and Kafatos, F.C. (1988) Functional cDNA libraries from Drosophila embryos. J. Mol Biol. 203, 425-37."

ORIGIN

Query Match 55.9%; Score 30.2; DB 3; Length 389;
Best Local Similarity 91.4%; Pred. No. 1.3;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAATTAATAGCACTCACTATAGGAGACCACATT 35

|||||
53 GAAATTAATAGCACTCACTATAGGAGACCACGAAT 19

RESULT 15

BQ102723/c

LOCUS BQ102723 Drosophila 8-12 hr embryonic cDNA library Drosophila

DEFINITION melanogaster cDNA 5', mRNA sequence.

ACCESSION BQ102723

VERSION BQ102723.1

KEYWORDS GI:20144206

ORGANISM Drosophila melanogaster (fruit fly)

DESCRIPTION Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 393)

REFERENCE 1. (bases 1 to 393)
AUTHORS Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B., Metherall,J.E. and Letsou,A.

TITLE An automated screen for spatially restricted transcripts in Drosophila embryogenesis

JOURNAL Genome Res. (2002) In press

COMMENT Contact: Letsou, A.

Department of Human Genetics

Eccles Institute of Human Genetics, University of Utah

15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA

Tel: 801 581-4422

Fax: 801 581-7796

Email: aletsou@genetics.utah.edu

Seq primer: SP6.

FEATURES Location/Qualifiers

source

1..393
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/dev_stage="embryonic 8-12 hr post-fertilization"
/clone_lib="Drosophila 8-12 hr embryonic cDNA library"
/note="Vector: plasmid pNB; see Brown, N.H. and Kafatos, F.C. (1988) Functional cDNA libraries from Drosophila embryos. J. Mol Biol. 203, 425-37."

ORIGIN

Query Match 55.9%; Score 30.2; DB 3; Length 393;
Best Local Similarity 91.4%; Pred. No. 1.3;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAATTAATAGCACTCACTATAGGAGACCACATT 35

|||||
43 GAAATTAATAGCACTCACTATAGGAGACCACGAAT 9

RESULT 16

BQ102707/c

LOCUS BQ102707 Drosophila 8-12 hr embryonic cDNA library Drosophila

DEFINITION melanogaster cDNA 5', mRNA sequence.

ACCESSION BQ102707

VERSION BQ102707.1

KEYWORDS GI:20144190

ORGANISM Drosophila melanogaster (fruit fly)

DESCRIPTION Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 395)

REFERENCE 1. (bases 1 to 395)

AUTHORS Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B., Metherall,J.E. and Letsou,A.

TITLE An automated screen for spatially restricted transcripts in Drosophila embryogenesis

JOURNAL Genome Res. (2002) In press

COMMENT Contact: Letsou, A.

Department of Human Genetics

Eccles Institute of Human Genetics, University of Utah

15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA

Tel: 801 581-4422

Fax: 801 581-7796

Email: aletsou@genetics.utah.edu

Seq primer: SP6.

FEATURES Location/Qualifiers

source

1..395
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/dev_stage="embryonic 8-12 hr post-fertilization"
/clone_lib="Drosophila 8-12 hr embryonic cDNA library"
/note="Vector: plasmid pNB; see Brown, N.H. and Kafatos, F.C. (1988) Functional cDNA libraries from Drosophila embryos. J. Mol Biol. 203, 425-37."

ORIGIN

Query Match 55.9%; Score 30.2; DB 3; Length 395;
Best Local Similarity 91.4%; Pred. No. 1.3;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAATTAATAGCACTCACTATAGGAGACCACATT 35

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46 GAAATTAATAGCACTCACTATAGGAGACCACGAAT 12

RESULT 17

BQ102746/c

LOCUS BQ102746 Drosophila 8-12 hr embryonic cDNA library Drosophila

DEFINITION melanogaster cDNA 5', mRNA sequence.

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ACCESSION BQ102746
VERSION BQ102746.1 GI:20144229
KEYWORDS EST.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 401)
AUTHORS Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B.,
Metherall,J.E. and Letsou,A.
TITLE An automated screen for spatially restricted transcripts in
Drosophila embryogenesis
JOURNAL Genome Res. (2002) In press
COMMENT Contact: Letsou, A.
Department of Human Genetics
Eccles Institute of Human Genetics, University of Utah
15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA
Tel: 801 581-4422
Fax: 801 581-7796
Email: aletsou@genetics.utah.edu
Seq primer: SP6.
FEATURES             location/Qualifiers
     source          1..401
                     /organism="Drosophila melanogaster"
                     /mol_type="mRNA"
                     /db_xref="taxon:7227"
                     /dev_stages="embryonic 8-12 hr post-fertilization"
                     /clone_lib="Drosophila 8-12 hr embryonic cDNA library"
                     /note="Vector: plasmid pNB; see Brown, N.H. and Kafatos,
                     F.C. (1988) Functional cDNA libraries from Drosophila
                     embryos. J. Mol Biol. 203, 425-37."
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Query Match      55.9%; Score 30.2; DB 3; Length 401;
Best Local Similarity 91.4%; Pred. No. 1.3;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCCACATT 35
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Db 56 GAAATTAATACGACTCACTATAGGAGACCCGGAAT 22
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RESULT 18
BQ102731/c
LOCUS BQ102731.1 GI:20144214
DEFINITION Drosophila melanogaster (fruit fly)
ACCESSION BQ102731
VERSION BQ102731.1
KEYWORDS EST.
SOURCE Drosophila melanogaster
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 427)
AUTHORS Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B.,
Metherall,J.E. and Letsou,A.
TITLE An automated screen for spatially restricted transcripts in
Drosophila embryogenesis
JOURNAL Genome Res. (2002) In press
COMMENT Contact: Letsou, A.
Department of Human Genetics
Eccles Institute of Human Genetics, University of Utah
15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA
Tel: 801 581-4422
Fax: 801 581-7796
Email: aletsou@genetics.utah.edu
Seq primer: SP6.
FEATURES             location/Qualifiers
     source          1..427
                     /organism="Drosophila melanogaster"

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/mol_type="mRNA"
/db_xref="taxon:7227"
/dev_stages="embryonic 8-12 hr post-fertilization"
/clone_lib="Drosophila 8-12 hr embryonic cDNA library"
/note="Vector: plasmid pNB; see Brown, N.H. and Kafatos,
F.C. (1988) Functional cDNA libraries from Drosophila
embryos. J. Mol Biol. 203, 425-37."
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Query Match      55.9%; Score 30.2; DB 3; Length 427;
Best Local Similarity 91.4%; Pred. No. 1.3;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCCACATT 35
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Db 48 GAAATTAATACGACTCACTATAGGAGACCCGGAAT 14
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RESULT 19
BQ102670/c
LOCUS BQ102670.1 GI:20144153
DEFINITION Drosophila melanogaster (fruit fly)
ACCESSION BQ102670
VERSION BQ102670.1
KEYWORDS EST.
SOURCE Drosophila melanogaster
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 452)
AUTHORS Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B.,
Metherall,J.E. and Letsou,A.
TITLE An automated screen for spatially restricted transcripts in
Drosophila embryogenesis
JOURNAL Genome Res. (2002) In press
COMMENT Contact: Letsou, A.
Department of Human Genetics
Eccles Institute of Human Genetics, University of Utah
15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA
Tel: 801 581-4422
Fax: 801 581-7796
Email: aletsou@genetics.utah.edu
Seq primer: SP6.
FEATURES             location/Qualifiers
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                     /organism="Drosophila melanogaster"
                     /mol_type="mRNA"
                     /db_xref="taxon:7227"
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                     /clone_lib="Drosophila 8-12 hr embryonic cDNA library"
                     /note="Vector: plasmid pNB; see Brown, N.H. and Kafatos,
                     F.C. (1988) Functional cDNA libraries from Drosophila
                     embryos. J. Mol Biol. 203, 425-37."
ORIGIN
Query Match      55.9%; Score 30.2; DB 3; Length 452;
Best Local Similarity 91.4%; Pred. No. 1.3;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCCACATT 35
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Db 54 GAAATTAATACGACTCACTATAGGAGACCCGGAAT 20
|||||

RESULT 20
BQ102693/c
LOCUS BQ102693.1 GI:20144176
DEFINITION Drosophila melanogaster (fruit fly)
ACCESSION BQ102693
VERSION BQ102693.1

```

[illegible]

SOURCE ORGANISM
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 739)
Liang, Z. and Biggin, M.D.
Eve and ftz regulate a wide array of genes in blastoderm embryos:
the selector homeoproteins directly or indirectly regulate most
genes in Drosophila
Development 125 (22), 4471-4482 (1998)
9778506
Contact: Biggin, M. D.
Department of Molecular Biophysics and Biochemistry
Yale University
P.O. Box 208114 266 Whitney Ave, New Haven, CT 06520-208114, USA
Tel: 203 432 6178
Fax: 203 432 5791
Email: mark.biggin@yale.edu
pair-rule, strong segmentally repeated patterns
Seq primer: SP6
High quality sequence stop: 739.

FEATURES
source
Location/Qualifiers
1..739
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/dev_stage="embryonic 8-12 hr post-fertilization"
/clone_lib="Drosophila 8-12 hr embryonic cDNA library"
/note="Vector: plasmid pNB; see Brown, N.H. and Kafatos,
F.C. (1988) Functional cDNA libraries from Drosophila
embryos. J. Mol Biol. 203, 425-37."

ORIGIN
Query Match 55.9%; Score 30.2; DB 1; Length 739;
Best Local Similarity 91.4%; Pred. No. 1.4;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACACACATT 35
|||||
Db 516 GAAATTAATACGACTCACTATAGGAGACCGGAAT 482
|||||

RESULT 24
A1124281/c
LOCUS 748 bp mRNA linear EST 28-SEP-1999
DEFINITION 1.53 Drosophila 8-12 hr embryonic cDNA library Drosophila
melanogaster cDNA 5', mRNA sequence.
ACCESSION A1124281
VERSION EST.
KEYWORDS Drosophila melanogaster (fruit fly)
SOURCE Drosophila melanogaster
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 748)
Liang, Z. and Biggin, M.D.
Eve and ftz regulate a wide array of genes in blastoderm embryos:
the selector homeoproteins directly or indirectly regulate most
genes in Drosophila
Development 125 (22), 4471-4482 (1998)
9778506
Contact: Biggin, M. D.
Department of Molecular Biophysics and Biochemistry
Yale University
P.O. Box 208114 266 Whitney Ave, New Haven, CT 06520-208114, USA
Tel: 203 432 6178
Fax: 203 432 5791
Email: mark.biggin@yale.edu
strong segmentally repeated patterns
Seq primer: SP6
High quality sequence stop: 748.

FEATURES
source
Location/Qualifiers
1..748
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
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/clone_lib="Drosophila 8-12 hr embryonic cDNA library"
/note="Vector: plasmid pNB; see Brown, N.H. and Kafatos,
F.C. (1988) Functional cDNA libraries from Drosophila
embryos. J. Mol Biol. 203, 425-37."

ORIGIN
Query Match 55.9%; Score 30.2; DB 1; Length 748;
Best Local Similarity 91.4%; Pred. No. 1.4;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACACACATT 35
|||||
Db 66 GAAATTAATACGACTCACTATAGGAGACCGGAAT 32
|||||

RESULT 25
A1124257/c
LOCUS 753 bp mRNA linear EST 28-SEP-1999
DEFINITION 1.17 Drosophila 8-12 hr embryonic cDNA library Drosophila
melanogaster cDNA 5', similar to EF-1-alpha F, mRNA sequence.
ACCESSION A1124257
VERSION EST.
KEYWORDS Drosophila melanogaster (fruit fly)
SOURCE Drosophila melanogaster
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 753)
Liang, Z. and Biggin, M.D.
Eve and ftz regulate a wide array of genes in blastoderm embryos:
the selector homeoproteins directly or indirectly regulate most
genes in Drosophila
Development 125 (22), 4471-4482 (1998)
9778506
Contact: Biggin, M. D.
Department of Molecular Biophysics and Biochemistry
Yale University
P.O. Box 208114 266 Whitney Ave, New Haven, CT 06520-208114, USA
Tel: 203 432 6178
Fax: 203 432 5791
Email: mark.biggin@yale.edu
weak segmentally repeated patterns
Seq primer: SP6
High quality sequence stop: 753.

FEATURES
source
Location/Qualifiers
1..753
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/dev_stage="embryonic 8-12 hr post-fertilization"
/clone_lib="Drosophila 8-12 hr embryonic cDNA library"
/note="Vector: plasmid pNB; see Brown, N.H. and Kafatos,
F.C. (1988) Functional cDNA libraries from Drosophila
embryos. J. Mol Biol. 203, 425-37."

ORIGIN
Query Match 55.9%; Score 30.2; DB 1; Length 753;
Best Local Similarity 91.4%; Pred. No. 1.4;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACACACATT 35
|||||
Db 343 GAAATTAATACGACTCACTATAGGAGACCGGAAT 309
|||||

RESULT 26


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BE391582/c
LOCUS       BE391582               181 bp    mRNA    linear    EST 21-JUL-2000
DEFINITION  601282148F1 NIH_MGC_44 Homo sapiens CDNA clone IMAGE:3604090 5',
            mRNA sequence.
ACCESSION   BE391582
VERSION     BE391582.1   GI:9136277
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1  (bases 1 to 181)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/
TITLE      NIH-MGC http://mgc.nci.nih.gov/
JOURNAL    National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT    Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: ATCC
            CDNA Library Preparation: Ling Hong/Rubin Laboratory
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
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                /db_xref="taxon:9606"
                /clone="IMAGE:3604090"
                /tissue_type="endometrium, adenocarcinoma cell line"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH MGC 44"
                /note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:
                EcoRI; CDNA made by oligo-dT priming. Directionally
                cloned into EcoRI/XhoI sites using the following 5'
                adaptor: GGCACGAG(G). Library constructed by Ling Hong
                in the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies)."

FEATURES             source
     source
Query Match      55.6%; Score 30; DB 7; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
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Db 143 GAAATTAATACGACTCACTATAGGAGACC 114

RESULT 27
BE262878/c
LOCUS       BE262878               182 bp    mRNA    linear    EST 26-OCT-2000
DEFINITION  601148014F1 NIH_MGC_19 Homo sapiens CDNA clone IMAGE:3163514 5',
            mRNA sequence.
ACCESSION   BE262878
VERSION     BE262878.1   GI:9136277
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1  (bases 1 to 182)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/
TITLE      NIH-MGC http://mgc.nci.nih.gov/
JOURNAL    National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT    Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.

```

```

Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CM124 row: k column: 03
High quality sequence start: 66
High quality sequence stop: 131.
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    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:3163514"
    /tissue_type="neuroblastoma"
    /lab_host="DH10B (phage-resistant)"
    /clone_lib="NIH_MGC_19"
    /note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
    EcoRI; CDNA made by oligo-dT priming. Directionally
    cloned into EcoRI/XhoI sites using the following 5'
    adaptor: GGCACGAG(G). Library constructed by Ling Hong
    in the laboratory of Gerald M. Rubin (University of
    California, Berkeley) using ZAP-cDNA synthesis kit
    (Stratagene) and Superscript II RT (Life Technologies)."
    Note: this is a NIH_MGC Library."

ORIGIN
Query Match      55.6%; Score 30; DB 7; Length 182;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
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Db 96 GAAATTAATACGACTCACTATAGGAGACC 67

RESULT 28
BF976190/c
LOCUS       BF976190               183 bp    mRNA    linear    EST 22-JAN-2001
DEFINITION  602245057F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4336023 5',
            mRNA sequence.
ACCESSION   BF976190
VERSION     BF976190.1   GI:12343405
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1  (bases 1 to 183)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/
TITLE      NIH-MGC http://mgc.nci.nih.gov/
JOURNAL    National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT    Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            CDNA Library Preparation: Ling Hong/Rubin Laboratory
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
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            High quality sequence start: 14
            High quality sequence stop: 106.
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                1..183
                /organism="Homo sapiens"
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                /db_xref="taxon:9606"
                /clone="IMAGE:4336023"

FEATURES             source
     source

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/tissue_type="primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_48"
 /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 55.6%; Score 30; DB 2; Length 183;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACC 30
 DB 77 GAAATTAATACGACTCACTATAGGAGACC 48

RESULT 29

BE314661/c
 LOCUS BE314661 185 bp mRNA linear EST 26-OCT-2000
 DEFINITION 60114677F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3161970 5',
 mRNA sequence.

ACCESSION BE314661
 VERSION BE314661.1 GI:9136063
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.

REFERENCE

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LLCM120 row: j column: 19
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 High quality sequence stop: 122.

FEATURES

Location/Qualifiers

1..185

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3161970"

/tissue_type="neuroblastoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_19"

/note="Organ: Brain; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 55.6%; Score 30; DB 7; Length 185;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACC 30
 DB 89 GAAATTAATACGACTCACTATAGGAGACC 60

RESULT 30

BE397962/c

LOCUS BE397962 195 bp mRNA linear EST 21-JUL-2000

DEFINITION 601290494F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620903 5',
 mRNA sequence.

ACCESSION BE397962

VERSION BE397962.1 GI:9343327

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.

REFERENCE 1 (bases 1 to 195)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM293 row: 1 column: 24

High quality sequence start: 5

High quality sequence stop: 143.

Location/Qualifiers

1..195

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3620903"

/tissue_type="Burkitt lymphoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_8"

/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 55.6%; Score 30; DB 7; Length 195;

Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACC 30

DB 109 GAAATTAATACGACTCACTATAGGAGACC 80

ORIGIN

Query Match 55.6%; Score 30; DB 7; Length 195;

Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACC 30

DB 109 GAAATTAATACGACTCACTATAGGAGACC 80

RESULT 31

BE410828/c

LOCUS BE410828 204 bp mRNA linear EST 21-JUL-2000

DEFINITION 601301490F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636046 5',
 mRNA sequence.

ACCESSION BE410828

VERSION BE410828.1 GI:9347278

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.

```

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 204)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
cDNA distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM333 row: c column: 23
High quality sequence start: 53
High quality sequence stop: 177.
FEATURES
    source
        Location/Qualifiers
            1..204
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:3636046"
                /tissue_type="choriocarcinoma"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH_MGC_21"
                /note="Organ: placenta; Vector: pOTB7; Site:1: XhoI;
                Site 2: EcoRI; cDNA made by oligo-dT priming.
                Directionally cloned into EcoRI/XhoI sites using the
                following 5' adaptor: GGCACGAG(G). Size-selected
                for average insert size 1.8kb. Library constructed by
                Ling Hong in the laboratory of Gerald M. Rubin (University
                of California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN
    Query Match 55.6%; Score 30; DB 7; Length 204;
    Best Local Similarity 100.0%; Pred. No. 1.4;
    Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
    |||
Db 144 GAAATTAATACGACTCACTATAGGAGACC 115
    |||
RESULT 32
BE398063/c
LOCUS BE398063 206 bp mRNA linear EST 21-JUL-2000
DEFINITION 601290252F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620772 5',
mRNA sequence.
ACCESSION BE398063.1 GI:9343428
VERSION BE398063.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 206)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
cDNA distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM293 row: g column: 13
High quality sequence start: 33
High quality sequence stop: 160.
FEATURES
    source
        Location/Qualifiers
            1..206
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:3620772"
                /tissue_type="Burkitt lymphoma"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH_MGC_8"
                /note="Organ: lymph; Vector: pOTB7; Site:1: XhoI; Site 2:
                EcoRI; cDNA made by oligo-dT priming. Directionally
                cloned into EcoRI/XhoI sites using the following 5'
                adaptor: GGCACGAG(G). Size-selected >500bp for average
                insert size 1.8kb. Library constructed by Ling Hong in
                the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN
    Query Match 55.6%; Score 30; DB 7; Length 206;
    Best Local Similarity 100.0%; Pred. No. 1.4;
    Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
    |||
Db 126 GAAATTAATACGACTCACTATAGGAGACC 97
    |||
RESULT 33
BF027436/c
LOCUS BF027436 227 bp mRNA linear EST 10-OCT-2000
DEFINITION 60167555F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955452 5',
mRNA sequence.
ACCESSION BF027436
VERSION BF027436.1 GI:10735148
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 227)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM829 row: p column: 13
High quality sequence start: 13
High quality sequence stop: 161.
FEATURES
    source
        Location/Qualifiers
            1..227
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:3955452"
                /tissue_type="melanotic melanoma"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH_MGC_20"
                /note="Organ: skin; Vector: pOTB7; Site:1: XhoI; Site 2:
                EcoRI; cDNA made by oligo-dT priming. Directionally
                cloned into EcoRI/XhoI sites using the following 5'
                adaptor: GGCACGAG(G). Size-selected >500bp for average
                insert size 1.8kb. Library constructed by Ling Hong in
                the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies)."

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FEATURES
    source
        Location/Qualifiers
            1..206
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:3620772"
                /tissue_type="Burkitt lymphoma"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH_MGC_8"
                /note="Organ: lymph; Vector: pOTB7; Site:1: XhoI; Site 2:
                EcoRI; cDNA made by oligo-dT priming. Directionally
                cloned into EcoRI/XhoI sites using the following 5'
                adaptor: GGCACGAG(G). Size-selected >500bp for average
                insert size 1.8kb. Library constructed by Ling Hong in
                the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN
    Query Match 55.6%; Score 30; DB 7; Length 206;
    Best Local Similarity 100.0%; Pred. No. 1.4;
    Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
    |||
Db 126 GAAATTAATACGACTCACTATAGGAGACC 97
    |||
RESULT 33
BF027436/c
LOCUS BF027436 227 bp mRNA linear EST 10-OCT-2000
DEFINITION 60167555F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955452 5',
mRNA sequence.
ACCESSION BF027436
VERSION BF027436.1 GI:10735148
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 227)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM829 row: p column: 13
High quality sequence start: 13
High quality sequence stop: 161.
FEATURES
    source
        Location/Qualifiers
            1..227
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:3955452"
                /tissue_type="melanotic melanoma"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH_MGC_20"
                /note="Organ: skin; Vector: pOTB7; Site:1: XhoI; Site 2:
                EcoRI; cDNA made by oligo-dT priming. Directionally
                cloned into EcoRI/XhoI sites using the following 5'
                adaptor: GGCACGAG(G). Size-selected >500bp for average
                insert size 1.8kb. Library constructed by Ling Hong in
                the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies)."

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ORIGIN

Query Match 55.6%; Score 30; DB 7; Length 227;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACC 30
 |||||
 Db 128 GAAATTAATACGACTCACTATAGGAGACC 99

RESULT 34

BE391744/c
 LOCUS BE391744.1 linear mRNA 272 bp EST 21-JUL-2000
 DEFINITION 601282029F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603943 5',
 mRNA sequence.

ACCESSION BE391744

VERSION BE391744.1 GI:9337109

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 272)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L1CM249 row: j column: 08

High quality sequence start: 102

High quality sequence stop: 217.

FEATURES

source

1..272

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3603943"

/tissue_type="endometrium, adenocarcinoma cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC_44"

/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Library constructed by Ling Hong

in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 55.6%; Score 30; DB 7; Length 272;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACC 30

|||||

Db 194 GAAATTAATACGACTCACTATAGGAGACC 165

RESULT 35

BG425691/c

LOCUS BG425691.1 linear mRNA 334 bp EST 14-MAR-2001

DEFINITION 602448292F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4586926 5',

mRNA sequence.

ACCESSION BG425691

VERSION

KEYWORDS

SOURCE

ORGANISM

BG425691.1 GI:13332197

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 334)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTF

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L1CM1316 row: g column: 23

High quality sequence start: 22

High quality sequence stop: 82.

FEATURES

source

1..334

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4586926"

/tissue_type="renal cell adenocarcinoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC 14"

/note="Organ: kidney; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match

Best Local Similarity 55.6%; Score 30; DB 2; Length 334;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACC 30

|||||

Db 51 GAAATTAATACGACTCACTATAGGAGACC 22

RESULT 36

BM043937/c

LOCUS BM043937.1 linear mRNA 347 bp EST 07-NOV-2001

DEFINITION 603620876F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5446338 5',

mRNA sequence.

ACCESSION BM043937

VERSION BM043937.1 GI:16773204

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo

1 (bases 1 to 347)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTF

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1928 row: h column: 19
High quality sequence stop: 93.
Location/Qualifiers

FEATURES
source

1. 347
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5446338"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_40"
/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 55.6%; Score 30; DB 2; Length 347;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
|||||
Db 58 GAAATTAATACGACTCACTATAGGAGACC 29
|||||

RESULT 37
BM041853/c
LOCUS
DEFINITION 603614347F1 NIH_MGC_108 Homo sapiens cDNA clone IMAGE:5420363 5',
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BM041853 349 bp mRNA linear EST 07-NOV-2001
603614347F1 NIH_MGC_108 Homo sapiens cDNA clone IMAGE:5420363 5',
mRNA sequence.
BM041853 GI:16771120
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 349)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LLCM1874 row: n column: 12
High quality sequence start: 34
High quality sequence stop: 157.
Location/Qualifiers

FEATURES
source

1. 349
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5420363"
/tissue_type="Wilms' tumor, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_108"
/note="Organ: kidney; Vector: pOTB7; Site_1: XhoI; Site_2:

EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 55.6%; Score 30; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
|||||
Db 125 GAAATTAATACGACTCACTATAGGAGACC 96
|||||

RESULT 38

BF974094/c

LOCUS
DEFINITION 602242718F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4331093 5',
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BF974094 351 bp mRNA linear EST 22-JAN-2001
602242718F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4331093 5',
mRNA sequence.
BF974094 GI:12341309
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 351)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM195 row: d column: 06
High quality sequence start: 93
High quality sequence stop: 210.
Location/Qualifiers

FEATURES
source

1. 351
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4331093"
/tissue_type="leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_46"
/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.0kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 55.6%; Score 30; DB 2; Length 351;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
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Db      175 GAAATTAATACGACTACTATAGGAGACC 146

RESULT 39
BE391553/c
LOCUS   BE391553
DEFINITION 601283214F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605139 5',
mRNA sequence.
ACCESSION BE391553
VERSION   BE391553.1 GI:9336918
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 394)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM252 row: 1 column: 04
High quality sequence start: 81
High quality sequence stop: 182.
Location/Qualifiers
FEATURES
source
1..394
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3605139"
/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_44"
/notes="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

Query Match 55.6%; Score 30; DB 7; Length 394;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTACTATAGGAGACC 30
 |||||
 Db 172 GAAATTAATACGACTACTATAGGAGACC 143

RESULT 40
 W91597/c
 LOCUS W91597
 DEFINITION MTA.G05.077.A MTA adult mouse thymus library Mus musculus cDNA
 clone MTA.G05.077 3' end similar to CT repeat, mRNA sequence.
 ACCESSION W91597
 VERSION W91597.1 GI:1408023
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Murioidea; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 418)

Query Match 55.6%; Score 30; DB 7; Length 394;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTACTATAGGAGACC 30
 |||||
 Db 172 GAAATTAATACGACTACTATAGGAGACC 143

RESULT 40
 W91597/c
 LOCUS W91597
 DEFINITION MTA.G05.077.A MTA adult mouse thymus library Mus musculus cDNA
 clone MTA.G05.077 3' end similar to CT repeat, mRNA sequence.
 ACCESSION W91597
 VERSION W91597.1 GI:1408023
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Murioidea; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 418)

Query Match 55.6%; Score 30; DB 10; Length 418;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTACTATAGGAGACC 30
 |||||
 Db 371 GAAATTAATACGACTACTATAGGAGACC 342

RESULT 41
 BG398598/c
 LOCUS BG398598
 DEFINITION 602439706F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4565904 5',
 mRNA sequence.
 ACCESSION BG398598
 VERSION BG398598.1 GI:13292046
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1 (bases 1 to 426)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM1283 row: 1 column: 01
 High quality sequence start: 17
 High quality sequence stop: 421.
 Location/Qualifiers

FEATURES

source

1..418
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="MTA.G05.077"
 /lab_host="MC1061 p3"
 /clone_lib="MTA adult mouse thymus library"
 /notes="Vector: pCDNAL; Site 1: NotI; Site 2: EcoRI; The
 cDNA library was constructed from poly(A)+ RNA of an adult
 mouse thymus by oligo-dT primed reverse transcription.
 cDNA was selected on gel for size above 800 nucleotides
 after second strand synthesis, then directionally cloned
 after adaptor ligation and restriction enzyme cleavage
 into the pCDNAL vector (Not I on polyA side, EcoR I on the
 5'side)."

AUTHORS Nguyen, C., Rocha, D., Granjeaud, S., Bernard, K., Naquet, P. and
 Jordan, B.R.
 TITLE Gene expression in different cell types of the mouse thymus
 JOURNAL Unpublished (1996)
 COMMENT Contact: Jordan BR
 Genome Structure and Immune Functions
 Centre d'Immunologie INSERM/CNRS
 Case 906, 13288 MARSEILLE Cedex 9, FRANCE
 Tel: 330491269496
 Fax: 330491269430
 Email: jordan@ciml.univ-mrs.fr
 This sequence was determined at Engelhardt Institute of Molecular
 Biology, Moscow, Russia (V Zakhariev)
 Seq primer: SP6.
 Location/Qualifiers

FEATURES

source

1..418
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="MTA.G05.077"
 /lab_host="MC1061 p3"
 /clone_lib="MTA adult mouse thymus library"
 /notes="Vector: pCDNAL; Site 1: NotI; Site 2: EcoRI; The
 cDNA library was constructed from poly(A)+ RNA of an adult
 mouse thymus by oligo-dT primed reverse transcription.
 cDNA was selected on gel for size above 800 nucleotides
 after second strand synthesis, then directionally cloned
 after adaptor ligation and restriction enzyme cleavage
 into the pCDNAL vector (Not I on polyA side, EcoR I on the
 5'side)."

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4565904"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site:1: XhoI;
Site:2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 55.6%; Score 30; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
|||||
Db 157 GAAATTAATACGACTCACTATAGGAGACC 128
|||||

RESULT 42

BE562252/c
LOCUS
DEFINITION
601344666F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677512 5',
mRNA sequence.

ACCESSION BE562252
VERSION BE562252.1 GI:9805972

KEYWORDS

EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 485)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM353 row: c column: 17

High quality sequence start: 12

High quality sequence stop: 480.

FEATURES

source

1. 485

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3677512"

/tissue_type="Burkitt lymphoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_8"

/note="Organ: lymph; Vector: pOTB7; Site:1: XhoI; Site:2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 55.6%; Score 30; DB 7; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
|||||
Db 143 GAAATTAATACGACTCACTATAGGAGACC 114
|||||

RESULT 43

BE398001/c
LOCUS
DEFINITION
601290550F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620700 5',
mRNA sequence.

ACCESSION BE398001

VERSION BE398001.1 GI:9343366

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 511)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM293 row: d column: 13

High quality sequence start: 2

High quality sequence stop: 506.

FEATURES

source

1. 511

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3620700"

/tissue_type="Burkitt lymphoma"

/lab_host="NIH_MGC_8"

/note="Organ: lymph; Vector: pOTB7; Site:1: XhoI; Site:2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

source

1. 511

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3620700"

/tissue_type="Burkitt lymphoma"

/lab_host="NIH_MGC_8"

/note="Organ: lymph; Vector: pOTB7; Site:1: XhoI; Site:2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

source

1. 511

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3620700"

/tissue_type="Burkitt lymphoma"

/lab_host="NIH_MGC_8"

/note="Organ: lymph; Vector: pOTB7; Site:1: XhoI; Site:2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM159 row: a column: 23
 High quality sequence start: 35
 High quality sequence stop: 490.

FEATURES
 source
 1..530
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4300318"
 /tissue_type="epitheloid carcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_42"
 /note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 55.6%; Score 30; DB 7; Length 530;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTAATACGACTCACTATAGGAGACC 30
 |||||
 DB 456 GAAATTAATACGACTCACTATAGGAGACC 427
 |||||

RESULT 45
BE410907/C
LOCUS BE410907 550 bp mRNA linear EST 21-JUL-2000
DEFINITION 601303550F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3637957 5',
 mRNA sequence.
ACCESSION BE410907
VERSION BE410907.1 GI:9347357
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LLCM338 row: C column: 14
 High quality sequence start: 95
 High quality sequence stop: 217.

FEATURES
 source
 1..550
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3637957"
 /tissue_type="choriocarcinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_21"
 /note="Organ: placenta; Vector: pOTB7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
 Query Match 55.6%; Score 30; DB 7; Length 550;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACC 30
 |||||
 DB 183 GAAATTAATACGACTCACTATAGGAGACC 154
 |||||

RESULT 46
BE281606/C
LOCUS BE281606 561 bp mRNA linear EST 13-JUL-2000
DEFINITION 601154965F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138329 5',
 mRNA sequence.
ACCESSION BE281606
VERSION BE281606.1 GI:9156628
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LLCM103 row: a column: 18
 High quality sequence start: 6
 High quality sequence stop: 560.

FEATURES
 source
 1..561
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3138329"
 /tissue_type="choriocarcinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_21"
 /note="Organ: placenta; Vector: pOTB7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming."

Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 55.6%; Score 30; DB 7; Length 561;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30

Db 124 GAAATTAATACGACTCACTATAGGAGACC 95

RESULT 47

LOCUS BG491845/c

DEFINITION 60253593271 NIH_MGC_41 Homo sapiens CDNA clone IMAGE:4685046 3',
mRNA sequence.

ACCESSION BG491845

VERSION BG491845.1 GI:13453357

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE

1 (bases 1 to 578)

NIH-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DRP

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LCM1493 row: p column: 07

High quality sequence stop: 569.

FEATURES

source

1..578
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4685046"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 41"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 55.6%; Score 30; DB 2; Length 578;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30

Db 543 GAAATTAATACGACTCACTATAGGAGACC 514

RESULT 48

BE737047/c

LOCUS

DEFINITION 601304208F1 NIH_MGC_39 Homo sapiens CDNA clone IMAGE:3639000 5',
mRNA sequence.

ACCESSION BE737047

VERSION BE737047.1 GI:10151039

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE

1 (bases 1 to 579)

NIH-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LCM340 row: o column: 01

High quality sequence stop: 502.

FEATURES

source

1..579
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3639000"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 39"
/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies)."

ORIGIN

Query Match 55.6%; Score 30; DB 7; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30

Db 96 GAAATTAATACGACTCACTATAGGAGACC 67

RESULT 49

BE728141/c

LOCUS

DEFINITION 601563696F1 NIH_MGC_20 Homo sapiens CDNA clone IMAGE:3833351 5',
mRNA sequence.

ACCESSION BE728141

VERSION BE728141.1 GI:10142133

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE

1 (bases 1 to 587)

NIH-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTF
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LLCW511 row: p column: 24
 High quality sequence stop: 587.
 Location/Qualifiers

FEATURES

source

```

1..587
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3833351"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_20"
/notes="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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ORIGIN

Query Match 55.6%; Score 30; DB 7; Length 587;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GAAATTAATACGACTCACTATAGGAGACC 30
 |||||||||||||||||||||||||||||||
 Db 121 GAAATTAATACGACTCACTATAGGAGACC 92

RESULT 50

BM007071/c
 LOCUS BM007071 617 bp mRNA linear EST 30-OCT-2001
 DEFINITION 603615464T1 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:5421543 3',
 mRNA sequence.

ACCESSION BM007071

VERSION BM007071.1 GI:16521425

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

1 (bases 1 to 617)

NIH-MGC http://mgs.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1877 row: o column: 16

High quality sequence start: 26

High quality sequence stop: 611.

Location/Qualifiers

FEATURES

source

```

1..617
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5421543"
```

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/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_110"
/notes="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
```

ORIGIN

Query Match 55.6%; Score 30; DB 2; Length 617;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GAAATTAATACGACTCACTATAGGAGACC 30
 |||||||||||||||||||||||||||||||
 Db 579 GAAATTAATACGACTCACTATAGGAGACC 550

RESULT 51

BG491861/c

LOCUS BG491861 634 bp mRNA linear EST 27-MAR-2001

DEFINITION 602535952T1 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:4684860 3',
 mRNA sequence.

ACCESSION BG491861

VERSION BG491861.1 GI:13453373

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 634)

NIH-MGC http://mgs.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTF

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1493 row: h column: 13

High quality sequence stop: 624.

Location/Qualifiers

FEATURES

source

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1..634
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4684860"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_41"
/notes="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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ORIGIN

Query Match 55.6%; Score 30; DB 2; Length 634;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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mRNA sequence.
ACCESSION BE397868
VERSION BE397868.1 GI:93433233
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
JOURNAL Hominidae; Homo.
COMMENT 1 (bases 1 to 775)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LNCM294 row: b column: 23
High quality sequence start: 16
High quality sequence stop: 513.
Location/Qualifiers
FEATURES
source
1..775
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3621046"
/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_8"
/notes="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

Query Match 55.6%; Score 30; DB 7; Length 775;
Best Local Similarity 100.0%; Pred. No. 1.7; Length 775;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
|||||
Db 111 GAAATTAATACGACTCACTATAGGAGACC 82

RESULT 58
CK199881/c
LOCUS CK199881.1
DEFINITION FGAS008388 Triticum aestivum FGAS: Library 3 Gate 6 Triticum
aestivum CDNA, mRNA sequence.
ACCESSION CK199881
VERSION CK199881.1 GI:39562271
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Pooidae; Triticeae; Triticum.
1 (bases 1 to 793)
Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,
Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,
Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,
Penniket, C., Roach, J.L. and Sarhan, F.
Functional Genomics of Abiotic Stress In Wheat and Canola Crops
Unpublished (2003)
Contact: Wm L Crosby

Query Match 55.6%; Score 30; DB 5; Length 793;
Best Local Similarity 86.8%; Pred. No. 1.7;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 6 TAATACGACTCACTATAGGAGACCACATTTGTGCAATA 43
|||||
Db 747 TAATACGACTCACTATAGGAGACCACATTTGTGCAAGA 710

RESULT 59
BE391895/c
LOCUS BE391895.1
DEFINITION BE391895.1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604880 5',
mRNA sequence.
ACCESSION BE391895
VERSION BE391895.1 GI:9337260
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
JOURNAL Hominidae; Homo.
COMMENT 1 (bases 1 to 793)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LNCM252 row: a column: 09
High quality sequence start: 65
High quality sequence stop: 189.
Location/Qualifiers
FEATURES
source
1..793
/organism="Homo sapiens"

Bioinformatics
University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas_esta@cs.usask.ca
This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [102,627].
Plate: L3C111 row: G column: 09.
Location/Qualifiers
1..793
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: Library 3 Gate 6"
/notes="Organ: Root; Vector: pCMV.SPORT6; Root tissue from
control, cold-acclimated and salt stressed wheat cultivar
Norstar. 7 mRNA populations were combined before
constructing the library; 7 day non-acclimated roots, 1,
23, and 53 days cold-acclimated at 4C, and 30 minutes, 3
hours and 6 hours treated roots with 200mM NaCl.
Non-acclimated and cold-acclimated plants were grown in
vermiculite while salt stressed plant were grown
hydroponically. First strand synthesis in this library was
done in the presence of methylated dCTP thereby protecting
from internal cleavage with NotI."

Matches	30; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
QY	1	GAATTAATACGACTCACTATAGGAGACC	30		
Db	127	GAATTAATACGACTCACTATAGGAGACC	98		
RESULT 61					
LOCUS	BE899343				
DEFINITION	60168118F1 NIH_MGC_9 Homo sapiens CDNA clone IMAGE:3951401 5', mRNA linear EST 29-SEP-2000				
ACCESSION	BE899343				
VERSION	BE899343.1	GI:10366945			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 830)				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTF CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM819 row: g column: 18 High quality sequence start: 30 High quality sequence stop: 228. Location/Qualifiers 1..830 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:3951401" /tissue_type="adenocarcinoma cell line" /lab_host="PH10B (phage-resistant)" /clone_lib="NIH MGC 9" /notes="Organ: ovary; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."				
FEATURES					
source					
ORIGIN					
Query Match	55.6%	Score 30; DB 7; Length 830;			
Best Local Similarity	100.0%;	Pred. No. 1.7;			
Matches	30; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
QY	1	GAATTAATACGACTCACTATAGGAGACC	30		
Db	73	GAATTAATACGACTCACTATAGGAGACC	102		
RESULT 62					
LOCUS	BE737520				
DEFINITION	601306689F1 NIH_MGC_39 Homo sapiens CDNA clone IMAGE:3640990 5', mRNA linear EST 15-SEP-2000				
ACCESSION	BE737520				
VERSION	BE737520.1	GI:10151512			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 909)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLCM346 row: a column: 23
High quality sequence start: 3
High quality sequence stop: 271.
High quality sequence stop: 271.

FEATURES
source

1..909

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3640990"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_39"

/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 55.6%; Score 30; DB 7; Length 909;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GAAATTAATACGACTCACTATAGGAGACC 30
Db 120 GAAATTAATACGACTCACTATAGGAGACC 91

RESULT 63
BE391677/c

LOCUS BE391677/c
DEFINITION 601284594F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606310 5',
mRNA sequence.

ACCESSION BE391677
VERSION BE391677.1 GI:9337042
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 932)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLCM355 row: l column: 23
High quality sequence start: 3
High quality sequence stop: 166.
High quality sequence stop: 166.

FEATURES
source

1..932
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3606310"
/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_44"

/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 55.6%; Score 30; DB 7; Length 932;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GAAATTAATACGACTCACTATAGGAGACC 30
Db 118 GAAATTAATACGACTCACTATAGGAGACC 89

RESULT 64

BE379428/c

LOCUS BE379428/c

DEFINITION 601237292F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609287 5',
mRNA sequence.

ACCESSION BE379428

VERSION BE379428.1 GI:9324793

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 944)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLCM363 row: h column: 24
High quality sequence start: 25
High quality sequence stop: 644.
High quality sequence stop: 644.

FEATURES
source

1..944
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3609287"
/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_44"

/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
Query Match 55.6%; Score 30; DB 7; Length 944;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTATACGACTCACTATAGGAGACC 30
|||||

Db 119 GAAATTATACGACTCACTATAGGAGACC 90
|||||

RESULT 65
BE515297/c
LOCUS BE515297 NIH_MGC_44 952 bp mRNA linear EST 07-AUG-2000
DEFINITION 601235832F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608286 5',
mRNA sequence.

ACCESSION BE515297

VERSION BE515297.1 GI:9722512

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE 1 (bases 1 to 952)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LCM260 row: o column: 07

High quality sequence stop: 447.

Location/Qualifiers

source

1..952
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3608286"
/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 44"
/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 55.6%; Score 30; DB 7; Length 952;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTATACGACTCACTATAGGAGACC 30
|||||

Db 121 GAAATTATACGACTCACTATAGGAGACC 92
|||||

RESULT 66

BE263035/c

LOCUS BE263035

DEFINITION 601147095F1 NIH_MGC_19 978 bp mRNA linear EST 26-OCT-2000

mRNA sequence.

ACCESSION

VERSION BE263035.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE 1 (bases 1 to 978)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LCM121 row: n column: 24

High quality sequence start: 94

High quality sequence stop: 214.

Location/Qualifiers

source

1..978
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3162455"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 19"
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 55.6%; Score 30; DB 7; Length 978;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTATACGACTCACTATAGGAGACC 30
|||||

Db 179 GAAATTATACGACTCACTATAGGAGACC 150
|||||

RESULT 67

BE391793/c

LOCUS BE391793

DEFINITION 601282531F1 NIH_MGC_44 986 bp mRNA linear EST 21-JUL-2000

mRNA sequence.

ACCESSION BE391793

VERSION BE391793.1 GI:9337158

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE 1 (bases 1 to 986)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM250 row: n column: 07
 High quality sequence start: 53
 High quality sequence stop: 187.

FEATURES

Location/Qualifiers

1..986
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:360442"
 /tissue_type="endometrium, adenocarcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_44"
 /note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 55.6%; Score 30; DB 7; Length 986;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
 |||||
 Db 153 GAAATTAATACGACTCACTATAGGAGACC 124

RESULT 68
 BE749185/c
 LOCUS BE749185 986 bp mRNA linear EST 15-SEP-2000
 DEFINITION 601123490F1 NIH_MGC_5 Homo sapiens cDNA clone IMAGE:3348070 5',
 mRNA sequence.

ACCESSION BE749185
 VERSION BE749185.1 GI:10163177
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 986)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LLCM140 row: d column: 23
 High quality sequence start: 44
 High quality sequence stop: 324.

FEATURES

Location/Qualifiers

1..986
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3348070"
 /tissue_type="carcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_5"
 /note="Organ: cervix; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 55.6%; Score 30; DB 7; Length 986;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
 |||||
 Db 104 GAAATTAATACGACTCACTATAGGAGACC 75

RESULT 69
 BE730535/c
 LOCUS BE730535 1064 bp mRNA linear EST 15-SEP-2000
 DEFINITION 601562507F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832128 5',
 mRNA sequence.

ACCESSION BE730535
 VERSION BE730535
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 1064)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC/BDT/DRP

cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LLCM508 row: n column: 01
 High quality sequence start: 62
 High quality sequence stop: 613.

FEATURES

Location/Qualifiers

1..1064
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3832128"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_20"
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 55.6%; Score 30; DB 7; Length 1064;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
 |||||
 Db 108 GAAATTAATACGACTCACTATAGGAGACC 79

```

RESULT 70
LOCUS      BF689216/c
DEFINITION 602184894T1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4299407 3',
            mRNA sequence.
ACCESSION  BF689216
VERSION     BF689216.1 GI:11974624
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE  1 (bases 1 to 1070)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs@mai.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLGW1156 row: k column: 24
            High quality sequence start: 4
            High quality sequence stop: 489.
            Location/Qualifiers
              1..1070
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:4299407"
                /tissue_type="normal pigmented retinal epithelium"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH_MGC_43"
                /note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:
                EcoRI; cDNA made by oligo-dT priming. Directionally
                cloned into EcoRI/XhoI sites using the following 5'
                adaptor: GGCACGAG(G). Library constructed by Ling Hong
                in the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies).
                Note: this is a NIH_MGC Library. |"
ORIGIN
Query Match      55.6%; Score 30; DB 7; Length 1070;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
    |||||
Db 455 GAAATTAATACGACTCACTATAGGAGACC 426

RESULT 71
LOCUS      BQ102683/c
DEFINITION BQ102683 Drosophila 8-12 hr embryonic cDNA library Drosophila
            melanogaster cDNA 5', mRNA sequence.
ACCESSION  BQ102683
VERSION     BQ102683.1 GI:20144166
KEYWORDS   EST.
SOURCE     Drosophila melanogaster (fruit fly)
ORGANISM   Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachyceta; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE  1 (bases 1 to 451)
AUTHORS   Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B.,
            Mcetherall,J.E. and Letsou,A.

TITLE
JOURNAL
COMMENT

An automated screen for spatially restricted transcripts in
Drosophila embryogenesis
Genome Res. (2002) In press
Contact: Letsou, A.
Department of Human Genetics
Eccles Institute of Human Genetics, University of Utah
15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA
Tel: 801 581-4422
Fax: 801 581-7796
Email: alestou@genetics.utah.edu
Seq primer: SP6.
Location/Qualifiers
  1..451
    /organism="Drosophila melanogaster"
    /mol_type="mRNA"
    /db_xref="taxon:7227"
    /dev_stages="embryonic 8-12 hr post-fertilization"
    /clone_lib="Drosophila 8-12 hr embryonic cDNA library"
    /note="Vector: plasmid pNB; see Brown, N.H. and Kafatos,
    F.C. (1988) Functional cDNA libraries from Drosophila
    embryos. J. Mol Biol. 203, 425-37."
ORIGIN
Query Match      54.1%; Score 29.2; DB 3; Length 451;
Best Local Similarity 88.6%; Pred. No. 3.2;
Matches 31; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACATT 35
    |||||
Db 54 GAAATTAATACGACTCACTATAGGAGCCGNAAT 20

RESULT 72
LOCUS      BE946471
DEFINITION UI-M-BZ0-axu-e-01-0-UI.s1 NIH BMAP_MH12 Mus musculus cDNA clone
            UI-M-BZ0-axu-e-01-0-UI 3', mRNA sequence.
ACCESSION  BE946471
VERSION     BE946471.1 GI:10524230
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 373)
AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
JOURNAL     Genome Res. 6 (9), 791-806 (1996)
PUBMED     8889548
COMMENT    Contact: Chin, H
            National Institute of Mental Health
            6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
            20892-9643, USA
            Tel: 301 443 1706
            Fax: 301 443 9890
            Email: m5t@mail.nih.gov
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. The sequence tag present in the cDNA between the NotI site
            and the oligo-dT track served to verify it as a clone from the
            hippocampus tissue cDNA library preparation: M.B. Soares Lab Clone
            distribution: Researchers may obtain BMAP cDNA clones from RESEARCH
            GENETICS. It should be noted that Bento Soares is generating a
            small number of additional specialized non-redundant arrays of BMAP
            cDNAs whose availability will be considered under appropriate and
            limited collaborative arrangements
            Seq primer: M13 Forward
            PolyA=yes.
Location/Qualifiers
  1..373

```

ACCESSION	AG368203
VERSION	AG368203.1 GI:47979408
KEYWORDS	GSS.
SOURCE	Mus musculus molossinus (Japanese wild mouse)
ORGANISM	Mus musculus molossinus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1
REFERENCE	Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T., Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and Shiroishi,T. Contribution of Asian mouse subspecies Mus musculus molossinus to genomic constitution of strain C57BL/6J, as defined by BAC-end Genome Res. 14 (12), 2439-2447 (2004) 15574823
TITLE	
JOURNAL	
PUBMED	
REFERENCE	2 (bases 1 to 723) Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y. Direct Submission Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgpc.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute of Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadaï, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199 e-mail: abe@rtc.riken.jp PRIMERS Sequencing : T7 LIBRARY Vector : pBACe3.6 R.Site 1 : EcoRI. R.Site 2 : EcoRI. Location/Qualifiers 1..723 /organism="Mus musculus molossinus" /mol_type="genomic DNA" /sub_species="molossinus" /db_xref="taxon:57486" /clone="MSMG01-172D11.T7" /sex="male" /tissue type="mixture of kidney and spleen" /clone_lib="MSMG01 Mouse Male BAC Library"
ORIGIN	
Query Match	53.3%; Score 28.8; DB 14; Length 723;
Best Local Similarity	75.0%; Pred. No. 4.9;
Matches	36; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Qy	6 TAATACGACTCACTATAGGGAGACCACATTGTGCATAATTTCCCGCATGC 53
Db	16 TAATACGACTCACTATAGGGAGAGATCCCGGAATTTCCTCCCGCATGC 63
RESULT 75	BQ102694 Drosophila 8-12 hr embryonic cdna library Drosophila
LOCUS	UUGC0075 Drosophila 8-12 hr embryonic cdna library Drosophila
DEFINITION	melanogaster cdna 5', mRNA sequence.
ACCESSION	BQ102694
VERSION	BQ102694.1 GI:20144177
KEYWORDS	EST.
SOURCE	Drosophila melanogaster (fruit fly)
ORGANISM	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 452)
REFERENCE	
/organism="Mus musculus"	
/mol_type="mRNA"	
/strain="C57BL/6J"	
/db_xref="taxon:10090"	
/clone="UI-M-B20-axu-e-01-0-UI"	
/dev_stage="27-32 days"	
/lab_host="DH10B (Life Technologies)"	
/clone_lib="NIH_BMAP_MHI2"	
/note="Vector: pT73D-PacI; Site 1: Not I; Site 2: Eco RI; The NIH BMAP MHI2 library is derived from mouse hippocampus tissue. For a detailed description of the library from which this clone was derived, please visit our web site at brainest.eng.uiowa.edu. TAG_TISSUE=hippocampus TAG_LIB=NIH_BMAP_MHI2 TAG_SEQ=CGGNA"	
ORIGIN	
Query Match	53.7%; Score 29; DB 7; Length 373;
Best Local Similarity	77.8%; Pred. No. 3.7;
Matches	35; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy	1 GAATTAATACGACTCACTATAGGGAGACCACATTGTCCAATTT 45
Db	329 GAATTAATACGACTCACTATAGGGAGCCCTCGGCCGAATTCIT 373
RESULT 73	CD630668 FLP Homo sapiens cDNA, mRNA linear EST 12-JAN-2004
LOCUS	55109686H1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION	CD630668
ACCESSION	CD630668
VERSION	CD630668.1 GI:40278934
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 597) Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L. Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes Genomics 84 (1), 205-210 (2004) 15203218 Contact: Fu GK Incyte Genomics, Inc. 3160 Porter Dr., Palo Alto, CA 94304, USA Tel: 6508454102 Email: gfu@incyte.com. Location/Qualifiers 1..597 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone_lib="FLP" /note="Vector: pDrive Cloning Vector"
ORIGIN	
Query Match	53.3%; Score 28.8; DB 5; Length 597;
Best Local Similarity	75.0%; Pred. No. 4.7;
Matches	36; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Qy	7 AATACGACTCACTATAGGGAGACCACATTGTGCAATATTTCCCGCATGC 54
Db	1 AATACGACTCACTATAGGGAGCCAGTGCTGTGGAAAGTGGCCACTGC 48
RESULT 74	AG368203 Mus musculus molossinus DNA, clone:MSMG01-172D11.T7, genomic survey
LOCUS	723 bp DNA linear GSS 21-DEC-2004
DEFINITION	Mus musculus molossinus DNA, clone:MSMG01-172D11.T7, genomic survey sequence.

AUTHORS Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B.,
Metherall,J.E. and Letsou,A.
TITLE An automated screen for spatially restricted transcripts in
Drosophila embryogenesis
JOURNAL Genome Res. (2002) In press
COMMENT Contact: Letsou, A.
Department of Human Genetics
Eccles Institute of Human Genetics, University of Utah
15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA
Tel: 801 581-4422
Fax: 801 581-7796
Email: aletsou@genetics.utah.edu
Seq primer: SP6.
FEATURES
source
1. .452
Location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/dev_stage="embryonic 8-12 hr post-fertilization"
/clone_lib="Drosophila 8-12 hr embryonic cDNA library"
/note="Vector: plasmid pNB; see Brown, N.H. and Kafatos,
F.C. (1988) Functional cDNA libraries from Drosophila
embryos. J. Mol Biol. 203, 425-37."
ORIGIN
Query Match 53.0%; Score 28.6; DB 3; Length 452;
Best Local Similarity 88.6%; Pred. No. 5.4;
Matches 31; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGGAGACCACTT 35
|||||
Db 59 GAAATTAATACGACTCACTATAGGAGACCGGAAT 25
|||||
RESULT 76
BE410822/c 214 bp mRNA linear EST 21-JUL-2000
LOCUS 601301472F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636328 5',
mRNA sequence.
DEFINITION BE410822
ACCESSION BE410822.1 GI:9347272
VERSION EST.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 214)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: c9apbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM333 row: o column: 17
High quality sequence start: 63
High quality sequence stop: 161.
Location/Qualifiers
FEATURES
source
1..214
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3636328"
/tissue_type="choriocarcinoma"
/lab_host="PH10B (phage-resistant)"
/clone_lib="NIH_MGC_21"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming."

Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
Query Match 52.6%; Score 28.4; DB 7; Length 214;
Best Local Similarity 96.7%; Pred. No. 5.8;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGGAGACC 30
|||||
Db 131 GAAATTAATACGACTCACTAGAGGAGACC 102
|||||
RESULT 77
CD625578 717 bp mRNA linear EST 12-JAN-2004
LOCUS 55147850H1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD625578
ACCESSION CD625578
VERSION CD625578.1 GI:40273844
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 717)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
PUBMED 15203218
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
1..717
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN
Query Match 52.6%; Score 28.4; DB 5; Length 717;
Best Local Similarity 76.1%; Pred. No. 6.9;
Matches 35; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 6 TAATACGACTCACTATAGGAGACCACTTGTGCAATATTCCTCCAC 51
|||||
Db 1 TAATACGACTCACTATAGGAGCCAGTCTGAGGAGGTCGCCGAC 46
|||||
RESULT 78
AG397294 730 bp DNA linear GSS 21-DEC-2004
LOCUS AG397294
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-217P04.T7, genomic survey
sequence.
ACCESSION AG397294
VERSION AG397294.1 GI:48032406
KEYWORDS GSS.
SOURCE Mus musculus molossinus (Japanese wild mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,

Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and Shiroishi,T.
 Contribution of Asian mouse subspecies *Mus musculus molossinus* to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis
 Genome Res. 14 (12), 2439-2447 (2004)
 15574823
 2 (bases 1 to 730)
 Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
 Direct Submission
 Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suihro-chou,Tsuri-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:hattori@psc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
 Clones are derived from the mouse BAC library MSNg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
 Tsukuba Institute, Bio Resource Center,
 The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan
 phone: 81-298-36-9189, fax: 81-298-36-9199
 e-mail: abe@rtc.riken.jp
 PRIMERS
 Sequencing : T7
 LIBRARY
 Vector : pBACe3.6
 R.Site 1 : EcoRI
 R.Site 2 : EcoRI.

FEATURES

source
 Location/Qualifiers
 1..730
 /organism="Mus musculus molossinus"
 /mol_type="genomic DNA"
 /sub_species="molossinus"
 /db_xref="taxon:57486"
 /clone="MSNg01-21P04.T7"
 /sex="male"
 /tissue type="mixture of kidney and spleen"
 /clone_lib="MSNg01 Mouse Male BAC Library"

ORIGIN

Query Match 52.6%; Score 28.4; DB 14; Length 730;
 Best Local Similarity 76.1%; Pred. NO. 6.9;
 Matches 35; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 Qy 6 TAATACGACTCCTATAGGAGACACATTCTGCAATATCCCCAC 51
 |||||
 Db 18 TAATACGACTCCTATAGGAGAGGAATCCGGGAATTTTACAC 63

RESULT 79
 BE737118/c
 LOCUS
 DEFINITION 601304503F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3638784 5', mRNA sequence.
 BE737118
 VERSION
 BE737118.1 GI:10151110
 EST.
 SOURCE Homo sapiens (human)

ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 784)
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LICM441 row: f column: 01
 High quality sequence start: 23
 High quality sequence stop: 157.
 Location/Qualifiers

FEATURES

source
 1..784
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3638784"
 /tissue_type="adenocarcinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_39"
 /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dr priming.
 Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 52.6%; Score 28.4; DB 7; Length 784;
 Best Local Similarity 96.7%; Pred. No. 7;
 Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GAAATTAATACGACTCTATAGGAGACC 30
 |||||
 Db 118 GAAATTAATACGACTCTATAGGAGACC 89
 RESULT 80
 BG491171/c
 LOCUS
 DEFINITION 602535205F1 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:4654152 5', mRNA sequence.
 BG491171
 VERSION
 BG491171.1 GI:13452683
 EST.
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 826)
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: DCTD/BTP
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LICM1441 row: i column: 01
 High quality sequence start: 46
 High quality sequence stop: 145.
 Location/Qualifiers

FEATURES

source
 1..826
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4654152"
 /tissue_type="amelanotic melanoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_41"
 /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 52.6%; Score 28.4; DB 2; Length 826;
Best Local Similarity 96.7%; Pred. No. 7.1;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTATACGACTCACTATAGGAGACC 30
|||||
Db 111 GAAATTATACGACTCACTATAGGAGACC 82
|||||

RESULT 81

BE727309/c
LOCUS BE727309 910 bp mRNA linear EST 15-SEP-2000
DEFINITION 601560609F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3830282 5',
mRNA sequence.

ACCESSION BE727309
VERSION BE727309
KEYWORDS BE727309.1 GI:10141402
SOURCE EST.

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1 (bases 1 to 910)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM504 row: a column: 03
High quality sequence start: 7
High quality sequence stop: 109.

FEATURES

source

1..910
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3830282"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_20"

/note="Organ: skin; Vector: pOTB7; Site: 1: XhoI; Site: 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAGGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 52.6%; Score 28.4; DB 7; Length 910;
Best Local Similarity 96.7%; Pred. No. 7.2;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTATACGACTCACTATAGGAGACC 30
|||||
Db 75 GAAATTATACGACTCACTATAGAGACC 46
|||||

RESULT 82

BG490614/c

LOCUS BG490614

DEFINITION 602519576F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4638019 5',
mRNA sequence.

ACCESSION BG490614

VERSION BG490614.1 GI:13452124

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1 (bases 1 to 1150)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTF/Gazdar

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLCM1399 row: h column: 20

High quality sequence stop: 120.

FEATURES

source

1..1150
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4638019"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_18"

/note="Organ: lung; Vector: pOTB7; Site: 1: XhoI; Site: 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 52.6%; Score 28.4; DB 2; Length 1150;

Best Local Similarity 96.7%; Pred. No. 7.4;

Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTATACGACTCACTATAGGAGACC 30
|||||

Db 84 GAAATTATACGACTCACTATAGGAGACC 55
|||||

RESULT 83

DR138757/c

LOCUS DR138757

DEFINITION 49194855 Drosophila pseudobscura embryonic cDNA library Drosophila
pseudobscura cDNA clone Al3 5', mRNA sequence.

ACCESSION DR138757

VERSION DR138757.1 GI:67883847

KEYWORDS EST.

SOURCE Drosophila pseudobscura

ORGANISM

Drosophila pseudobscura
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1201)

Richards S., Liu, Y., Bettencourt, B.R., Hradscky, P., Letovsky, S.,

Nielsen, R., Thornton, K., Hubisz, M.J., Chen, R., Meisel, R.P.,

Couronne, O., Hua, S., Smith, M.A., Zhang, P., Liu, J., Bussemaker, H.J.,

EST.

van Batenburg, M.F., Howells, S.L., Scherer, S.E., Sodergren, E.,
 Matthews, B.B., Crosby, M.A., Schroeder, A.J., Ortiz-Barrientos, D.,
 Rives, C.M., Metzker, M.L., Muzny, D.M., Scott, G., Steffen, D.,
 Wheeler, D.A., Worley, K.C., Havlak, P., Durbin, K.J., Egan, A.,
 Gill, R., Hume, J., Morgan, M.B., Miner, G., Hamilton, C., Huang, Y.,
 Waldron, L., Verduzco, D., Clerc-Blankenburg, K.P., Dubchak, I.,
 Noor, M.A., Anderson, W., White, K.P., Clark, A.G., Schaeffer, S.W.,
 Gelbart, W., Weinstein, G.M., and Gibbs, R.A.
 Comparative genome sequencing of *Drosophila pseudoobscura*:
 Chromosomal, gene, and cis-element evolution
 Genome Res. 15 (1), 1-18 (2005)
 15632085
 Contact: Stephen Richards
 Human Genome Sequencing Center
 Baylor College of Medicine
 One Baylor Plaza, Houston, TX 77030, USA
 Tel: 713-798-6667
 Email: stephenr@bcm.tmc.edu
 NCBI Trace Archive: 226708009
 Insert Length: 1750 Std Error: 0.25.
 Location/Qualifiers

FEATURES

1..1201
 /organism="Drosophila pseudoobscura"
 /mol_type="mRNA"
 /db_xref="taxon:7237"
 /clone="Al3"
 /dev_stage="0-18h embryos"
 /clone_lib="Drosophila pseudoobscura embryonic cDNA
 library"
 /note="Vector: pOTB7; Site 1: EcoRI; Site 2: XhoI; oligo
 dt priming from poly A+ RNA, directionally cloned"

ORIGIN

Query Match 52.6%; Score 28.4; DB 9; Length 1201;
 Best Local Similarity 96.7%; Pred. No. 7.4;
 Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTTATAGCACTCACTATAGGAGACC 30
 |||||
 Db 502 GAAATTTATAGCACTCACTATAGGAGACC 473

RESULT 84
 BQ102668/c
 LOCUS BQ102668 403 bp mRNA linear EST 12-APR-2002
 DEFINITION U00C0047 Drosophila 8-12 hr embryonic cDNA library Drosophila
 melanogaster cDNA 5', mRNA sequence.

ACCESSION BQ102668
 VERSION BQ102668.1 GI:20144151
 KEYWORDS EST.
 ORGANISM Drosophila melanogaster (fruit fly)
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 403)
 AUTHORS Simin, K., Scuderi, A., Reamey, J., Dunn, D.M., Weiss, R.B.,
 Metherall, J.E. and Letsou, A.
 TITLE An automated screen for spatially restricted transcripts in
 Drosophila embryogenesis

JOURNAL Drosophila embryogenesis
 COMMENT Genome Res. (2002) In press
 Department of Human Genetics
 Eccles Institute of Human Genetics, University of Utah
 15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA
 Tel: 801 581-4422
 Fax: 801 581-7796
 Email: aletsou@genetics.utah.edu

Seq primer: SP6
 Location/Qualifiers
 1..403
 /organism="Drosophila melanogaster"
 /mol_type="mRNA"

FEATURES

/db_xref="taxon:7227"
 /dev_stage="embryonic 8-12 hr post-fertilization"
 /clone_lib="Drosophila 8-12 hr embryonic cDNA library"
 /note="Vector: plasmid pNB; see Brown, N.H. and Kafatos,
 F.C. (1988) Functional cDNA libraries from *Drosophila*
 embryos. J. Mol Biol. 203, 425-37."

ORIGIN

Query Match 52.2%; Score 28.2; DB 3; Length 403;
 Best Local Similarity 90.9%; Pred. No. 7.6;
 Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AATTAATACGACTCACTATAGGAGACCACTT 35
 |||||
 Db 51 AATTAATACGACTCACTATAGGAGACCGAAT 19

RESULT 85
 CD629304

LOCUS CD629304 707 bp mRNA linear EST 12-JAN-2004
 DEFINITION 5514282SH1 FLP Homo sapiens cDNA, mRNA sequence.

ACCESSION CD629304
 VERSION CD629304.1 GI:40277570
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 707)
 AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
 TITLE Circular rapid amplification of cDNA ends for high-throughput
 extension cloning of partial genes
 JOURNAL Genomics 84 (1), 205-210 (2004)
 PUBMED 15203218

COMMENT Contact: Fu GK
 Incyte Genomics, Inc.
 3160 Porter Dr., Palo Alto, CA 94304, USA
 Tel: 6508454102
 Email: gfu@incyte.com.
 Location/Qualifiers

FEATURES

1..707
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="FLP"
 /note="Vector: pDrive Cloning Vector"

ORIGIN

Query Match 52.2%; Score 28.2; DB 5; Length 707;
 Best Local Similarity 73.5%; Pred. No. 8.3;
 Matches 36; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 6 TAATACGACTCACTATAGGAGACCACTTGTGCAATATTCCTCCACTGC 54
 |||||
 Db 1 TAATACGACTCACTATAGGAGACCACTGTGCTGGAAGTCGCTCAGC 49

RESULT 86
 AG399005

LOCUS AG399005 737 bp DNA linear GSS 21-DEC-2004
 DEFINITION Mus musculus molossinus DNA, clone:MSMg01-232110.T7, genomic survey
 sequence.

ACCESSION AG399005
 VERSION AG399005.1 GI:48037712
 KEYWORDS GSS.
 SOURCE Mus musculus molossinus
 ORGANISM Mus musculus molossinus (Japanese wild mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1
 AUTHORS Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T.,

Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and Shiroishi,T.
 Contribution of Asian mouse subspecies *Mus musculus molossinus* to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis
 Genome Res. 14 (12), 2439-2447 (2004)
 15574823
 2 (bases 1 to 737)
 Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
 Direct Submission
 Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Japan
 1-7-22 Suehiro-chou, Tsukuba, Ibaraki, 305-0856, Japan
 (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
 Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
 Tsukuba Institute, Bio Resource Center,
 The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan
 phone: 81-298-36-9189, fax: 81-298-36-9199
 e-mail: abe@rtc.riken.jp
 PRIMERS
 Sequencing : T7
 LIBRARY
 Vector : pBACe3.6
 R.Site 1 : EcoRI
 R.Site 2 : EcoRI

FEATURES

source

1..737
 /organism="Mus musculus molossinus"
 /mol_type="genomic DNA"
 /sub_species="molossinus"
 /db_xref="taxon:57486"
 /clone="MSMg01-232110.T7"
 /sex="male"
 /tissue_type="mixture of kidney and spleen"
 /clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN

Query Match 52.2%; Score 28.2; DB 14; Length 737;
 Best Local Similarity 73.5%; Pred. No. 8.3;
 Matches 36; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 QY 6 TAATAGCACTACTATAGGAGACCATTTGCAATATCCCACTGC 54
 |||||
 Db 18 TAATAGCACTACTATAGGAGAGGACTCCGGGATTCATCACTAC 66
 |||||

RESULT 87
 BE749102/c
 LOCUS
 DEFINITION
 mRNA sequence.
 BE749102
 BE749102.1 GI:10163094
 EST.
 SOURCE
 Homo sapiens (human)

1507 bp mRNA linear EST 15-SEP-2000
 601123149F1 NIH_MGC_5 Homo sapiens cDNA clone IMAGE:3347988 5',
 mRNA sequence.
 BE749102
 BE749102.1 GI:10163094
 EST.
 SOURCE
 Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 1 (bases 1 to 1507)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be

FEATURES

source

1..1507
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3347988"
 /tissue_type="carcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_5"
 /note="Organ: cervix; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 52.2%; Score 28.2; DB 7; Length 1507;
 Best Local Similarity 90.9%; Pred. No. 9.2;
 Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GAATTAATACGACTCACTATAGGAGACCA 33
 |||||
 Db 68 GAATTAATACGACTCACTATAGGAGAACGGCA 36
 |||||

RESULT 88

BE749102/c

LOCUS

DEFINITION

mRNA sequence.

BE749102

BE749102.1 GI:13145090

EST.

KEYWORDS

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 1 (bases 1 to 385)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1253 row: n column: 02

High quality sequence stop: 351.

Location/Qualifiers

1..385

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4554433"

/tissue_type="leiomyosarcoma cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_46"

/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LLCM140 row: a column: 13
 High quality sequence start: 38
 High quality sequence stop: 273.
 Location/Qualifiers

1..1507
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3347988"
 /tissue_type="carcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_5"
 /note="Organ: cervix; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 52.2%; Score 28.2; DB 7; Length 1507;
 Best Local Similarity 90.9%; Pred. No. 9.2;
 Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GAATTAATACGACTCACTATAGGAGACCA 33
 |||||
 Db 68 GAATTAATACGACTCACTATAGGAGAACGGCA 36
 |||||

RESULT 88

BE749102/c

LOCUS

DEFINITION

mRNA sequence.

BE749102

BE749102.1 GI:13145090

EST.

KEYWORDS

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 1 (bases 1 to 385)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1253 row: n column: 02

High quality sequence stop: 351.

Location/Qualifiers

1..385

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4554433"

/tissue_type="leiomyosarcoma cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_46"

/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size

1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 51.9%; Score 28; DB 2; Length 385;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AATTAAATACGACTCTACTATAGGAGACC 30
|||||
Db 314 AATTAAATACGACTCTACTATAGGAGACC 287

RESULT 89

BG438290/c
LOCUS BG438290
DEFINITION 602489239F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4621616 5', mRNA sequence.
ACCESSION BG438290
VERSION BG438290.1 GI:13344796
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 648)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLCW1384 row: m column: 09
High quality sequence start: 8
High quality sequence stop: 128.

FEATURES

source

1..648
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4621616"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 18"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCCAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 51.9%; Score 28; DB 2; Length 648;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AATTAAATACGACTCTACTATAGGAGACC 30
|||||
Db 91 AATTAAATACGACTCTACTATAGGAGACC 64

RESULT 90

CW951343/c

LOCUS

DEFINITION

TCB36.4_C02.T7 Tribolium BAC library Tribolium castaneum genomic, genomic_survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Triolium castaneum (red flour beetle)

Triolium castaneum

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia; Tenebrionidae; Tribolium.

1 (bases 1 to 907)

Savard, J. and Tautz, D.

Triolium castaneum BAC-ends sequencing project

Unpublished (2003)

CONTACT: Savard, J.

Abteilung fur Evolutionsgenetik, AG Tautz

Institut fur Genetik, Universitat zu Koln

Weyertal 121, 50931 Koln, Germany

Tel: 49 221 470 6911

Fax: 49 221 470 5975

Email: savard@uni-koeln.de

Class: BAC ends

Location/Qualifiers

1..907

/organism="Tribolium castaneum"

/mol_type="genomic DNA"

/strain="GA-2"

/db_xref="taxon:7070"

/clone_lib="Tribolium BAC library"

/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; Library constructed by Exelixis Inc."

ORIGIN

Query Match 51.9%; Score 28; DB 13; Length 907;

Best Local Similarity 71.2%; Pred. No. 10;

Matches 37; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 2 AAATTAATACGACTCTACTATAGGAGACCACATTGTGCAATATTCCCACTG 53

|||||

Db 66 AAATTAATACGACTCTACTATAGGAGTCTATAGGCGATTATACGCTCGAATG 15

RESULT 91

AG375696

LOCUS

DEFINITION

Mus musculus molossinus DNA, clone:MSMg01-182P08.TJ, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus molossinus (Japanese wild mouse)

Mus musculus molossinus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

1

Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T., Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriawaki, K. and Shiroishi, T.

Contribution of Asian mouse subspecies Mus musculus molossinus to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis

Genome Res. 14 (12), 2439-2447 (2004)

15574823

2 (bases 1 to 704)

Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

Direct Submission

Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

(E-mail: hattori@sc.riken.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center, Research (RIKEN) 3-1-1
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp

PRIMERS
Sequencing : T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI
Location/Qualifiers
1. .707
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-169M02.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

FEATURES
source
1. .704
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-182P08.TJ"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN
Query Match 51.5%; Score 27.8; DB 14; Length 704;
Best Local Similarity 74.5%; Pred. No. 12;
Matches 35; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 6 TAATACGACTCACTATAGGAGACACACATTGTGCAATATTCCTCCACT 52
|||||
Db 18 TAATACGACTCACTATAGGAGATCGCGGAATTCCTACCCACT 64
|||||

RESULT 92
AG366526 707 bp DNA linear GSS 21-DEC-2004
LOCUS Mus musculus molossinus DNA, clone: MSMg01-169M02.T7, genomic survey
DEFINITION
ACCESSION AG366526.1 GI:47977731
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus molossinus (Japanese wild mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T.,
Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriaki, K. and
Shiroishi, T.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
(E-mail: hattori@sc.riken.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp

JOURNAL
PUBMED
REFERENCE
2 (bases 1 to 707)
AUTHORS
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
(E-mail: hattori@sc.riken.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp

PRIMERS
Sequencing : T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI
Location/Qualifiers
1. .707
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-169M02.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

FEATURES
source
1. .707
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-169M02.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN
Query Match 51.5%; Score 27.8; DB 14; Length 707;
Best Local Similarity 74.5%; Pred. No. 12;
Matches 35; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 6 TAATACGACTCACTATAGGAGACACACATTGTGCAATATTCCTCCACT 52
|||||
Db 18 TAATACGACTCACTATAGGAGATCGCGGAATTCCTACCCACT 64
|||||

RESULT 93
AG409074 737 bp DNA linear GSS 21-DEC-2004
LOCUS Mus musculus molossinus DNA, clone: MSMg01-268L24.T7, genomic survey
DEFINITION
ACCESSION AG409074
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus molossinus (Japanese wild mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T.,
Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriaki, K. and
Shiroishi, T.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
(E-mail: hattori@sc.riken.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp

JOURNAL
PUBMED
REFERENCE
2 (bases 1 to 737)
AUTHORS
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
(E-mail: hattori@sc.riken.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp

JOURNAL
PUBMED
REFERENCE
2 (bases 1 to 737)
AUTHORS
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
(E-mail: hattori@sc.riken.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp

```

/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-268J24.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

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ORIGIN

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Query Match      51.5%; Score 27.8; DB 14; Length 737;
Best Local Similarity 74.5%; Pred. No. 12;
Matches 35; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Qy      6 TAATACGACTCATTAGGAGACACATTGTGCAATATCCCACT 52
          |||||
Db     18 TAATACGACTCATTAGGAGAGATCCGCGGAATCTTTCCCACT 64
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RESULT 94
AG409684
LOCUS
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-269J20.T7, genomic survey
sequence.
ACCESSION AG409684
VERSION AG409684.1 GI:48052370
KEYWORDS GSS.
SOURCE Mus musculus molossinus (Japanese wild mouse)
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1

```

```

REFERENCE
AUTHORS Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,
Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and
Shiroishi,T.

```

```

TITLE Contribution of Asian mouse subspecies Mus musculus molossinus to
genomic constitution of strain C57BL/6J, as defined by BAC-end
sequence-SNP analysis
Genome Res. 14 (12), 2439-2447 (2004)
15574823
2 (bases 1 to 742)
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission

```

```

JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
(E-mail:hattori@psc.riken.jp, URL:http://hgp.9sc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
Location/Qualifiers
1..742
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-269J20.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

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FEATURES source

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1..742
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-269J20.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

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ORIGIN

```

Query Match      51.5%; Score 27.8; DB 14; Length 742;
Best Local Similarity 74.5%; Pred. No. 12;
Matches 35; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

```

```

Qy      6 TAATACGACTCATTAGGAGACACATTGTGCAATATCCCACT 52
          |||||
Db     14 TAATACGACTCATTAGGAGAGATCCGCGGAATCTTCTCACT 60
          |||||

```

```

RESULT 95
AG357071
LOCUS
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-156E17.T7, genomic survey
sequence.
ACCESSION AG357071
VERSION AG357071.1 GI:47930381
KEYWORDS GSS.
SOURCE Mus musculus molossinus (Japanese wild mouse)
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1

```

```

REFERENCE
AUTHORS Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,
Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and
Shiroishi,T.
TITLE Contribution of Asian mouse subspecies Mus musculus molossinus to
genomic constitution of strain C57BL/6J, as defined by BAC-end
sequence-SNP analysis
Genome Res. 14 (12), 2439-2447 (2004)
15574823
2 (bases 1 to 743)
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission

```

```

JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
(E-mail:hattori@psc.riken.jp, URL:http://hgp.9sc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
Location/Qualifiers
1..743
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-156E17.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

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ORIGIN

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Query Match      51.5%; Score 27.8; DB 14; Length 743;
Best Local Similarity 74.5%; Pred. No. 12;
Matches 35; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Qy      6 TAATACGACTCATTAGGAGACACATTGTGCAATATCCCACT 52
          |||||
Db     17 TAATACGACTCATTAGGAGAGATCCGCGGAATCTTCTCACT 63
          |||||

```

```

RESULT 96
AG377287
LOCUS
DEFINITION
Mus musculus molossinus DNA, clone:MSMg01-185D18.T7, genomic survey
sequence.
ACCESSION
AG377287
VERSION
GI:47988492
KEYWORDS
Mus musculus molossinus (Japanese wild mouse)
SOURCE
GSS.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1
Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,
Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriaki,K. and
Shiroishi,T.
TITLE
Contribution of Asian mouse subspecies Mus musculus molossinus to
genomic constitution of strain C57BL/6J, as defined by BAC-end
sequence-SNP analysis
JOURNAL
Genome Res. 14 (12), 2439-2447 (2004)
PUBMED
15574823
REFERENCE
2 (bases 1 to 767)
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
TITLE
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
(E-mail:hattori@gsc.riken.jp URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY
Vector : pBAC3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
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Db 31 TAATACGACTACTATAGGAGGATCCGCGAATTTCTTCCCACT 77
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RESULT 97
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DEFINITION
KBRH118G04 genomic clone, KBrH (HindIII) BAC library Brassica rapa
subsp. pekinensis, genomic survey sequence.
ACCESSION
CT010966
VERSION
GI:71479007
KEYWORDS
Brassica rapa subsp. pekinensis
SOURCE
GSS.
ORGANISM
Brassica rapa subsp. pekinensis
REFERENCE
1
Viehöver,P., Holtgraewe,D. and Weishaar,B.
BAC end sequences of Brassica rapa
Unpublished
REFERENCE
2 (bases 1 to 874)
Li,Y. and Weishaar,B.
Direct Submission
TITLE
Submitted (09-AUG-2005) Weishaar B., Bielefeld University,
Institute for Genome Research, Universitätsstrasse 25, D-33594
Bielefeld, Germany
COMMENT
Contact: Bernd Weishaar
Bielefeld University, Institute for Genome Research
Universitätsstrasse 25, D-33594 Bielefeld, Germany Email:
bernd.weishaar@uni-bielefeld.de
BAC end sequences of Brassica rapa BAC clone KBrH118G04; generated
as contribution to the 'Multinational Brassica rapa Sequencing
Project' Seq primer: sp6B ATTTAGGTGACACTATAG
Class: BAC ends
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RESULT 98
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LOCUS
DEFINITION
TCB29.4 A01.T7 Tribolium BAC library Tribolium castaneum genomic,
genomic survey sequence.
ACCESSION
CW946685
VERSION
GI:56729300
KEYWORDS
Tribolium castaneum (red flour beetle)
SOURCE
Tribolium castaneum
ORGANISM
Tribolium castaneum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Tenebrionidae; Tribolium.
REFERENCE
1 (bases 1 to 897)
Savard,J. and Tautz,D.
Tribolium castaneum BAC-ends sequencing project
Unpublished (2003)
COMMENT
Contact: Savard, J.
Abteilung für Evolutionsgenetik, AG Tautz
Institut für Genetik, Universität zu Köln
Weyertal 121, 50931 Köln, Germany
Tel: 49 221 470 6911
Fax: 49 221 470 5975
Email: savard@uni-koeln.de
Class: BAC ends.
FEATURES
source
Location/Qualifiers
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Best Local Similarity 76.7%; Pred. No. 15;
Matches 33; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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RESULT 99
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DEFINITION    BOHSZ75TF BOHS Brassica oleracea genomic clone BOHSZ75, genomic
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ACCESSION     BH501537
VERSION       BH501537.1 GI:17709634
KEYWORDS      GSS
SOURCE        Brassica oleracea
ORGANISM      Brassica oleracea
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               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
               rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE     1 (bases 1 to 317)
AUTHORS       Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
               Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
TITLE         Whole genome shotgun sequencing of Brassica oleracea and its
               application to gene discovery and annotation in Arabidopsis
JOURNAL       Genome Res. 15 (4), 487-495 (2005)
PUBMED        15805490
COMMENT       Contact: Chris Town
               TIGR
               9712 Medical Center Drive, Rockville, MD 20850, USA.
               Tel: 301-838-3523
               Fax: 301-838-0208
               Email: cdtown@tigr.org
               DNA is from a doubled haploid provided by Tom Osborn.
               Seq primer: TF
               Class: sheared ends.
               Location/Qualifiers
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Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DEFINITION    BOGJM68TF BOGJ Brassica oleracea genomic clone BOGJM68, genomic
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ACCESSION     BH523081

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VERSION          BH523081.1 GI:17731166
KEYWORDS         GSS.
SOURCE           Brassica oleracea
ORGANISM         Brassica oleracea
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               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
               rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE     1 (bases 1 to 317)
AUTHORS       Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
               Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
TITLE         Whole genome shotgun sequencing of Brassica oleracea and its
               application to gene discovery and annotation in Arabidopsis
JOURNAL       Genome Res. 15 (4), 487-495 (2005)
PUBMED        15805490
COMMENT       Contact: Chris Town
               TIGR
               9712 Medical Center Drive, Rockville, MD 20850, USA.
               Tel: 301-838-3523
               Fax: 301-838-0208
               Email: cdtown@tigr.org
               DNA is from a doubled haploid provided by Tom Osborn.
               Seq primer: TF
               Class: sheared ends.
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Query Match      50.7%; Score 27.4; DB 11; Length 317;
Best Local Similarity 96.6%; Pred. No. 15;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AATTAATACGACTCACTATAGGAGACCA 31
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Db 19 AATTAATACGACTCACTATAGGAGACGA 47

Search completed: May 19, 2006, 07:06:15
Job time : 3625.49 secs

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2006, 23:59:38 ; Search time 165.253 Seconds
 (without alignments)
 611.425 Million cell updates/sec

Title: US-10-665-708-11
 Perfect score: 54
 Sequence: 1 gaattaatacagctacta.....tgtgaataatccccactgc 54

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 300 summaries

Database : Issued Patents_NA.*
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 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	41	75.9	57	3	US-09-738-274-10	Sequence 10, Appl	
4	40	74.1	59	3	US-09-738-274-9	Sequence 9, Appl	
5	37.6	69.6	54	3	US-09-944-036-9	Sequence 9, Appl	
6	37.6	69.6	54	3	US-10-425-975-9	Sequence 9, Appl	
7	37	68.5	53	3	US-09-944-036-42	Sequence 42, Appl	
8	37	68.5	53	3	US-10-425-975-42	Sequence 42, Appl	
9	37	68.5	57	3	US-09-738-274-7	Sequence 7, Appl	
10	37	68.5	57	3	US-09-738-972-3	Sequence 3, Appl	
C	11	37	68.5	57	3	US-09-738-972-13	Sequence 13, Appl
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13	36	66.7	37	3	US-10-425-975-2	Sequence 2, Appl	
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16	35.8	66.3	53	3	US-09-944-036-34	Sequence 34, Appl	
17	35.8	66.3	53	3	US-09-944-036-36	Sequence 36, Appl	
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19	35.8	66.3	53	3	US-10-425-975-36	Sequence 36, Appl	
20	35.4	65.6	54	3	US-09-493-491-49	Sequence 49, Appl	
21	35.4	65.6	54	3	US-09-493-491A-49	Sequence 49, Appl	
22	35.4	65.6	54	3	US-10-273-707-49	Sequence 49, Appl	
23	35.4	65.6	55	3	US-09-944-036-10	Sequence 10, Appl	

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32	34.4	63.7	62	3	US-10-140-545-48	Sequence 48, Appl
33	34	63.0	53	3	US-09-944-036-38	Sequence 38, Appl
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38	34	63.0	55	3	US-09-944-036-45	Sequence 45, Appl
39	34	63.0	55	3	US-10-425-975-45	Sequence 45, Appl
40	34	63.0	61	3	US-09-738-972-2	Sequence 2, Appl
41	34	63.0	61	3	US-09-738-972-12	Sequence 12, Appl
42	33.8	62.6	52	3	US-09-493-491-33	Sequence 33, Appl
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56	33	61.1	51	2	US-08-902-623-33	Sequence 33, Appl
57	33	61.1	51	3	US-09-944-036-41	Sequence 41, Appl
58	33	61.1	51	3	US-10-425-975-41	Sequence 41, Appl
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61	33	61.1	53	3	US-09-944-036-37	Sequence 37, Appl
62	33	61.1	53	3	US-10-425-975-37	Sequence 37, Appl
63	33	61.1	55	2	US-08-162-836-14	Sequence 14, Appl
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65	33	61.1	55	3	US-08-116-984A-13	Sequence 13, Appl
66	33	61.1	55	3	US-09-502-966-10	Sequence 10, Appl
67	33	61.1	55	3	US-09-944-036-44	Sequence 44, Appl
68	33	61.1	55	3	US-10-425-975-44	Sequence 44, Appl
69	33	61.1	55	5	US-08-480-472A-1	Sequence 1, Appl
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71	33	61.1	59	3	US-09-738-972-1	Sequence 1, Appl
72	33	61.1	59	3	US-09-738-972-11	Sequence 11, Appl
73	33	61.1	60	2	US-07-971-819A-36	Sequence 36, Appl
74	33	61.1	60	2	US-08-475-231-36	Sequence 36, Appl
75	33	61.1	62	2	US-08-345-861-1	Sequence 1, Appl
76	33	61.1	63	3	US-09-425-585-5	Sequence 5, Appl
77	33	61.1	63	3	US-09-953-321-5	Sequence 5, Appl
78	33	61.1	66	5	US-10-124-663A-2	Sequence 2, Appl
79	33	61.1	67	3	US-09-518-813B-14	Sequence 14, Appl
80	33	61.1	75	3	US-09-486-356-16	Sequence 16, Appl
81	33	61.1	75	3	US-09-577-528B-16	Sequence 16, Appl
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83	33	61.1	90	2	US-08-902-623-24	Sequence 24, Appl
84	33	61.1	102	3	US-08-678-735A-2	Sequence 2, Appl
85	33	61.1	102	3	US-08-418-992-5	Sequence 5, Appl
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94	33	61.1	187	7	PCT-US94-08327-7	Sequence 7, Appl
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98	33	61.1	2839	3	US-09-809-517A-36	Sequence 36, Appl	171	32.6	60.4	55	5	US-08-480-472A-21	Sequence 21, Appl
99	33	61.1	2865	3	US-09-795-872-9	Sequence 9, Appl	c 172	32	59.3	158	3	US-09-722-393A-6	Sequence 6, Appl
100	33	61.1	2869	3	US-09-795-872-8	Sequence 8, Appl	173	32	59.3	3331	3	US-09-582-761B-32	Sequence 32, Appl
101	33	61.1	3984	2	US-08-040-753-1	Sequence 1, Appl	174	32	59.3	4421	3	US-08-952-674-1	Sequence 1, Appl
102	33	61.1	4009	2	US-08-152-483B-6	Sequence 6, Appl	175	32	59.3	7463	2	US-08-715-808-13	Sequence 13, Appl
103	33	61.1	4100	3	US-09-813-718-5	Sequence 5, Appl	176	31.8	58.9	50	3	US-08-972-799A-25	Sequence 25, Appl
104	33	61.1	4294	2	US-08-152-483B-2	Sequence 2, Appl	177	31.8	58.9	50	3	US-09-506-282-25	Sequence 25, Appl
105	33	61.1	4682	3	US-09-813-718-3	Sequence 3, Appl	178	31.8	58.9	50	7	PCT-US95-03339-25	Sequence 25, Appl
106	33	61.1	4682	3	US-09-813-718-7	Sequence 7, Appl	179	31.8	58.9	50	9	US-10-165-281-25	Sequence 25, Appl
c 107	33	61.1	4701	3	US-08-651-472-64	Sequence 64, Appl	180	31.8	58.9	50	9	US-10-164-833-25	Sequence 25, Appl
c 108	33	61.1	4701	3	US-08-358-928-64	Sequence 64, Appl	181	31.8	58.9	75	7	PCT-US93-04950-3	Sequence 3, Appl
109	33	61.1	4742	3	US-09-813-718-15	Sequence 15, Appl	182	31.8	58.9	644	3	US-09-043-506A-17	Sequence 17, Appl
110	33	61.1	4811	3	US-09-813-718-13	Sequence 13, Appl	183	31.8	58.9	3944	2	US-07-678-408A-1	Sequence 1, Appl
111	33	61.1	4819	2	US-08-450-257-20	Sequence 20, Appl	184	31.8	58.9	5437	2	US-08-416-872-1	Sequence 1, Appl
112	33	61.1	4819	2	US-08-450-246-20	Sequence 20, Appl	185	31.8	58.9	5437	2	US-09-035-241-1	Sequence 1, Appl
113	33	61.1	4819	2	US-08-450-098-20	Sequence 20, Appl	186	31.6	58.9	5437	7	PCT-US94-06197-1	Sequence 1, Appl
114	33	61.1	4819	2	US-08-451-233-20	Sequence 20, Appl	187	31.6	58.5	760	3	US-09-043-506A-14	Sequence 14, Appl
115	33	61.1	4819	2	US-08-450-236-20	Sequence 20, Appl	188	31.6	58.5	5053	3	US-09-311-784A-35	Sequence 35, Appl
116	33	61.1	4819	2	US-08-235-403-20	Sequence 20, Appl	189	31.6	58.5	6200	3	US-09-439-923-1	Sequence 1, Appl
117	33	61.1	4877	3	US-09-813-718-11	Sequence 11, Appl	190	31.6	58.5	6200	3	US-09-711-202A-1	Sequence 1, Appl
118	33	61.1	4910	2	US-08-450-257-11	Sequence 11, Appl	191	31.6	58.5	6200	3	US-09-711-205A-1	Sequence 1, Appl
119	33	61.1	4910	2	US-08-450-246-11	Sequence 11, Appl	192	31.6	58.5	6200	3	US-09-993-241-1	Sequence 1, Appl
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121	33	61.1	4910	2	US-08-451-233-11	Sequence 11, Appl	194	31.4	58.1	104	2	US-08-482-182-24	Sequence 24, Appl
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127	33	61.1	4977	2	US-08-450-246-17	Sequence 17, Appl	200	31	57.4	55	3	US-09-493-491-47	Sequence 47, Appl
128	33	61.1	4977	2	US-08-450-098-14	Sequence 14, Appl	201	31	57.4	55	3	US-09-493-491A-47	Sequence 47, Appl
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138	33	61.1	5098	2	US-08-450-257-10	Sequence 10, Appl	211	30.4	56.3	32	3	US-09-944-036-3	Sequence 3, Appl
139	33	61.1	5098	2	US-08-450-246-10	Sequence 10, Appl	212	30.4	56.3	32	3	US-10-425-975-3	Sequence 3, Appl
140	33	61.1	5098	2	US-08-450-098-10	Sequence 10, Appl	213	30.4	56.3	49	3	US-09-493-491-34	Sequence 34, Appl
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143	33	61.1	5098	2	US-08-235-403-10	Sequence 10, Appl	216	30.4	56.3	50	3	US-09-944-036-8	Sequence 8, Appl
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150	33	61.1	5574	3	US-08-235-403-22	Sequence 22, Appl	223	30.4	56.3	10494	4	US-10-138-727A-40	Sequence 40, Appl
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152	33	61.1	6714	2	US-08-021-623C-5	Sequence 5, Appl	225	30.2	55.9	51	3	US-10-425-975-40	Sequence 40, Appl
153	33	61.1	6873	3	US-09-131-028A-1	Sequence 1, Appl	226	30.2	55.9	52	3	US-09-493-491-39	Sequence 39, Appl
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c 155	33	61.1	8430	3	US-09-131-028A-6	Sequence 6, Appl	228	30.2	55.9	52	3	US-10-273-707-42	Sequence 42, Appl
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ALIGNMENTS

RESULT 1
US-09-738-274-11
US-09-738-11, Application US/09738274
; Sequence 11, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc

```

% TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
%
% TITLE OF INVENTION: MYCOBACTERIUM SPECIES
%
% FILE REFERENCE: GP107-02.UT
%
% CURRENT APPLICATION NUMBER: US/09/738,274
%
% CURRENT FILING DATE: 2000-12-15
%
% PRIOR APPLICATION NUMBER: 60/172,190
%
% PRIOR FILING DATE: 1999-12-17
%
% NUMBER OF SEQ ID NOS: 42
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% SOFTWARE: PatentIn Ver. 2.0
%
% SEQ ID NO 11
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% LENGTH: 54
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% TYPE: DNA
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% ORGANISM: Artificial Sequence
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% FEATURE:
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% OTHER INFORMATION: Description of Artificial Sequence: primer
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% OTHER INFORMATION: oligonucleotide
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% NAME/KEY: promoter
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% LOCATION: (1)..(33)
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% US-09-738-274-11

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; Patent NO. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02 UT
; CURRENT APPLICATION NUMBER: US/09/738, 274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-738-274-8

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RESULT 3
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; Sequence 10, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:

; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
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US-09-738-274-10

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; Sequence 9, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
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; FEATURE:
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; OTHER INFORMATION: oligonucleotide
; NAME/KEY: promoter
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US-09-738-274-9

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RESULT 5
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; Sequence 9, Application US/09944036
; Patent No. 6582920
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-9

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RESULT 6
US-10-425-975-9
; Sequence 9, Application US/10425975
; Patent No. 6946254
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
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; SEQ ID NO 9
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-9

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Query Match      69.6%; Score 37.6; DB 3; Length 54;
Best Local Similarity 90.9%; Pred. No. 3.1e-05;
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RESULT 7
US-09-944-036-42
; Sequence 42, Application US/09944036
; Patent No. 6582920
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-42

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RESULT 8
US-10-425-975-42
; Sequence 42, Application US/10425975
; Patent No. 6946254
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 53
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-42

Query Match      68.5%; Score 37; DB 3; Length 53;
Best Local Similarity 88.9%; Pred. No. 5.2e-05;
Matches 40; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATAT 45
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATAT 45
    |||||

RESULT 9
US-09-738-274-7
; Sequence 7, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-738-274-7

Query Match      68.5%; Score 37; DB 3; Length 57;
Best Local Similarity 91.2%; Pred. No. 5.3e-05;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTTGCAATATTTCCCACT 52
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATTTCCCACT 57
    |||||

RESULT 10
US-09-738-972-3
; Sequence 3, Application US/09738972
; Patent No. 6747141
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
```

; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: promoter-primer
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-738-972-3

Query Match 68.5%; Score 37; DB 3; Length 57;
Best Local Similarity 91.2%; Pred. No. 5.3e-05;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTCCTCACT 52
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCAAGCCCATTTGTGCAATATTCCTCACT 57
|||||

RESULT 11

US-09-738-972-13/c
; Sequence 13, Application US/09738972
; Patent No. 6747141
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; TITLE OF INVENTION: AVIUM COMPLEX SPECIES
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: probe
US-09-738-972-13

Query Match 68.5%; Score 37; DB 3; Length 57;
Best Local Similarity 91.2%; Pred. No. 5.3e-05;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTCCTCACT 52
|||||
Db 57 GAAATTAATACGACTCACTATAGGAGACCAAGCCCATTTGTGCAATATTCCTCACT 1
|||||

RESULT 12

US-09-944-036-2
; Sequence 2, Application US/09944036
; Patent No. 6582920
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01

; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 37
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: T7 promoter
; OTHER INFORMATION: sequence
; NAME/KEY: promoter
; LOCATION: (1)..(29)
US-09-944-036-2

Query Match 66.7%; Score 36; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36
|||||

RESULT 13

US-10-425-975-2
; Sequence 2, Application US/10425975
; Patent No. 6946254
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 37
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: T7 promoter
; OTHER INFORMATION: sequence
; NAME/KEY: promoter
; LOCATION: (1)..(29)
US-10-425-975-2

Query Match 66.7%; Score 36; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36
|||||

RESULT 14

US-09-944-036-6
; Sequence 6, Application US/09944036
; Patent No. 6582920
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie

APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; NAME/KEY: modified_base
; LOCATION: (46)
; OTHER INFORMATION: Nebularine
US-09-944-036-6

Query Match 66.7%; Score 36; DB 3; Length 54;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGAGACCATTTG 36
Db 1 GAAATTAATACGACTCACTATAGGAGAGACCATTTG 36

RESULT 15
US-10-425-975-6
; Sequence 6, Application US/10425975
; Patent No. 6946254
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; NAME/KEY: modified_base
; LOCATION: (46)
; OTHER INFORMATION: Nebularine
US-10-425-975-6

Query Match 66.7%; Score 36; DB 3; Length 54;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGAGACCATTTG 36
Db 1 GAAATTAATACGACTCACTATAGGAGAGACCATTTG 36

RESULT 16
US-09-944-036-34
; Sequence 34, Application US/09944036
; Patent No. 6582920
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; NAME/KEY: modified_base
; LOCATION: (45)
; OTHER INFORMATION: Nebularine
US-09-944-036-34

Query Match 66.3%; Score 35.8; DB 3; Length 53;
Best Local Similarity 94.9%; Pred. No. 0.00015;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGAGACCATTTGTC 39
Db 1 GAAATTAATACGACTCACTATAGGAGAGACCATGTC 39

RESULT 17
US-09-944-036-36
; Sequence 36, Application US/09944036
; Patent No. 6582920
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:

```
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; NAME/KEY: Promoter
; LOCATION: (1)..(33)
US-09-944-036-36

Query Match          66.3%; Score 35.8; DB 3; Length 53;
Best Local Similarity 94.9%; Pred. No. 0.00015;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCAATTGTGC 39
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCAATTGTGC 39
|||||

RESULT 18
US-10-425-975-34
; Sequence 34, Application US/10425975
; Patent No. 6946254
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; NAME/KEY: modified_base
; LOCATION: (45)
; OTHER INFORMATION: Nebularine
US-10-425-975-34

Query Match          66.3%; Score 35.8; DB 3; Length 53;
Best Local Similarity 94.9%; Pred. No. 0.00015;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCAATTGTGC 39
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCAATTGTGC 39
|||||

RESULT 19
US-10-425-975-36
; Sequence 36, Application US/10425975
; Patent No. 6946254
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
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; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-36

Query Match          66.3%; Score 35.8; DB 3; Length 53;
Best Local Similarity 94.9%; Pred. No. 0.00015;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCAATTGTGC 39
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCAATTGTGC 39
|||||

RESULT 20
US-09-493-491-49
; Sequence 49, Application US/09493491
; Patent No. 6391556
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-02.UT
; CURRENT APPLICATION NUMBER: US/09/493,491
; CURRENT FILING DATE: 2000-01-28
; EARLIER APPLICATION NUMBER: 60/117,640 US
; EARLIER FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
US-09-493-491-49

Query Match          65.6%; Score 35.4; DB 3; Length 54;
Best Local Similarity 79.2%; Pred. No. 0.00022;
Matches 42; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 2 AAATTAATACGACTCACTATAGGAGACCAATTGTGCAATATTTCCCACTGC 54
|||||
Db 2 AAATTAATACGACTCACTATAGGAGACCAAAATTTCTTGTGCATCCAGCTTGC 54
|||||

RESULT 21
US-09-493-491A-49
; Sequence 49, Application US/09493491A
; Patent No. 6551778
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-02.UT
```

; CURRENT APPLICATION NUMBER: US/09/493,491A
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-09-493-491A-49

Query Match 65.6%; Score 35.4; DB 3; Length 54;
Best Local Similarity 79.2%; Pred. No. 0.00022;
Matches 42; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2 AAATTAATACGACTCACTATAGGAGACCACATTGTGCAATATTCCTCCACTGC 54
|||||
DB 2 AAATTAATACGACTCACTATAGGAGACCACAAATCTTCTGCAATCCAGCTTGC 54
|||||

RESULT 22

US-10-273-707-49
; Sequence 49, Application US/10273707
; Patent No. 6811985
; GENERAL INFORMATION:
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-49

Query Match 65.6%; Score 35.4; DB 3; Length 54;
Best Local Similarity 79.2%; Pred. No. 0.00022;
Matches 42; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2 AAATTAATACGACTCACTATAGGAGACCACATTGTGCAATATTCCTCCACTGC 54
|||||
DB 2 AAATTAATACGACTCACTATAGGAGACCACAAATCTTCTGCAATCCAGCTTGC 54
|||||

RESULT 23

US-09-944-036-10
; Sequence 10, Application US/09944036
; Patent No. 6582920
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.

; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-10

Query Match 65.6%; Score 35.4; DB 3; Length 55;
Best Local Similarity 97.3%; Pred. No. 0.00022;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACATTGT 37
|||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCACATTGT 37
|||||

RESULT 24

US-10-425-975-10
; Sequence 10, Application US/10425975
; Patent No. 6946254
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-10

Query Match 65.6%; Score 35.4; DB 3; Length 55;
Best Local Similarity 97.3%; Pred. No. 0.00022;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACATTGT 37
|||||

Db 1 GAAATTAATACGACTCACTATAGGAGACCACTGT 37

RESULT 25

US-09-944-036-43
; Sequence 43, Application US/09944036
; Patent No. 6582920
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-43

Query Match 64.8%; Score 35; DB 3; Length 52;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTT 35

Db 1 GAAATTAATACGACTCACTATAGGAGACCACTT 35

RESULT 26

US-09-738-274-12
; Sequence 12, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAI, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-738-274-12

Query Match 64.8%; Score 35; DB 3; Length 52;
Best Local Similarity 80.4%; Pred. No. 0.00031;
Matches 41; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATTCCTCCAC 51

Db 1 GAAATTAATACGACTCACTATAGGAGACCACTATGATGCTTGGCCCC 51

RESULT 27

US-10-425-975-43
; Sequence 43, Application US/10425975
; Patent No. 6946254
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-43

Query Match 64.8%; Score 35; DB 3; Length 52;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTT 35

Db 1 GAAATTAATACGACTCACTATAGGAGACCACTT 35

RESULT 28

US-09-944-036-35
; Sequence 35, Application US/09944036
; Patent No. 6582920
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 53

```
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:
/ OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
/ NAME/KEY: promoter
/ LOCATION: (1)..(33)
US-09-944-036-35
```

```
Query Match          64.4%; Score 34.8; DB 3; Length 53;
Best Local Similarity 84.8%; Pred. No. 0.00037;
Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATTC 46
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATTC 46
    |||||
```

```
RESULT 29
US-10-425-975-35
; Sequence 35, Application US/10425975
; Patent No. 6946254
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-35
```

```
Query Match          64.4%; Score 34.8; DB 3; Length 53;
Best Local Similarity 84.8%; Pred. No. 0.00037;
Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATTC 46
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATTC 46
    |||||
```

```
RESULT 30
US-09-944-036-33
; Sequence 33, Application US/09944036
; Patent No. 6582920
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
```

```
/ CURRENT APPLICATION NUMBER: US/09/944,036
/ CURRENT FILING DATE: 2001-08-31
/ PRIOR APPLICATION NUMBER: US 60/229,790
/ PRIOR FILING DATE: 2000-09-01
/ NUMBER OF SEQ ID NOS: 70
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 33
/ LENGTH: 54
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:
/ OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
/ NAME/KEY: promoter
/ LOCATION: (1)..(33)
US-09-944-036-33
```

```
Query Match          63.7%; Score 34.4; DB 3; Length 54;
Best Local Similarity 97.2%; Pred. No. 0.00053;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTG 36
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTG 36
    |||||
```

```
RESULT 31
US-10-425-975-33
; Sequence 33, Application US/10425975
; Patent No. 6946254
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-33
```

```
Query Match          63.7%; Score 34.4; DB 3; Length 54;
Best Local Similarity 97.2%; Pred. No. 0.00053;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTG 36
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTG 36
    |||||

RESULT 32
US-10-140-545-48
; Sequence 48, Application US/10140545
; Patent No. 6943242
; GENERAL INFORMATION:
```



```
; APPLICANT: Daniel, Stevan G
; APPLICANT: Turner, Leah
; APPLICANT: Samartzidou, Hrisi
; APPLICANT: Houts, Thomas M
; TITLE OF INVENTION: DESIGN OF ARTIFICIAL GENES FOR USE AS CONTROLS IN GENE EXPRESSION
; TITLE OF INVENTION: ANALYSIS SYSTEMS
; FILE REFERENCE: PB0120
; CURRENT APPLICATION NUMBER: US/10/140,545
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/289,202
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: US 60/312,420
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 62
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-140-545-48

Query Match      63.7%; Score 34.4; DB 3; Length 62;
Best Local Similarity 97.2%; Pred. No. 0.00054;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTATACGACTCACTATAGGAGACCAATTTG 36
    |||||
Db 15 GAAATTATACGACTCACTATAGGAGACCAATTTG 50

RESULT 33
US-09-944-036-38
; Sequence 38, Application US/09944036
; Patent No. 6582920
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Protease target
; OTHER INFORMATION: sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-38

Query Match      63.0%; Score 34; DB 3; Length 53;
Best Local Similarity 88.1%; Pred. No. 0.00075;
Matches 37; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAAATTATACGACTCACTATAGGAGACCAATTTGCAAT 42
    |||||
Db 1 GAAATTATACGACTCACTATAGGAGACCAATTTGCAAT 42

RESULT 34
US-10-425-975-38
; Sequence 38, Application US/10425975
; Patent No. 6946254
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Protease target
; OTHER INFORMATION: sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-38

Query Match      63.0%; Score 34; DB 3; Length 54;
Best Local Similarity 80.0%; Pred. No. 0.00076;
Matches 40; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 2 AAATTATACGACTCACTATAGGAGACCAATTTGCAATATTTCCAC 51
    |||||
Db 2 AAATTATACGACTCACTATAGGAGACCAATTTGCAATATTTCCAC 51

RESULT 35
US-09-493-491-27
; Sequence 27, Application US/09493491
; Patent No. 6391556
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-02.UT
; CURRENT APPLICATION NUMBER: US/09/493,491
; CURRENT FILING DATE: 2000-01-28
; EARLIER APPLICATION NUMBER: 60/117,640 US
; EARLIER FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
US-09-493-491-27

Query Match      63.0%; Score 34; DB 3; Length 54;
Best Local Similarity 80.0%; Pred. No. 0.00076;
Matches 40; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 2 AAATTATACGACTCACTATAGGAGACCAATTTGCAATATTTCCAC 51
    |||||
Db 2 AAATTATACGACTCACTATAGGAGACCAATTTGCAATATTTCCAC 51
```

```
RESULT 36
US-09-493-491A-30
; Sequence 30, Application US/09493491A
; Patent No. 6551778
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-02.UT
; CURRENT APPLICATION NUMBER: US/09/493,491A
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-09-493-491A-30

Query Match      63.0%; Score 34; DB 3; Length 54;
Best Local Similarity 80.0%; Pred. No. 0.00076;
Matches 40; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2 AAATTAATACGACTCACTATAGGAGACCACCATTTGTGCAATATTCGCCAC 51
    |||||||
DB 2 AAATTAATACGACTCACTATAGGAGACCACCATTTGTGCAATATTCGCCAC 51
    |||||||

RESULT 37
US-10-273-707-30
; Sequence 30, Application US/10273707
; Patent No. 6811985
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-30

Query Match      63.0%; Score 34; DB 3; Length 54;
Best Local Similarity 80.0%; Pred. No. 0.00076;
Matches 40; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2 AAATTAATACGACTCACTATAGGAGACCACCATTTGTGCAATATTCGCCAC 51
    |||||||
DB 2 AAATTAATACGACTCACTATAGGAGACCACCATTTGTGCAATATTCGCCAC 51
    |||||||

RESULT 38
US-09-944-036-45
; Sequence 45, Application US/09944036
; Patent No. 6582920
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-45

Query Match      63.0%; Score 34; DB 3; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.00076;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACCAT 34
    |||||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCACCAT 34
    |||||||

RESULT 39
US-10-425-975-45
; Sequence 45, Application US/10425975
; Patent No. 6946254
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; OTHER INFORMATION: target sequence
US-10-425-975-45

Query Match      63.0%; Score 34; DB 3; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.00076;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACCAT 34
    |||||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCACCAT 34
    |||||||
```

```
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-45

Query Match      63.0%; Score 34; DB 3; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.00076;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACAT 34
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACAT 34

RESULT 40
US-09-738-972-2
; Sequence 2, Application US/09738972
; Patent No. 6747141
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-738-972-2

Query Match      63.0%; Score 34; DB 3; Length 61;
Best Local Similarity 100.0%; Pred. No. 0.00077;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACAT 34
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACAT 34

RESULT 41
US-09-738-972-12/c
; Sequence 12, Application US/09738972
; Patent No. 6747141
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(33)
```

```
US-09-738-972-12

Query Match      63.0%; Score 34; DB 3; Length 61;
Best Local Similarity 100.0%; Pred. No. 0.00077;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACAT 34
    |||||
Db 61 GAAATTAATACGACTCACTATAGGAGACCACAT 28

RESULT 42
US-09-493-491-33
; Sequence 33, Application US/09493491
; Patent No. 6391556
; GENERAL INFORMATION:
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-02.UT
; CURRENT APPLICATION NUMBER: US/09/493,491
; CURRENT FILING DATE: 2000-01-28
; EARLIER APPLICATION NUMBER: 60/117,640 US
; EARLIER FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
US-09-493-491-33

Query Match      62.6%; Score 33.8; DB 3; Length 52;
Best Local Similarity 94.6%; Pred. No. 0.0009;
Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAATTAATACGACTCACTATAGGAGACCACATTGTG 38
    |||||
Db 2 AAATTAATACGACTCACTATAGGAGACCACCTTCTG 38

RESULT 43
US-09-493-491A-36
; Sequence 36, Application US/09493491A
; Patent No. 6551778
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-02.UT
; CURRENT APPLICATION NUMBER: US/09/493,491A
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-09-493-491A-36
```

```
Query Match          62.6%; Score 33.8; DB 3; Length 52;
Best Local Similarity 94.6%; Pred. No. 0.0009;
Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAATTAATACGACTCACTATAGGAGACACACATTGTG 38
    |||||
Db 2 AAATTAATACGACTCACTATAGGAGACACACATTGTG 38
    |||||

RESULT 44
US-10-273-707-36
; Sequence 36, Application US/10273707
; Patent No. 6811985
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-36

Query Match          62.6%; Score 33.8; DB 3; Length 52;
Best Local Similarity 94.6%; Pred. No. 0.0009;
Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAATTAATACGACTCACTATAGGAGACACACATTGTG 38
    |||||
Db 2 AAATTAATACGACTCACTATAGGAGACACACATTGTG 38
    |||||

RESULT 45
US-10-001-407-19
; Sequence 19, Application US/10001407
; Patent No. 6870045
; GENERAL INFORMATION:
; APPLICANT: Yang, Yeasing
; APPLICANT: Burrell, Terrie
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)
; FILE REFERENCE: GP117-03.UT
; CURRENT APPLICATION NUMBER: US/10/001,407
; CURRENT FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/242,620
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/280,058
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 58
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T7 promoter primer having a promoter sequence
; OTHER INFORMATION: appended at the 5' end of an HIV-2 complementary
```

```
; OTHER INFORMATION: primer sequence
US-10-001-407-19

Query Match          61.5%; Score 33.2; DB 3; Length 58;
Best Local Similarity 92.1%; Pred. No. 0.0016;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACACACATTGTG 38
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACACACATTGTG 38
    |||||

RESULT 46
US-09-944-036-4
; Sequence 4, Application US/09944036
; Patent No. 6582920
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: T7 promoter
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-4

Query Match          61.1%; Score 33; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACACACA 33
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACACACA 33
    |||||

RESULT 47
US-09-738-274-36
; Sequence 36, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 33
; TYPE: DNA
```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: promoter
US-09-738-274-36

Query Match 61.1%; Score 33; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.0017;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 48

US-09-738-972-10
; Sequence 10, Application US/09738972
; Patent No. 6747141
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE OF INVENTION: AVIUM COMPLEX SPECIES
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: promoter
US-09-738-972-10

Query Match 61.1%; Score 33; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.0017;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 49

US-10-001-407-29
; Sequence 29, Application US/10001407
; Patent No. 6870045
; GENERAL INFORMATION:
; APPLICANT: Yang, Yeasing
; APPLICANT: Burrell, Terrie
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP117-03.UT
; CURRENT APPLICATION NUMBER: US/10/001,407
; CURRENT FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/242,620
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/280,058
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 33
; TYPE: DNA
; ORGANISM: HIV-2
US-10-001-407-29

Query Match 61.1%; Score 33; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.0017;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 50

US-10-425-975-4
; Sequence 4, Application US/10425975
; Patent No. 6946254
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: T7 promoter
US-10-425-975-4

Query Match 61.1%; Score 33; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.0017;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 51

US-09-425-585-15
; Sequence 15, Application US/09425585
; Patent No. 6348315
; GENERAL INFORMATION:
; APPLICANT: PLUCKTHUN, ANDREAS
; APPLICANT: HANES, JOZEF
; TITLE OF INVENTION: METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING
; FILE REFERENCE: PLUCK/1
; CURRENT APPLICATION NUMBER: US/09/425,585
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: PCT/EP98/02420
; PRIOR FILING DATE: 1998-04-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide T7B
US-09-425-585-15

```
Query Match          61.1%; Score 33; DB 3; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
   |||||||
Db 5 GAAATTAATACGACTCACTATAGGAGACCACA 37

RESULT 52
US-09-953-321-15
; Sequence 15, Application US/09953321
; Patent No. 6589741
; GENERAL INFORMATION:
; APPLICANT: HANES, JOZEF
; APPLICANT: JERMUTUS, LUTZ
; TITLE OF INVENTION: NOVEL METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING
; FILE REFERENCE: PLUCK/1 CON2
; CURRENT APPLICATION NUMBER: US/09/953,321
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/425,585
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide T7B
US-09-953-321-15

Query Match          61.1%; Score 33; DB 3; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
   |||||||
Db 5 GAAATTAATACGACTCACTATAGGAGACCACA 37

RESULT 53
US-08-678-735A-9
; Sequence 9, Application US/08678735A
; Patent No. 6150179
; GENERAL INFORMATION:
; APPLICANT: Deem, Michael W.
; APPLICANT: Rothberg, Jonathan M.
; TITLE OF INVENTION: CONSENSUS CONFIGURATIONAL BIAS MONTE
; TITLE OF INVENTION: CARLO METHOD AND SYSTEM FOR PHARMACOPHORE STRUCTURE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/678,735A
; FILING DATE: 1996-JUL-11
; CLASSIFICATION: 436
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirostock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-678-735A-9

Query Match          61.1%; Score 33; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
   |||||||
Db 6 GAAATTAATACGACTCACTATAGGAGACCACA 38

RESULT 54
US-08-418-992-9
; Sequence 9, Application US/08418992
; Patent No. 6341256
; GENERAL INFORMATION:
; APPLICANT: Deem, Michael W.
; APPLICANT: Rothberg, Jonathan M.
; APPLICANT: Went, Gregory T.
; TITLE OF INVENTION: CONSENSUS CONFIGURATIONAL BIAS MONTE
; TITLE OF INVENTION: CARLO METHOD AND SYSTEM FOR PHARMACOPHORE STRUCTURE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/418,992
; FILING DATE: On Even Date Herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirostock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-418-992-9

Query Match          61.1%; Score 33; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.0018;
```

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTATACGACTCACTATAGGAGACCACA 33
DB 6 GAAATTATACGACTCACTATAGGAGACCACA 38

RESULT 55

US-09-518-813B-15

; Sequence 15, Application US/09518813B

; Patent No. 6927025

; GENERAL INFORMATION:

; APPLICANT: CARR, Francis Joseph

; APPLICANT: CARTER, Graham

; APPLICANT: HAMILTON, Anita Anne

; APPLICANT: ADAIR, Fiona Suzanne

; APPLICANT: WILLIAMS, Stephen

; TITLE OF INVENTION: METHODS FOR PROTEIN SCREENING

; FILE REFERENCE: 112408-122

; CURRENT APPLICATION NUMBER: US/09/518,813B

; CURRENT FILING DATE: 2000-03-03

; PRIOR APPLICATION NUMBER: PCT/GB98/02649

; PRIOR FILING DATE: 1998-09-03

; PRIOR APPLICATION NUMBER: US 60/070,063

; PRIOR FILING DATE: 1997-12-30

; PRIOR APPLICATION NUMBER: US 60/070,062

; PRIOR FILING DATE: 1997-12-30

; PRIOR APPLICATION NUMBER: US 60/070,037

; PRIOR FILING DATE: 1997-12-30

; PRIOR APPLICATION NUMBER: US 60/070,050

; PRIOR FILING DATE: 1997-12-30

; PRIOR APPLICATION NUMBER: GB 9718552.4

; PRIOR FILING DATE: 1997-09-03

; PRIOR APPLICATION NUMBER: GB 9719834.5

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: GB 9720184.2

; PRIOR FILING DATE: 1997-09-14

; PRIOR APPLICATION NUMBER: GB 9720522.3

; PRIOR FILING DATE: 1997-09-29

; PRIOR APPLICATION NUMBER: GB 9720523.1

; PRIOR FILING DATE: 1997-09-29

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 15

; LENGTH: 50

; TYPE: DNA

; ORGANISM: synthetic oligonucleotide

US-09-518-813B-15

Query Match 61.1%; Score 33; DB 3; Length 50;

Best Local Similarity 100.0%; Pred. No. 0.0018;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTATACGACTCACTATAGGAGACCACA 33

DB 15 GAAATTATACGACTCACTATAGGAGACCACA 47

RESULT 56

US-08-902-623-33

; Sequence 33, Application US/08902623

; Patent No. 5922545

; GENERAL INFORMATION:

; APPLICANT: MATTHEAKIS, LARRY C.

; APPLICANT: DOWER, WILLIAM J.

; TITLE OF INVENTION: IN VITRO PEPTIDE AND ANTIBODY DISPLAY

; TITLE OF INVENTION: LIBRARIES

; NUMBER OF SEQUENCES: 75

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW LLP

; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,623
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/586,176
; FILING DATE: 17-JAN-1996
; APPLICATION NUMBER: US 08/300,262
; FILING DATE: 02-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/144,775
; FILING DATE: US 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/12206
; FILING DATE: US 25-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: DUNN, TRACY J.
; REGISTRATION NUMBER: 34,587
; REFERENCE/DOCKET NUMBER: 16528X-0032310US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-902-623-33

Query Match 61.1%; Score 33; DB 2; Length 51;

Best Local Similarity 100.0%; Pred. No. 0.0018;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTATACGACTCACTATAGGAGACCACA 33

DB 6 GAAATTATACGACTCACTATAGGAGACCACA 38

RESULT 57

US-09-944-036-41

; Sequence 41, Application US/09944036

; Patent No. 6582920

; GENERAL INFORMATION:

; APPLICANT: YANG, Yeasing Y.

; APPLICANT: BRENTANO, Steven T.

; APPLICANT: BABOLA, Odile

; APPLICANT: TRAN, Nathalie

; APPLICANT: VERNET, Guy

; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF

; FILE REFERENCE: GP114-02.UT

; CURRENT APPLICATION NUMBER: US/09/944,036

; CURRENT FILING DATE: 2001-08-31

; PRIOR APPLICATION NUMBER: US 60/229,790

; PRIOR FILING DATE: 2000-09-01

; NUMBER OF SEQ ID NOS: 70

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 41

; LENGTH: 51

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:

; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase

; OTHER INFORMATION: target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-41

Query Match 61.1%; Score 33; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 58

US-10-425-975-41
; Sequence 41, Application US/10425975
; Patent No. 6946254
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; OTHER INFORMATION: target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-41

Query Match 61.1%; Score 33; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 59

US-09-944-036-39
; Sequence 39, Application US/09944036
; Patent No. 6582920
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790

; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; OTHER INFORMATION: target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-39

Query Match 61.1%; Score 33; DB 3; Length 52;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 60

US-10-425-975-39
; Sequence 39, Application US/10425975
; Patent No. 6946254
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; OTHER INFORMATION: target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-39

Query Match 61.1%; Score 33; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 61

US-09-944-036-37
; Sequence 37, Application US/09944036
; Patent No. 6582920
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.


```
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Protease target
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-37

Query Match          61.1%; Score 33; DB 3; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 62
US-10-425-975-37
; Sequence 37, Application US/10425975
; Patent No. 6946254
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Protease target
; OTHER INFORMATION: sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-37

Query Match          61.1%; Score 33; DB 3; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
```

```
DB 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||

RESULT 63
US-08-162-836-14
; Sequence 14, Application US/08162836
; Patent No. 5554516
; GENERAL INFORMATION:
; APPLICANT: Daniel L. Kacian
; APPLICANT: Diane L. McAllister
; APPLICANT: Sherrol H. McDonough
; APPLICANT: Nani Bhushan Dattagupta
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE AMPLIFICATION
; TITLE OF INVENTION: METHOD, COMPOSITION AND KIT
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,836
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/879,686
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 55
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-162-836-14

Query Match          61.1%; Score 33; DB 2; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 64
US-08-479-105A-1
; Sequence 1, Application US/08479105A
; Patent No. 5908744
; GENERAL INFORMATION:
; APPLICANT: Diane L. McAllister
; APPLICANT: Philip Hammond
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE
; TITLE OF INVENTION: AMPLIFICATION
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
```

STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS DOS (5.0)
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,105A
FILING DATE: June 6, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/345,861
FILING DATE: No. 590874ember 28, 1994
APPLICATION NUMBER: 07/925,405
FILING DATE: August 4, 1992
APPLICATION NUMBER: 07/855,732
FILING DATE: March 19, 1992
APPLICATION NUMBER: 07/550,837
FILING DATE: July 10, 1990
APPLICATION NUMBER: 07/379,501
FILING DATE: July 11, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/067
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
US-08-479-105A-1

Query Match 61.1%; Score 33; DB 2; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 65
US-08-116-984A-13
; Sequence 13, Application US/08116984A
; Patent No. 6136529
; GENERAL INFORMATION:
; APPLICANT: Philip W. Hammond
; TITLE OF INVENTION: NUCLEIC ACID PROBES TO
; TITLE OF INVENTION: MYCOBACTERIUM AVIUM
; TITLE OF INVENTION: COMPLEX
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,984A
FILING DATE: September 3, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 203/188
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 55
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
US-08-116-984A-13

Query Match 61.1%; Score 33; DB 3; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 66
US-09-502-966-10
; Sequence 10, Application US/09502966
; Patent No. 6245519
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: MCDONOUGH, Sherrol H.
; APPLICANT: NELSON, No. 6245519man C.
; TITLE OF INVENTION: PROTECTION PROBES
; FILE REFERENCE: GPI02-02.UT
; CURRENT APPLICATION NUMBER: US/09/502,966
; CURRENT FILING DATE: 2000-02-11
; EARLIER APPLICATION NUMBER: 60/120,019 US
; EARLIER FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: a synthetic
; OTHER INFORMATION: amplification primer
US-09-502-966-10

Query Match 61.1%; Score 33; DB 3; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 67
US-09-944-036-44
; Sequence 44, Application US/09944036
; Patent No. 6582920

GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; PRIORITY FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; OTHER INFORMATION: target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-44

Query Match 61.1%; Score 33; DB 3; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 68
US-10-425-975-44
; Sequence 44, Application US/10425975
; Patent No. 6946254
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; OTHER INFORMATION: target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-44

Query Match 61.1%; Score 33; DB 3; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 69
US-08-480-472A-1
; Sequence 1, Application US/08480472A
; Patent No. 7009041
; GENERAL INFORMATION:
; APPLICANT: Sherrol H. McDonough
; APPLICANT: Daniel L. Kacian
; APPLICANT: Nanibhushan Dattagupta
; APPLICANT: Diane L. McAllister
; APPLICANT: Philip Hammond
; APPLICANT: Thomas B. Ryder
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE
; TITLE OF INVENTION: AMPLIFICATION
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,472A
; FILING DATE: June 6, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/345,861
; FILING DATE: No. 7009041ember 28, 1994
; APPLICATION NUMBER: 07/925,405
; FILING DATE: August 4, 1992
; APPLICATION NUMBER: 07/855,732
; FILING DATE: March 19, 1992
; APPLICATION NUMBER: 07/550,837
; FILING DATE: July 10, 1990
; APPLICATION NUMBER: 07/379,501
; FILING DATE: July 11, 1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 213/066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 55 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-480-472A-1

Query Match 61.1%; Score 33; DB 5; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

```
RESULT 70
US-10-001-407-18
; Sequence 18, Application US/10001407
; Patent No. 6870045
; GENERAL INFORMATION:
; APPLICANT: Yang, Yeasing
; APPLICANT: Burrell, Terrie
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)
; FILE REFERENCE: GP117-03 UT
; CURRENT APPLICATION NUMBER: US/10/001,407
; CURRENT FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/242,620
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/280,058
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T7 promoter primer having a promoter sequence
; OTHER INFORMATION: appended at the 5' end of the sequence given as
; OTHER INFORMATION: SEQ ID NO:13
US-10-001-407-18

Query Match      61.1%; Score 33; DB 3; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 71
US-09-738-972-1
; Sequence 1, Application US/09738972
; Patent No. 6747141
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; TITLE OF INVENTION: AVIUM COMPLEX SPECIES
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 59
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: promoter-primer
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-738-972-1

Query Match      61.1%; Score 33; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 72
US-09-738-972-11/c
; Sequence 11, Application US/09738972
; Patent No. 6747141
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; TITLE OF INVENTION: AVIUM COMPLEX SPECIES
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 59
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: probe
US-09-738-972-11

Query Match      61.1%; Score 33; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 59 GAAATTAATACGACTCACTATAGGAGACCACA 27

RESULT 73
US-07-971-819A-36
; Sequence 36, Application US/07971819A
; Patent No. 5420029
; GENERAL INFORMATION:
; APPLICANT: Gelfand, David H.
; APPLICANT: Lawyer, Frances C.
; APPLICANT: Stoffel, Susanne
; TITLE OF INVENTION: Purified Thermostable Nucleic Acid
; TITLE OF INVENTION: Polymerase Enzyme from Thermotoga Maritima
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/971,819A
; FILING DATE: 19930203
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stacey R. Sias, Ph.D.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 814-2977
; TELEX:
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 bases
```

```
;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other Nucleic Acid
US-07-971-819A-36

Query Match          61.1%; Score 33; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
    |||||||
Db 16 GAAATTAATACGACTCACTATAGGAGACCACA 48

RESULT 74
US-08-475-231-36
; Sequence 36, Application US/08475231
; Patent No. 5624833
; GENERAL INFORMATION:
; APPLICANT: Gelfand, David H.
; APPLICANT: Lawyer, Frances C.
; APPLICANT: Stoffel, Susanne
; TITLE OF INVENTION: Purified Thermostable Nucleic Acid
; TITLE OF INVENTION: Polymerase Enzyme from Thermotoga Maritima
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,231
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/971,819
; FILING DATE: 03-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stacey R. Sias, Ph.D.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 814-2977
; TELEX:
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other Nucleic Acid
US-08-475-231-36

Query Match          61.1%; Score 33; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
    |||||||
Db 16 GAAATTAATACGACTCACTATAGGAGACCACA 48

RESULT 75
US-08-345-861-1
; Sequence 1, Application US/08345861
; Patent No. 5766849
; GENERAL INFORMATION:
; APPLICANT: Sherrol H. McDonough
; APPLICANT: Daniel L. Kacian
; APPLICANT: Nanibhushan Datta Gupta
; APPLICANT: Diane L. McAllister
; APPLICANT: Philip Hammond
; APPLICANT: Thomas B. Ryder
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE AMPLIFICATION
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/345,861
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/925,405
; FILING DATE: August 4, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 197/136
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 552-8400
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 62
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-345-861-1

Query Match          61.1%; Score 33; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
    |||||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 76
US-09-425-585-5
; Sequence 5, Application US/09425585
; Patent No. 6348315
; GENERAL INFORMATION:
; APPLICANT: PLUCKTHUN, ANDREAS
; APPLICANT: HANES, JOZEF
; TITLE OF INVENTION: METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: (POLY) PEPTIDES THAT INTERACT WITH TARGET MOLECULES
; FILE REFERENCE: PLUCK/1
; CURRENT APPLICATION NUMBER: US/09/425,585
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: PCT/EP98/02420
; PRIOR FILING DATE: 1998-04-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 63
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide ON3
US-09-425-585-5

Query Match      61.1%; Score 33; DB 3; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGGAGACCACA 33
Db 13 GAAATTAATACGACTCACTATAGGGAGACCACA 45

RESULT 77
US-09-953-321-5
; Sequence 5, Application US/09953321
; Patent No. 6589741
; GENERAL INFORMATION:
; APPLICANT: HANES, JOSEF
; APPLICANT: JERMUTUS, LUTZ
; TITLE OF INVENTION: NOVEL METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING
; FILE REFERENCE: PLUCK/1 CON2
; CURRENT APPLICATION NUMBER: US/09/953,321
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/425,585
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 63
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide ON3
US-09-953-321-5

Query Match      61.1%; Score 33; DB 3; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGGAGACCACA 33
Db 13 GAAATTAATACGACTCACTATAGGGAGACCACA 45

RESULT 78
US-10-124-663A-2
; Sequence 2, Application US/10124663A
; Patent No. 7011958
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics Corp.
; TITLE OF INVENTION: Method for Improving the Stability of Linear DNA in Cell-free in
; FILE REFERENCE: RDID 0104905
; CURRENT APPLICATION NUMBER: US/10/124,663A
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 66
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sense primer
US-10-124-663A-2

Query Match      61.1%; Score 33; DB 5; Length 66;
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Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGGAGACCACA 33
Db 26 GAAATTAATACGACTCACTATAGGGAGACCACA 58

RESULT 79
US-09-518-813B-14
; Sequence 14, Application US/09518813B
; Patent No. 6927025
; GENERAL INFORMATION:
; APPLICANT: CARR, Francis Joseph
; APPLICANT: CARTER, Graham
; APPLICANT: HAMILTON, Anita Anne
; APPLICANT: ADAIR, Fiona Suzanne
; APPLICANT: WILLIAMS, Stephen
; TITLE OF INVENTION: METHODS FOR PROTEIN SCREENING
; FILE REFERENCE: 112408-122
; CURRENT APPLICATION NUMBER: US/09/518,813B
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: PCT/GB98/02649
; PRIOR FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: US 60/070,063
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: US 60/070,062
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: US 60/070,037
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: US 60/070,050
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: GB 9718552.4
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: GB 9719834.5
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: GB 9720184.2
; PRIOR FILING DATE: 1997-09-14
; PRIOR APPLICATION NUMBER: GB 9720522.3
; PRIOR FILING DATE: 1997-09-29
; PRIOR APPLICATION NUMBER: GB 9720523.1
; PRIOR FILING DATE: 1997-09-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 67
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-09-518-813B-14

Query Match      61.1%; Score 33; DB 3; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGGAGACCACA 33
Db 15 GAAATTAATACGACTCACTATAGGGAGACCACA 47

RESULT 80
US-09-486-356-16
; Sequence 16, Application US/09486356
; Patent No. 6383770
; GENERAL INFORMATION:
; APPLICANT: Roberts, Richard J.
; APPLICANT: Byrd, Devon R.
; APPLICANT: Morgan, Richard D.
; APPLICANT: Patti, Jay
; APPLICANT: No. 6383770en, Christopher J.
; TITLE OF INVENTION: Method For Screening Restriction Endonucleases
; FILE REFERENCE: NEB-130PCT-U
; CURRENT APPLICATION NUMBER: US/09/486,356
```

```
; CURRENT FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: PCT/US98/18124
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/135,541
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 75
; TYPE: DNA
; ORGANISM: Pseudomonas alcaligenes
US-09-486-356-16

Query Match 61.1%; Score 33; DB 3; Length 75;
Best Local Similarity 87.8%; Pred. No. 0.002;
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAAATTAATAGCACTCACTATAGGAGACCACTTGTCGAA 41
   |||||||
Db 2 GAAATTAATAGCACTCACTATAGGAGACCACTTGTCGAA 42
   |||||||

RESULT 81
US-09-577-528B-16
; Sequence 16, Application US/09577528B
; Patent No. 6689573
; GENERAL INFORMATION:
; APPLICANT: Roberts, Richard J.
; APPLICANT: Byrd, Devon R.
; APPLICANT: Morgan, Richard D.
; APPLICANT: Patti, Jay
; APPLICANT: No. 6689573en, Christopher J.
; TITLE OF INVENTION: Method For Screening Restriction Endonucleases
; FILE REFERENCE: NEB-130PCTPR
; CURRENT APPLICATION NUMBER: US/09/577,528B
; CURRENT FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 60/135,541
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 75
; TYPE: DNA
; ORGANISM: Pseudomonas alcaligenes
US-09-577-528B-16

Query Match 61.1%; Score 33; DB 3; Length 75;
Best Local Similarity 87.8%; Pred. No. 0.002;
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAAATTAATAGCACTCACTATAGGAGACCACTTGTCGAA 41
   |||||||
Db 2 GAAATTAATAGCACTCACTATAGGAGACCACTTGTCGAA 42
   |||||||

RESULT 82
US-10-208-557-16
; Sequence 16, Application US/10208557
; Patent No. 6905837
; GENERAL INFORMATION:
; APPLICANT: Roberts, Richard J.
; APPLICANT: Byrd, Devon R.
; APPLICANT: Morgan, Richard D.
; APPLICANT: Patti, Jay
; APPLICANT: No. 6905837en, Christopher J.
; TITLE OF INVENTION: Method For Screening Restriction Endonucleases
; FILE REFERENCE: NEB-130PCT-U
; CURRENT APPLICATION NUMBER: US/10/208,557
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US/09/486,356
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: PCT/US98/18124
; PRIOR FILING DATE: 1998-09-01
```

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; PRIOR APPLICATION NUMBER: 60/135,541
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 75
; TYPE: DNA
; ORGANISM: Pseudomonas alcaligenes
US-10-208-557-16

Query Match 61.1%; Score 33; DB 3; Length 75;
Best Local Similarity 87.8%; Pred. No. 0.002;
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAAATTAATAGCACTCACTATAGGAGACCACTTGTCGAA 41
   |||||||
Db 2 GAAATTAATAGCACTCACTATAGGAGACCACTTGTCGAA 42
   |||||||

RESULT 83
US-08-902-623-24
; Sequence 24, Application US/08902623
; Patent No. 5922545
; GENERAL INFORMATION:
; APPLICANT: MATTHEAKIS, LARRY C.
; APPLICANT: DOWER, WILLIAM J.
; TITLE OF INVENTION: IN VITRO PEPTIDE AND ANTIBODY DISPLAY
; LIBRARIES
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,623
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/586,176
; FILING DATE: 17-JAN-1996
; APPLICATION NUMBER: US 08/300,262
; FILING DATE: 02-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/144,775
; FILING DATE: US 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/12206
; FILING DATE: US 25-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: DUNN, TRACY J.
; REGISTRATION NUMBER: 34,587
; REFERENCE/DOCKET NUMBER: 16528x-003230US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 90 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-902-623-24

Query Match 61.1%; Score 33; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.002;
```

```
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
   |||||
Db 6 GAAATTAATACGACTCACTATAGGAGACCACA 38

RESULT 84
US-08-678-735A-2
; Sequence 2, Application US/08678735A
; Patent No. 6150179
; GENERAL INFORMATION:
; APPLICANT: Deem, Michael W.
; APPLICANT: Rothberg, Jonathan M.
; APPLICANT: Went, Gregory T.
; TITLE OF INVENTION: CONSENSUS CONFIGURATIONAL BIAS MONTE
; TITLE OF INVENTION: CARLO METHOD AND SYSTEM FOR PHARMACOPHORE STRUCTURE
; DETERMINATION
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/678,735A
; FILING DATE: 1996-JUL-11
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-678-735A-2

Query Match 61.1%; Score 33; DB 3; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
   |||||
Db 6 GAAATTAATACGACTCACTATAGGAGACCACA 38

RESULT 85
US-08-418-992-2
; Sequence 2, Application US/08418992
; Patent No. 6341256
; GENERAL INFORMATION:
; APPLICANT: Deem, Michael W.
; APPLICANT: Rothberg, Jonathan M.
; APPLICANT: Went, Gregory T.
; TITLE OF INVENTION: CONSENSUS CONFIGURATIONAL BIAS MONTE
; TITLE OF INVENTION: CARLO METHOD AND SYSTEM FOR PHARMACOPHORE STRUCTURE
; DETERMINATION
; NUMBER OF SEQUENCES: 10
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/418,992
; FILING DATE: On Even Date Herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-418-992-2

Query Match 61.1%; Score 33; DB 3; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
   |||||
Db 6 GAAATTAATACGACTCACTATAGGAGACCACA 38

RESULT 86
US-08-538-875-5/c
; Sequence 5, Application US/08538875
; Patent No. 5773582
; GENERAL INFORMATION:
; APPLICANT: Shin, Hang-Cheol
; APPLICANT: Shin, Nam-Kyu
; APPLICANT: Lee, Inkyung
; APPLICANT: Kang, Sungzong
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR MUTAINS
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shin, Hang-Cheol
; STREET: Jukong Gocheung Apt. 1014-806, Haan-dong
; CITY: Kwangmyung-shi
; STATE: Kyungki-do
; COUNTRY: Republic of Korea
; ZIP: 423-060
; ADDRESSEE: Shin, Nam-Kyu
; STREET: #181-404 Sadang-4-dong, Dongjak-ku
; CITY: Seoul
; STATE:
; COUNTRY: Republic of Korea
; ZIP: 156-094
; ADDRESSEE: Lee, Inkyung
; STREET: 11/2, #302-39 Juan-4-dong, Nam-ku
; CITY: Incheon
; STATE:
; COUNTRY: Republic of Korea
; ZIP: 402-204
; ADDRESSEE: Kang, Sungzong
```



```
; STREET: #84-4 Daeshin-dong, Seodaemun-ku
; CITY: Seoul
; STATE:
; COUNTRY: Republic of Korea
; ZIP: 120-160
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.5inch 2.0Mb storage
; COMPUTER: IBM PC/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/538.875
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/193.336
; FILING DATE:
; APPLICATION NUMBER: KR 93-1751
; FILING DATE: 9-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: 17 promoter region DNA
; US-08-538-875-5

Query Match 61.1%; Score 33; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 91 GAAATTAATACGACTCACTATAGGAGACCACA 59

RESULT 87
US-09-284-627-21
; Sequence 21, Application US/09284627
; Patent No. 6361943
; GENERAL INFORMATION:
; APPLICANT: Mitsubishi Chemical Corporation
; TITLE OF INVENTION: Molecule assigning genotype to
; phenotype and use thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mitsubishi Chemical Corporation
; STREET: 5-2, Marunouchi 2-chome
; CITY: Chiyoda-ku
; STATE: Tokyo
; COUNTRY: JAPAN
; ZIP: 103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/284,627
; FILING DATE: 02-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 1996274855
; FILING DATE: 17.10.96
; INFORMATION FOR SEQ ID NO: 21:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 118
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: synthetic DNA
; FEATURE:
; OTHER INFORMATION: includes a promoter region of T7
; RNA polymerase, a kozak sequence, and a DNA sequence
; corresponding to amino acid numbers 1-25 of a human tau protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-284-627-21

Query Match 61.1%; Score 33; DB 3; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 9 GAAATTAATACGACTCACTATAGGAGACCACA 41

RESULT 88
US-09-655-378A-163
; Sequence 163, Application US/09655378A
; Patent No. 6673616
; GENERAL INFORMATION:
; APPLICANT: BROW, MARY ANN D.
; LYAMICHEV, VICTOR I.
; OLIVE, DAVID M.
; TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
; PATHOGENS
; NUMBER OF SEQUENCES: 165
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/655.378A
; FILING DATE: 05-Sep-2000
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: FORS-01756
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 163:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 163:
US-09-655-378A-163

Query Match 61.1%; Score 33; DB 3; Length 144;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
```

Db 16 GAAATTAATACGACTCACTATAGGGAGACCACA 48

RESULT 89

US-08-902-623-44
; Sequence 44, Application US/08902623
; Patent No. 5922545
; GENERAL INFORMATION:
; APPLICANT: MATTHEAKIS, LARRY C.
; APPLICANT: DOWER, WILLIAM J.
; TITLE OF INVENTION: IN VITRO PEPTIDE AND ANTIBODY DISPLAY
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,623
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/586,176
; FILING DATE: 17-JAN-1996
; APPLICATION NUMBER: US 08/300,262
; FILING DATE: 02-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/144,775
; FILING DATE: US 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/12206
; FILING DATE: US 25-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: DUNN, TRACY J.
; REGISTRATION NUMBER: 34,587
; REFERENCE/DOCKET NUMBER: 16528X-001230US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-902-623-44

Query Match 61.1%; Score 33; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGGAGACCACA 33
Db 6 GAAATTAATACGACTCACTATAGGGAGACCACA 38

RESULT 90

US-08-875-277A-12
; Sequence 12, Application US/08875277A
; Patent No. 6171808
; GENERAL INFORMATION:
; APPLICANT: SOUIRELL, DAVID J.
; APPLICANT: LOWE, CHRISTOPHER R.
; APPLICANT: WHITE, PETER J.
; APPLICANT: MURRAY, JAMES A.H.

; TITLE OF INVENTION: MUTANT LUCIFERASES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,277A
; FILING DATE: 01-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9501172.2
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9508301.0
; FILING DATE: 24-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAWFORD, ARTHUR R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 124-588
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 186 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "PLASMID"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 124..186
US-08-875-277A-12

Query Match 61.1%; Score 33; DB 3; Length 186;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGGAGACCACA 33
Db 39 GAAATTAATACGACTCACTATAGGGAGACCACA 71

RESULT 91

US-08-096-182A-7
; Sequence 7, Application US/08096182A
; Patent No. 5439808
; GENERAL INFORMATION:
; APPLICANT: Blake, Milan S.
; APPLICANT: Tai, Joseph Y.
; APPLICANT: Qi, Huilin L.
; APPLICANT: Liang, Shu-Mei
; APPLICANT: Hronowski, Lucjan J.J.
; APPLICANT: Pullen, Jeffrey K.
; TITLE OF INVENTION: Method for the High Level Expression,
; Purification and Refolding of the Outer Membrane Group B
; PROTEINS FROM NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: D.C.

```
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/096.182A
; FILING DATE: 23-JUL-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1438.0060000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 101..187
; US-08-096-182A-7

Query Match 61.1%; Score 33; DB 2; Length 187;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAAATACGACTCACTATAGGAGACCACA 33
Db 16 GAAATTAAATACGACTCACTATAGGAGACCACA 48

RESULT 92
US-08-877-109-7
; Sequence 7, Application US/08877109
; Patent No. 5747287
; GENERAL INFORMATION:
; APPLICANT: Blake, Milan S.
; APPLICANT: Tai, Joseph Y.
; APPLICANT: Qi, Huilin L.
; APPLICANT: Liang, Shu-Mei
; APPLICANT: Hronowski, Lucjan J.J.
; APPLICANT: Pullen, Jeffrey K.
; TITLE OF INVENTION: Method for the High Level Expression,
; TITLE OF INVENTION: Purification and Refolding of the Outer Membrane Group B
; TITLE OF INVENTION: Porin Proteins from Neisseria meningitidis
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Ave., NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/877.109
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/431,264
; FILING DATE: 28-APR-1995
; APPLICATION NUMBER: 08/096.182
```

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; FILING DATE: 23-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1438.0060001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 101..187
; US-08-877-109-7

Query Match 61.1%; Score 33; DB 2; Length 187;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAAATACGACTCACTATAGGAGACCACA 33
Db 16 GAAATTAAATACGACTCACTATAGGAGACCACA 48

RESULT 93
US-08-798-760-7
; Sequence 7, Application US/08798760
; Patent No. 6013267
; GENERAL INFORMATION:
; APPLICANT: Blake, Milan S.
; APPLICANT: Tai, Joseph Y.
; APPLICANT: Qi, Huilin L.
; APPLICANT: Liang, Shu-Mei
; APPLICANT: Hronowski, Lucjan J.J.
; APPLICANT: Pullen, Jeffrey K.
; TITLE OF INVENTION: Method for the High Level Expression,
; TITLE OF INVENTION: Purification and Refolding of the Outer Membrane Group B
; TITLE OF INVENTION: Porin Proteins from Neisseria Meningitidis
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798.760
; FILING DATE: 11-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1438.0060002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
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NAME/KEY: CDS
LOCATION: 101..187
US-08-798-760-7

Query Match 61.1%; Score 33; DB 3; Length 187;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
DB 16 GAAATTAATACGACTCACTATAGGAGACCACA 48

RESULT 94

PCT-US94-08327-7
Sequence 7, Application PC/TUS9408327
GENERAL INFORMATION:
APPLICANT: The Rockefeller University
APPLICANT: 1230 York Avenue
APPLICANT: New York, New York 10021
APPLICANT: United States of America
APPLICANT: 12103 Indian Creek Court
APPLICANT: Beltsville, Maryland 20705
APPLICANT: United States of America
APPLICANT: Tai, Joseph Y.
APPLICANT: Qi, Huilin L.
APPLICANT: Liang, Shu-Mei
APPLICANT: Hronowski, Lucjan J.J.
APPLICANT: Pullen, Jeffrey K.
TITLE OF INVENTION: Method for the High Level
TITLE OF INVENTION: Expression,
TITLE OF INVENTION: Purification and Refolding of the Outer Membrane
TITLE OF INVENTION: Group B
TITLE OF INVENTION: Porin Proteins from Neisseria Meningitidis
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Ave., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/08327
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,182
FILING DATE: 23 July 1993
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438.006PC00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: 101..187
PCT-US94-08327-7

Query Match 61.1%; Score 33; DB 7; Length 187;

Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
DB 16 GAAATTAATACGACTCACTATAGGAGACCACA 48

RESULT 95

US-08-178-477B-33
Sequence 33, Application US/08178477B
Patent No. 5756343
GENERAL INFORMATION:
APPLICANT: WU, CARL; CLOS, JOACHIM;
APPLICANT: WESTWOOD, J. TIMOTHY.; RABINDRAN, SRIDHAR
TITLE OF INVENTION: CELL STRESS
TITLE OF INVENTION: TRANSCRIPTIONAL FACTORS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/178,477B
FILING DATE: 07-JAN-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/617,910
FILING DATE: 26-NOV-1990
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4103US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 278
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: (DNA) genomic
US-08-178-477B-33

Query Match 61.1%; Score 33; DB 2; Length 278;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
DB 18 GAAATTAATACGACTCACTATAGGAGACCACA 50

RESULT 96

US-08-014-944-1
Sequence 1, Application US/08014944
Patent No. 5376549
GENERAL INFORMATION:
APPLICANT: Guilfoyle, Richard A.
APPLICANT: Smith, Lloyd M.
TITLE OF INVENTION: CLONING VECTOR
NUMBER OF SEQUENCES: 6

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: QUARLES & BRADY
;; STREET: 411 East Wisconsin Avenue
;; CITY: Milwaukee
;; STATE: Wisconsin
;; COUNTRY: United States
;; ZIP: 53202
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/014,944
;; FILING DATE: 19930205
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Baker, Jean C.
;; REGISTRATION NUMBER: 35,433
;; REFERENCE/DOCKET NUMBER: 96-296-9243-3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (414) 277-5709
;; TELEFAX: (414) 277-5591
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 451 base pairs
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: double
;; TOPOLOGY: unknown
;; MOLECULE TYPE: RNA (genomic)
US-08-014-944-1

Query Match 61.1%; Score 33; DB 2; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 24 GAAATTAATACGACTCACTATAGGAGACCACA 56

RESULT 97
US-09-450-972-6
; Sequence 6, Application US/09450972
; Patent No. 6440728
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PHAGE VECTORS AND METHODS OF USE
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/450,972
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/072,222
; FILING DATE: 22-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/049,072
; FILING DATE: 09-JUN-1997
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 967 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-09-450-972-6

Query Match 61.1%; Score 33; DB 3; Length 967;

Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 673 GAAATTAATACGACTCACTATAGGAGACCACA 705

RESULT 98
US-09-809-517A-36
; Sequence 36, Application US/09809517A
; Patent No. 6753136
; GENERAL INFORMATION:
; APPLICANT: Lohning, Corinna
; TITLE OF INVENTION: No. 6753136el methods for displaying (poly)peptides/proteins on b.
; FILE REFERENCE: MORPHO/11
; CURRENT APPLICATION NUMBER: US/09/809,517A
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: EP 99114072.4
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: EP 00103551.8
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 2839
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: vector
US-09-809-517A-36

Query Match 61.1%; Score 33; DB 3; Length 2839;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 14 GAAATTAATACGACTCACTATAGGAGACCACA 46

RESULT 99
US-09-795-872-9
; Sequence 9, Application US/09795872
; Patent No. 6653068
; GENERAL INFORMATION:
; APPLICANT: Frisch, Christian
; APPLICANT: Kretzschmar, Titus
; APPLICANT: Hoss, Adolf
; APPLICANT: Von Ruden, Thomas
; TITLE OF INVENTION: Generation of specific binding partners binding to (poly)peptides
; FILE REFERENCE: Morpho/10
; CURRENT APPLICATION NUMBER: US/09/795,872
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/EP00/06137
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: EP 99 11 2815.8
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 2865
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(2865)
; OTHER INFORMATION: synthetic construct
; OTHER INFORMATION: expression vector
US-09-795-872-9

Query Match 61.1%; Score 33; DB 3; Length 2865;
 Best Local Similarity 100.0%; Pred. No. 0.0039;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAAATACGACTCACTATAGGGAGACCACA 33
 |||||
 DB 14 GAAATTAAATACGACTCACTATAGGGAGACCACA 46

RESULT 100
 US-09-795-872-8
 ; Sequence 8, Application US/09795872
 ; Patent No. 6653068
 ; GENERAL INFORMATION:
 ; APPLICANT: Frisch, Christian
 ; APPLICANT: Kretschmar, Titus
 ; APPLICANT: Hoss, Adolf
 ; APPLICANT: Von Ruden, Thomas
 ; TITLE OF INVENTION: Generation of specific binding partners binding to (poly)peptides
 ; FILE REFERENCE: Morpho/10
 ; CURRENT APPLICATION NUMBER: US/09/795,872
 ; PRIOR FILING DATE: 2001-02-28
 ; PRIOR APPLICATION NUMBER: PCT/EP00/06137
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: EP 99 11 2815.8
 ; PRIOR FILING DATE: 1999-07-02
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 8
 ; LENGTH: 2869
 ; TYPE: DNA
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (1)..(2869)
 ; OTHER INFORMATION: synthetic construct
 ; OTHER INFORMATION: expression vector
 US-09-795-872-8

Query Match 61.1%; Score 33; DB 3; Length 2869;
 Best Local Similarity 100.0%; Pred. No. 0.0039;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAAATACGACTCACTATAGGGAGACCACA 33
 |||||
 DB 14 GAAATTAAATACGACTCACTATAGGGAGACCACA 46

Search completed: May 19, 2006, 01:01:36
 Job time : 167.253 secs

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GenCore version 5.1.8
 Copyright (c) 1993 - 2006 Bioceleration Ltd.
 OM nucleic - nucleic search, using sw model
 Run on: May 19, 2006, 03:46:33 ; Search time 2166.18 Seconds
 (without alignments)
 306.314 Million cell updates/sec

Title: US-10-665-708-11
 Perfect score: 54
 Sequence: 1 gaataataacagctacta.....tgtgcaatattcccaatgc 54

Scoring table: IDENTITY NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications_NA_Main:*

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3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*

12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*

13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10H_PUBCOMB.seq:*

14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*

15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*

16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description	
		Match	Length				
1	54	100.0	54	3	US-09-738-274-11	Sequence 11, Appl	
2	54	100.0	54	10	US-10-665-708-11	Sequence 11, Appl	
3	42	77.8	58	3	US-09-738-274-8	Sequence 8, Appl	
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14	37	68.5	53	13	US-11-145-272-42	Sequence 42, Appl	
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119	33	61.1	144	16	US-11-198-657-163	Sequence 163, App	192	33	61.1	4742	16	US-11-196-019A-6	Sequence 6, Appl
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ALIGNMENTS

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; Sequence 11, Application US/09738274
; Publication No. US200301658241

Sequence 86, Appl
Sequence 9, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 168, App
Sequence 204, App
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 34, Appl
Sequence 5, Appli
Sequence 121, App
Sequence 2, Appli
Sequence 26, Appl
Sequence 15, Appl
Sequence 5, Appli
Sequence 14, Appl
Sequence 33, Appl
Sequence 4, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 9, Appli
Sequence 1, Appli
Sequence 35, Appl
Sequence 6, Appli
Sequence 7, Appli
Sequence 69, Appl
Sequence 31, Appl
Sequence 30, Appl
Sequence 29, Appl
Sequence 66, Appl
Sequence 10, Appl
Sequence 29, Appl
Sequence 17, Appl
Sequence 29, Appl
Sequence 18, Appl
Sequence 87, Appl
Sequence 20, Appl
Sequence 26, Appl
Sequence 1, Appli
Sequence 78, Appl
Sequence 37, Appl
Sequence 36, Appl
Sequence 70, Appl
Sequence 32, Appl
Sequence 35, Appl
Sequence 62, Appl
Sequence 38, Appl
Sequence 95, Appl
Sequence 95, Appl
Sequence 49, Appl
Sequence 19, Appl
Sequence 50, Appl
Sequence 20, Appl
Sequence 67, Appl
Sequence 1, Appli
Sequence 8, Appli
Sequence 15, Appl
Sequence 15, Appl

GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-738-274-11

Query Match 100.0%; Score 54; DB 3; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.1e-10; Mismatches 0; Indels 0; Gaps 0;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCTACTATAGGAGACACATTGTGCAATATTTCCCACTGC 54
DB 1 GAAATTAATACGACTCTACTATAGGAGACACATTGTGCAATATTTCCCACTGC 54

RESULT 2
US-10-665-708-11
; Sequence 11, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-665-708-11

Query Match 100.0%; Score 54; DB 10; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.1e-10; Mismatches 0; Indels 0; Gaps 0;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCTACTATAGGAGACACATTGTGCAATATTTCCCACTGC 54

```
Db 1 GAAATTAATACGACTCACTATAGGAGACCAATTGTGCAATATTTCCCACTGC 54
|||||
Query Match 77.8%; Score 42; DB 3; Length 58;
Best Local Similarity 98.1%; Pred. No. 7.9e-06;
Matches 53; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

RESULT 3
US-09-738-274-8
; Sequence 8, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 58
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-738-274-8
Query Match 77.8%; Score 42; DB 3; Length 58;
Best Local Similarity 98.1%; Pred. No. 7.9e-06;
Matches 53; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCAATTGTGCAATATTTCCCACTGC 54
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCA-TGTGCAATATTTCCCACTGC 53

RESULT 4
US-10-665-708-8
; Sequence 8, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 58
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; NAME/KEY: promoter
```

```
; LOCATION: (1)..(33)
US-10-665-708-8
Query Match 77.8%; Score 42; DB 10; Length 58;
Best Local Similarity 98.1%; Pred. No. 7.9e-06;
Matches 53; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCAATTGTGCAATATTTCCCACTGC 54
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCA-TGTGCAATATTTCCCACTGC 53

RESULT 5
US-09-738-274-10
; Sequence 10, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-738-274-10
Query Match 75.9%; Score 41; DB 3; Length 57;
Best Local Similarity 94.7%; Pred. No. 1.9e-05;
Matches 54; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 54
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATTTCCCACTGC 57

RESULT 6
US-10-665-708-10
; Sequence 10, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
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; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-665-708-10

Query Match      75.9%; Score 41; DB 10; Length 57;
Best Local Similarity 94.7%; Pred. No. 1.9e-05;
Matches 54; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 54
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 57

RESULT 7
US-09-738-274-9
; Sequence 9, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 59
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-738-274-9

Query Match      74.1%; Score 40; DB 3; Length 59;
Best Local Similarity 93.1%; Pred. No. 4.6e-05;
Matches 54; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 54
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 58

RESULT 8
US-10-665-708-9
; Sequence 9, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
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; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 59
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-665-708-9

Query Match      74.1%; Score 40; DB 10; Length 59;
Best Local Similarity 93.1%; Pred. No. 4.6e-05;
Matches 54; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 54
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 58

RESULT 9
US-09-944-036-9
; Sequence 9, Application US/09944036
; Patent No. US20020055095A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-9

Query Match      69.6%; Score 37.6; DB 3; Length 54;
Best Local Similarity 90.9%; Pred. No. 0.00037;
Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 44
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 44

RESULT 10
US-10-425-975-9
; Sequence 9, Application US/10425975
; Publication No. US20030228574A1
; GENERAL INFORMATION:
```

```
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; OTHER INFORMATION: target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-9
```

```
Query Match          69.6%; Score 37.6; DB 7; Length 54;
Best Local Similarity 90.9%; Pred. No. 0.00037;
Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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```
Qy 1 GAAATTAATAGACTCACTATAGGAGACCAATGTGCAATAT 44
    |||||
Db 1 GAAATTAATAGACTCACTATAGGAGACCAATGTGATAAATTT 44
```

RESULT 11

```
US-11-145-272-9
; Sequence 9, Application US/11/45272
; Publication No. US2005022727A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated with drug-resistance mutations
; FILE REFERENCE: GP114-04.DV2
; CURRENT APPLICATION NUMBER: US/11/145,272
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/425,975
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for Reverse Transcriptase target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; OTHER INFORMATION:
US-11-145-272-9
```

```
Query Match          69.6%; Score 37.6; DB 13; Length 54;
Best Local Similarity 90.9%; Pred. No. 0.00037;
Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 1 GAAATTAATAGACTCACTATAGGAGACCAATGTGCAATAT 44
    |||||
Db 1 GAAATTAATAGACTCACTATAGGAGACCAATGTGATAAATTT 44
```

RESULT 12

```
US-09-944-036-42
; Sequence 42, Application US/09944036
; Patent No. US20020055095A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-42
```

```
Query Match          68.5%; Score 37; DB 3; Length 53;
Best Local Similarity 88.9%; Pred. No. 0.00063;
Matches 40; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy 1 GAAATTAATAGACTCACTATAGGAGACCAATGTGCAATAT 45
    |||||
Db 1 GAAATTAATAGACTCACTATAGGAGACCAATCTTGATAAATTT 45
```

RESULT 13

```
US-10-425-975-42
; Sequence 42, Application US/10425975
; Publication No. US20030228574A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 53
; TYPE: DNA
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```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; OTHER INFORMATION: target sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-42

Query Match          68.5%; Score 37; DB 7; Length 53;
Best Local Similarity 88.9%; Pred. No. 0.00063;
Matches 40; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATT 45
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGATAAATT 45

RESULT 14
US-11-145-272-42
; Sequence 42, Application US/11145272
; Publication No. US2005022727A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated with drug-resistance mutations
; FILE REFERENCE: GP114-04.DV2
; CURRENT APPLICATION NUMBER: US/11/145,272
; PRIOR FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/425,975
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for Reverse Transcriptase target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; OTHER INFORMATION:
US-11-145-272-42

Query Match          68.5%; Score 37; DB 13; Length 53;
Best Local Similarity 88.9%; Pred. No. 0.00063;
Matches 40; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATT 45
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGATAAATT 45

RESULT 15
US-09-738-972-3
; Sequence 3, Application US/09738972
; Patent No. US20020012918A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; TITLE OF INVENTION: AVIUM COMPLEX SPECIES
; FILE REFERENCE: GP119-02.UT

```

```

; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: promoter-primer
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-738-972-3

Query Match          68.5%; Score 37; DB 3; Length 57;
Best Local Similarity 91.2%; Pred. No. 0.00064;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTTCCCACT 52
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATTTCCCACT 57

RESULT 16
US-09-738-972-13/c
; Sequence 13, Application US/09738972
; Patent No. US20020012918A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; TITLE OF INVENTION: AVIUM COMPLEX SPECIES
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: probe
US-09-738-972-13

Query Match          68.5%; Score 37; DB 3; Length 57;
Best Local Similarity 91.2%; Pred. No. 0.00064;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTTCCCACT 52
    |||||
Db 57 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATTTCCCACT 1

RESULT 17
US-09-738-274-7
; Sequence 7, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT

```

```
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-738-274-7

Query Match      68.5%; Score 37; DB 3; Length 57;
Best Local Similarity 91.2%; Pred. No. 0.00064;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy 1 GAAATTATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTTCCCACT 52
    |||||||
Db 1 GAAATTATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTTCCCACT 57
    |||||||

RESULT 18
US-10-862-026-3
; Sequence 3, Application US/10862026
; Publication No. US20040224348A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/10/862,026
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-862-026-3

Query Match      68.5%; Score 37; DB 9; Length 57;
Best Local Similarity 91.2%; Pred. No. 0.00064;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy 1 GAAATTATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTTCCCACT 52
    |||||||
Db 1 GAAATTATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTTCCCACT 57
    |||||||

RESULT 19
US-10-862-026-13/c
; Sequence 13, Application US/10862026
; Publication No. US20040224348A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GP119-02.UT
```

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; CURRENT APPLICATION NUMBER: US/10/862,026
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: probe
; LOCATION: (1)..(33)
US-10-862-026-13

Query Match      68.5%; Score 37; DB 9; Length 57;
Best Local Similarity 91.2%; Pred. No. 0.00064;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy 1 GAAATTATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTTCCCACT 52
    |||||||
Db 57 GAAATTATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTTCCCACT 1
    |||||||

RESULT 20
US-10-665-708-7
; Sequence 7, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAI, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-665-708-7

Query Match      68.5%; Score 37; DB 10; Length 57;
Best Local Similarity 91.2%; Pred. No. 0.00064;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy 1 GAAATTATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTTCCCACT 52
    |||||||
Db 1 GAAATTATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTTCCCACT 57
    |||||||

RESULT 21
US-09-944-036-2
; Sequence 2, Application US/09944036
; Publication No. US2002005095A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
```

APPLICANT: BABOLA, Odile
APPLICANT: TRAN, Nathalie
APPLICANT: VERNET, Guy
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
FILE REFERENCE: GP114-02.UT
CURRENT APPLICATION NUMBER: US/09/944,036
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,790
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: T7 promoter
NAME/KEY: promoter
LOCATION: (1)..(29)
US-09-944-036-2

Query Match 66.7%; Score 36; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36
|||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36

RESULT 22
US-10-425-975-2
Sequence 2, Application US/10425975
Publication No. US20030228574A1
GENERAL INFORMATION:
APPLICANT: YANG, Yeasing Y.
APPLICANT: BRENTANO, Steven T.
APPLICANT: BABOLA, Odile
APPLICANT: TRAN, Nathalie
APPLICANT: VERNET, Guy
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
FILE REFERENCE: GP114-02.UT
CURRENT APPLICATION NUMBER: US/10/425,975
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US/09/944,036
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,790
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: T7 promoter
NAME/KEY: promoter
LOCATION: (1)..(29)
US-10-425-975-2

Query Match 66.7%; Score 36; DB 7; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36
|||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36

RESULT 23
US-11-145-272-2
Sequence 2, Application US/11145272
Publication No. US20050227227A1
GENERAL INFORMATION:
APPLICANT: YANG, Yeasing Y.
APPLICANT: BRENTANO, Steven T.
APPLICANT: BABOLA, Odile
APPLICANT: TRAN, Nathalie
APPLICANT: VERNET, Guy
TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated with drug-resistance mutations
FILE REFERENCE: GP114-04.DV2
CURRENT APPLICATION NUMBER: US/11/145,272
CURRENT FILING DATE: 2005-06-03
PRIOR APPLICATION NUMBER: US 10/425,975
PRIOR FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: 09/944,036
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 60/229,790
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: T7 promoter
US-11-145-272-2

Query Match 66.7%; Score 36; DB 13; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36
|||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36

RESULT 24
US-09-944-036-6
Sequence 6, Application US/09944036
Patent No. US20020055095A1
GENERAL INFORMATION:
APPLICANT: YANG, Yeasing Y.
APPLICANT: BRENTANO, Steven T.
APPLICANT: BABOLA, Odile
APPLICANT: TRAN, Nathalie
APPLICANT: VERNET, Guy
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
FILE REFERENCE: GP114-02.UT
CURRENT APPLICATION NUMBER: US/09/944,036
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,790
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
NAME/KEY: promoter
LOCATION: (1)..(33)
NAME/KEY: modified_base
LOCATION: (46)
OTHER INFORMATION: Nebularine
US-09-944-036-6


```
; Query Match 66.7%; Score 36; DB 3; Length 54;
; Best Local Similarity 100.0%; Pred. No. 0.0015;
; Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36

RESULT 25
US-10-425-975-6
; Sequence 6, Application US/10425975
; Publication No. US200302285741
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; NAME/KEY: modified_base
; LOCATION: (46)
; OTHER INFORMATION: Nebularine
US-10-425-975-6

Query Match 66.7%; Score 36; DB 7; Length 54;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36

RESULT 26
US-11-145-272-6
; Sequence 6, Application US/11145272
; Publication No. US2005022727A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated with drug-resistance mutations
; FILE REFERENCE: GP114-04.DV2
; CURRENT APPLICATION NUMBER: US/11/145,272
; PRIOR FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/425,975
; PRIOR FILING DATE: 2003-04-28
```

```
; PRIOR APPLICATION NUMBER: 09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for Gag target sequence
; NAME/KEY: misc_feature
; LOCATION: (46)..(46)
; OTHER INFORMATION: Nebularine
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; OTHER INFORMATION:
US-11-145-272-6

Query Match 66.7%; Score 36; DB 13; Length 54;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36

RESULT 27
US-09-944-036-34
; Sequence 34, Application US/09944036
; Patent No. US20020055095A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; NAME/KEY: modified_base
; LOCATION: (45)
; OTHER INFORMATION: Nebularine
US-09-944-036-34

Query Match 66.3%; Score 35.8; DB 3; Length 53;
Best Local Similarity 94.9%; Pred. No. 0.0018;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTC 39
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTATGC 39
```

```
RESULT 28
US-09-944-036-36
; Sequence 36, Application US/09944036
; Patent No. US20020055095A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-36

Query Match      66.3%; Score 35.8; DB 3; Length 53;
Best Local Similarity 94.9%; Pred. No. 0.0018;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCATTTGTC 39
|||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCATTTGTC 39

RESULT 29
US-10-425-975-34
; Sequence 34, Application US/10425975
; Publication No. US20030228574A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-34

Query Match      66.3%; Score 35.8; DB 3; Length 53;
Best Local Similarity 94.9%; Pred. No. 0.0018;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCATTTGTC 39
|||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCATTTGTC 39
```

```
; OTHER INFORMATION: Nebularine
US-10-425-975-34

Query Match      66.3%; Score 35.8; DB 7; Length 53;
Best Local Similarity 94.9%; Pred. No. 0.0018;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCATTTGTC 39
|||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCATTTGTC 39

RESULT 30
US-10-425-975-36
; Sequence 36, Application US/10425975
; Publication No. US20030228574A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-36

Query Match      66.3%; Score 35.8; DB 7; Length 53;
Best Local Similarity 94.9%; Pred. No. 0.0018;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCATTTGTC 39
|||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCATTTGTC 39

RESULT 31
US-11-145-272-34
; Sequence 34, Application US/11145272
; Publication No. US2005022727A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associ
; TITLE OF INVENTION: with drug-resistance mutations
; FILE REFERENCE: GP114-04.DV2
; CURRENT APPLICATION NUMBER: US/11/145,272
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/425,975
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 09/944,036
; PRIOR FILING DATE: 2001-08-31
```

; PRIOR APPLICATION NUMBER: 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for Gag target sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (45)..(45)
; OTHER INFORMATION: Nebularine
US-11-145-272-34

Query Match 66.3%; Score 35.8; DB 13; Length 53;
Best Local Similarity 94.9%; Pred. No. 0.0018;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACATTGTGC 39
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACATTGTGC 39

RESULT 32
US-11-145-272-36
; Sequence 36, Application US/11145272
; Publication No. US2005022727A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated with drug-resistance mutations
; FILE REFERENCE: GP114-04.DV2
; CURRENT APPLICATION NUMBER: US/11/145,272
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/425,975
; PRIOR FILING DATE: 2003-04-28
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for Gag target sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; OTHER INFORMATION:
US-11-145-272-36

Query Match 66.3%; Score 35.8; DB 13; Length 53;
Best Local Similarity 94.9%; Pred. No. 0.0018;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACATTGTGC 39
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACATTGTGC 39

RESULT 33
US-10-500-646-241
; Sequence 241, Application US/10500646
; Publication No. US20050069890A1
; GENERAL INFORMATION:
; APPLICANT: MABILAT, Claude
; APPLICANT: DESVARENNE, Sabine
; APPLICANT: BABOLA, Odile
; APPLICANT: LACROIX, Bruno
; APPLICANT: BELLO PIGEM, Natalia
; TITLE OF INVENTION: Method for the detection and/or identification of the original animal species in animal matter contained in a sample
; FILE REFERENCE: 120162
; CURRENT APPLICATION NUMBER: US/10/500,646
; CURRENT FILING DATE: 2004-07-02
; PRIOR APPLICATION NUMBER: FR 0200265
; PRIOR FILING DATE: 2002-01-10
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 241
; LENGTH: 53
; TYPE: DNA
; ORGANISM: primer sequence CBHT7 20
US-10-500-646-241

Query Match 65.6%; Score 35.4; DB 10; Length 53;
Best Local Similarity 86.7%; Pred. No. 0.0026;
Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACATTGTGCAATATT 45
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACAGATGATATT 45

RESULT 34
US-10-273-707-49
; Sequence 49, Application US/10273707
; Publication No. US2003010448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-49

Query Match 65.6%; Score 35.4; DB 6; Length 54;
Best Local Similarity 79.2%; Pred. No. 0.0026;
Matches 42; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 2 AAATTAATACGACTCACTATAGGAGACCACATTGTGCAATATTCCTCCACTGC 54
|||||
Db 2 AAATTAATACGACTCACTATAGGAGACCACAAATTTCTTGCATCCCACTTGC 54

```
RESULT 35
US-10-978-145-49
; Sequence 49, Application US/10978145
; Publication No. US20050118630A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/978,145
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: US/10/273,707
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-978-145-49

Query Match          65.6%; Score 35.4; DB 10; Length 54;
Best Local Similarity 79.2%; Pred. No. 0.0026;
Matches 42; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY  2 AAATTAATACGACTCACTATAGGAGACACATTTGTGCAATATCCCACTGC 54
    |||||
DB   2 AAATTAATACGACTCACTATAGGAGACCAAAATTTCTTGCATCCAGCTGC 54

RESULT 36
US-09-944-036-10
; Sequence 10, Application US/09944036
; Patent No. US2002005095A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-10

Query Match          65.6%; Score 35.4; DB 3; Length 55;
Best Local Similarity 79.2%; Pred. No. 0.0026;
Matches 42; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
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Best Local Similarity 97.3%; Pred. No. 0.0026;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 GAAATTAATACGACTCACTATAGGAGACACATTTGT 37
    |||||
DB   1 GAAATTAATACGACTCACTATAGGAGACACATTTGT 37

RESULT 37
US-10-425-975-10
; Sequence 10, Application US/10425975
; Publication No. US20030228574A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-10

Query Match          65.6%; Score 35.4; DB 7; Length 55;
Best Local Similarity 97.3%; Pred. No. 0.0026;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 GAAATTAATACGACTCACTATAGGAGACACATTTGT 37
    |||||
DB   1 GAAATTAATACGACTCACTATAGGAGACACATTTGT 37

RESULT 38
US-11-145-272-10
; Sequence 10, Application US/11145272
; Publication No. US20050227227A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated
; FILE REFERENCE: GP114-04.DV2
; CURRENT APPLICATION NUMBER: US/11/145,272
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/425,975
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
```

```

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for Reverse Transcriptase target sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; OTHER INFORMATION:
US-11-145-272-10

Query Match          65.6%; Score 35.4; DB 13; Length 55;
Best Local Similarity 97.3%; Pred. No. 0.0026;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTAAATAGCACTCACTATAGGAGACCACTGT 37
|||||
Db 1 GAAATTAAATAGCACTCACTATAGGAGACCACTGT 37

RESULT 39
US-09-944-036-43
; Sequence 43, Application US/09944036
; Patent No. US20020055095A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-43

Query Match          64.8%; Score 35; DB 3; Length 52;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAAATAGCACTCACTATAGGAGACCACTT 35
|||||
Db 1 GAAATTAAATAGCACTCACTATAGGAGACCACTT 35

RESULT 40
US-09-738-274-12
; Sequence 12, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF

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; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-738-274-12

Query Match          64.8%; Score 35; DB 3; Length 52;
Best Local Similarity 80.4%; Pred. No. 0.0036;
Matches 41; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 GAAATTAAATAGCACTCACTATAGGAGACCACTTGTGCAATATTCCTCCAC 51
|||||
Db 1 GAAATTAAATAGCACTCACTATAGGAGACCACTGTCATCAGGCTTGCCCC 51

RESULT 41
US-10-425-975-43
; Sequence 43, Application US/10425975
; Publication No. US20030228574A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; OTHER INFORMATION: target sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-43

Query Match          64.8%; Score 35; DB 7; Length 52;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAAATAGCACTCACTATAGGAGACCACTT 35
|||||
Db 1 GAAATTAAATAGCACTCACTATAGGAGACCACTT 35

RESULT 42
US-10-665-708-12

```

Sequence 12, Application US/10665708
Publication No. US20050100915A1
GENERAL INFORMATION:
APPLICANT: BRENTANO, Steven T.
APPLICANT: JUCKER, Markus T.
APPLICANT: DELGADO, Francisco D.
APPLICANT: CLEUZIAT, Philippe
APPLICANT: RODRIGUE, Marc
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
TITLE OF INVENTION: MYCOBACTERIUM SPECIES
FILE REFERENCE: GP107-02.UT
CURRENT APPLICATION NUMBER: US/10/665,708
PRIOR FILING DATE: 2003-09-18
PRIOR APPLICATION NUMBER: US/09/738,274
PRIOR FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: 60/172,190
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 52
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
OTHER INFORMATION: oligonucleotide
NAME/KEY: promoter
LOCATION: (1)..(33)
US-10-665-708-12

Query Match 64.8%; Score 35; DB 10; Length 52;
Best Local Similarity 80.4%; Pred. No. 0.0036;
Matches 41; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGGAGACCATTTGTGCAATATCCAC 51
DB 1 GAAATTAATACGACTCACTATAGGAGACCATTTGTGCAATATCCAC 51

RESULT 43
US-11-145-272-43
Sequence 43, Application US/11145272
Publication No. US2005022727A1
GENERAL INFORMATION:
APPLICANT: YANG, Yeasing Y.
APPLICANT: BRENTANO, Steven T.
APPLICANT: BABOLA, Odile
APPLICANT: TRAN, Nathalie
APPLICANT: VERNET, Guy
TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated with drug-resistance mutations
FILE REFERENCE: GP114-04.DV2
CURRENT APPLICATION NUMBER: US/11/145,272
CURRENT FILING DATE: 2005-06-03
PRIOR APPLICATION NUMBER: US/10/425,975
PRIOR FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: 09/944,036
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 60/229,790
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn version 3.1
SEQ ID NO 43
LENGTH: 52
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: primer for Reverse Transcriptase target sequence
NAME/KEY: promoter
LOCATION: (1)..(33)
OTHER INFORMATION:

US-11-145-272-43
Query Match 64.8%; Score 35; DB 13; Length 52;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGGAGACCATTT 35
DB 1 GAAATTAATACGACTCACTATAGGAGACCATTT 35
RESULT 44
US-09-944-036-35
Sequence 35, Application US/09944036
Patent No. US20020055095A1
GENERAL INFORMATION:
APPLICANT: YANG, Yeasing Y.
APPLICANT: BRENTANO, Steven T.
APPLICANT: BABOLA, Odile
APPLICANT: TRAN, Nathalie
APPLICANT: VERNET, Guy
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
FILE REFERENCE: GP114-02.UT
CURRENT APPLICATION NUMBER: US/09/944,036
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,790
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 35
LENGTH: 53
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
NAME/KEY: promoter
LOCATION: (1)..(33)
US-09-944-036-35

Query Match 64.4%; Score 34.8; DB 3; Length 53;
Best Local Similarity 84.8%; Pred. No. 0.0043;
Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGGAGACCATTTGCAATATTC 46
DB 1 GAAATTAATACGACTCACTATAGGAGACCATTTGCTCCTTC 46
RESULT 45
US-10-425-975-35
Sequence 35, Application US/10425975
Publication No. US20030228574A1
GENERAL INFORMATION:
APPLICANT: YANG, Yeasing Y.
APPLICANT: BRENTANO, Steven T.
APPLICANT: BABOLA, Odile
APPLICANT: TRAN, Nathalie
APPLICANT: VERNET, Guy
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
FILE REFERENCE: GP114-02.UT
CURRENT APPLICATION NUMBER: US/10/425,975
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US/09/944,036
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,790
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 35
LENGTH: 53

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-35

Query Match 64.4%; Score 34.8; DB 7; Length 53;
Best Local Similarity 84.8%; Pred. No. 0.0043;
Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTGTCGAATATTC 46
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTGTCGAATATTC 46
|||||

RESULT 46
US-11-145-272-35
; Sequence 35, Application US/11145272
; Publication No. US20050227227A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated with drug-resistance mutations
; FILE REFERENCE: GP114-04.DV2
; CURRENT APPLICATION NUMBER: US/11/145,272
; CURRENT FILING DATE: 2005-08-03
; PRIOR APPLICATION NUMBER: US 10/425,975
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for Gag target sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; OTHER INFORMATION:
US-11-145-272-35

Query Match 64.4%; Score 34.8; DB 13; Length 53;
Best Local Similarity 84.8%; Pred. No. 0.0043;
Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTGTCGAATATTC 46
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTGTCGAATATTC 46
|||||

RESULT 47
US-09-944-036-33
; Sequence 33, Application US/09944036
; Patent No. US20020055095A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy

; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-33

Query Match 63.7%; Score 34.4; DB 3; Length 54;
Best Local Similarity 97.2%; Pred. No. 0.0062;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTG 36
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTG 36
|||||

RESULT 48
US-10-425-975-33
; Sequence 33, Application US/10425975
; Publication No. US20030228574A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-33

Query Match 63.7%; Score 34.4; DB 7; Length 54;
Best Local Similarity 97.2%; Pred. No. 0.0062;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTG 36
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTG 36
|||||

RESULT 49
US-11-145-272-33

; Sequence 33, Application US/11145272
; Publication No. US20050227227A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated with drug-resistance mutations
; FILE REFERENCE: GP114-04.DV2
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/425,975
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for Gag target sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; OTHER INFORMATION:
US-11-145-272-33

Query Match 63.7%; Score 34.4; DB 13; Length 54;
Best Local Similarity 97.2%; Pred. No. 0.0064;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36

RESULT 50
US-10-140-545-48
; Sequence 48, Application US/10140545
; Publication No. US2003017526A1
; GENERAL INFORMATION:
; APPLICANT: Daniel, Steven G
; APPLICANT: Turner, Leah
; APPLICANT: Samartzidou, Hrisi
; APPLICANT: Houts, Thomas M
; TITLE OF INVENTION: DESIGN OF ARTIFICIAL GENES FOR USE AS CONTROLS IN GENE EXPRESSION
; FILE REFERENCE: PB0120
; CURRENT APPLICATION NUMBER: US/10/140,545
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/289,202
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: US 60/312,420
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 62
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-140-545-48

Query Match 63.7%; Score 34.4; DB 7; Length 62;
Best Local Similarity 97.2%; Pred. No. 0.0064;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36

Db 15 GAAATTAATACGACTCACTATAGGAGACCACTTG 50
|||||
RESULT 51
US-11-013-179-48
; Sequence 48, Application US/11013179
; Publication No. US20050095640A1
; GENERAL INFORMATION:
; APPLICANT: SAMARTZIDOU, Hrisi
; APPLICANT: TURNER, Leah
; APPLICANT: HOUTS, Steven
; APPLICANT: HOUTS, Thomas
; TITLE OF INVENTION: DESIGN OF ARTIFICIAL GENES FOR USE AS CONTROLS IN GENE EXPRESSION
; FILE REFERENCE: PB0120
; CURRENT APPLICATION NUMBER: US/11/013,179
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: US 10/140,545
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/289,202
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: US 60/312,420
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 48
; LENGTH: 62
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-11-013-179-48

Query Match 63.7%; Score 34.4; DB 13; Length 62;
Best Local Similarity 97.2%; Pred. No. 0.0064;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36
|||||
Db 15 GAAATTAATACGACTCACTATAGGAGACCACTTG 50

RESULT 52
US-09-944-036-38
; Sequence 38, Application US/09944036
; Patent No. US20020050595A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Protease target
; OTHER INFORMATION: sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-38

Query Match 63.0%; Score 34; DB 3; Length 53;

Best Local Similarity 88.1%; Pred. No. 0.0088;
Matches 37; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 GAAATTAATACGACTCACTATAGGAGACCACTGTGCAAT 42
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTCCATT 42
|||||

RESULT 53

US-10-425-975-38
; Sequence 38, Application US/10425975
; Publication No. US20030228574A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR FILING DATE: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Protease target
; OTHER INFORMATION: sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-38

Query Match 63.0%; Score 34; DB 7; Length 53;
Best Local Similarity 88.1%; Pred. No. 0.0088;
Matches 37; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 GAAATTAATACGACTCACTATAGGAGACCACTGTGCAAT 42
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTCCATT 42
|||||

RESULT 54

US-11-145-272-38
; Sequence 38, Application US/11145272
; Publication No. US2005022727A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated with drug-resistance mutations
; FILE REFERENCE: GP114-04.DV2
; CURRENT APPLICATION NUMBER: US/11/145,272
; CURRENT FILING DATE: 2005-06-03
; PRIOR FILING DATE: US 10/425,975
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for Protease target sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; OTHER INFORMATION:
US-11-145-272-38

Query Match 63.0%; Score 34; DB 13; Length 53;
Best Local Similarity 88.1%; Pred. No. 0.0088;
Matches 37; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 GAAATTAATACGACTCACTATAGGAGACCACTGTGCAAT 42
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTCCATT 42
|||||

RESULT 55

US-10-273-707-30
; Sequence 30, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-30

Query Match 63.0%; Score 34; DB 6; Length 54;
Best Local Similarity 80.0%; Pred. No. 0.0088;
Matches 40; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy 2 AAATTAATACGACTCACTATAGGAGACCACTGTGCAATATTTCCAC 51
|||||
Db 2 AAATTAATACGACTCACTATAGGAGACCACTGAACTTGGCACAC 51
|||||

RESULT 56

US-10-978-145-30
; Sequence 30, Application US/10978145
; Publication No. US20050118630A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/978,145
; CURRENT FILING DATE: 2004-10-28

```
; PRIOR APPLICATION NUMBER: US/10/273,707
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1998-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-978-145-30
```

```
Query Match 63.0%; Score 34; DB 10; Length 54;
Best Local Similarity 80.0%; Pred. No. 0.0088;
Matches 40; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2 AAATTAATACGACTCACTATAGGAGACACATTTGTGAATATCCGCAC 51
|||||
DB 2 AAATTAATACGACTCACTATAGGAGACACATTTGTGAATATCCGCAC 51
|||||
```

```
RESULT 57
US-09-944-036-45
; Sequence 45, Application US/09944036
; Patent No. US20020055095A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-45
```

```
Query Match 63.0%; Score 34; DB 3; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACACAT 34
|||||
DB 1 GAAATTAATACGACTCACTATAGGAGACACAT 34
|||||
```

```
RESULT 58
US-10-425-975-45
; Sequence 45, Application US/10425975
; Publication No. US20030228574A1
```

```
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-45
```

```
Query Match 63.0%; Score 34; DB 7; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GAAATTAATACGACTCACTATAGGAGACACAT 34
|||||
DB 1 GAAATTAATACGACTCACTATAGGAGACACAT 34
|||||
```

```
RESULT 59
US-11-145-272-45
; Sequence 45, Application US/11145272
; Publication No. US20050227227A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated with drug-resistance mutations
; FILE REFERENCE: GP114-04.DV2
; CURRENT APPLICATION NUMBER: US/11/145,272
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/425,975
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for Reverse Transcriptase target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; OTHER INFORMATION:
US-11-145-272-45
```

```
Query Match          63.0%; Score 34; DB 13; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACAT 34
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACAT 34
    |||||

RESULT 60
US-09-738-972-2
; Sequence 2, Application US/09738972
; Patent No. US20020012918A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: Gp119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-738-972-2

Query Match          63.0%; Score 34; DB 3; Length 61;
Best Local Similarity 100.0%; Pred. No. 0.009;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACAT 34
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACAT 34
    |||||

RESULT 61
US-09-738-972-12/c
; Sequence 12, Application US/09738972
; Patent No. US20020012918A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: Gp119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-738-972-12

Query Match          63.0%; Score 34; DB 3; Length 61;
Best Local Similarity 100.0%; Pred. No. 0.009;
```

```
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACAT 34
    |||||
Db 61 GAAATTAATACGACTCACTATAGGAGACCACAT 28

RESULT 62
US-10-862-026-2
; Sequence 2, Application US/10862026
; Publication No. US20040224348A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: Gp119-02.UT
; CURRENT APPLICATION NUMBER: US/10/862,026
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-862-026-2

Query Match          63.0%; Score 34; DB 9; Length 61;
Best Local Similarity 100.0%; Pred. No. 0.009;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACAT 34
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACAT 34
    |||||

RESULT 63
US-10-862-026-12/c
; Sequence 12, Application US/10862026
; Publication No. US20040224348A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: Gp119-02.UT
; CURRENT APPLICATION NUMBER: US/10/862,026
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-862-026-12

Query Match          63.0%; Score 34; DB 9; Length 61;
Best Local Similarity 100.0%; Pred. No. 0.009;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 GAAATTAATACGACTCACTATAGGAGACCAT 34
|||
Db 61 GAAATTAATACGACTCACTATAGGAGACCAT 28

RESULT 64

US-10-273-707-36
; Sequence 36, Application US/10273707
; Publication No. US2003010448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-03.DV1
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-36

Query Match 62.6%; Score 33.8; DB 6; Length 52;
Best Local Similarity 94.6%; Pred. No. 0.01;
Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAATTAATACGACTCACTATAGGAGACCATTTGTG 38
|||
Db 2 AAATTAATACGACTCACTATAGGAGACCATTTGTG 38

RESULT 65

US-10-78-145-36
; Sequence 36, Application US/10978145
; Publication No. US20050118630A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-03.DV1
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: US/10/273,707
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter

; LOCATION: (1)..(28)
US-10-978-145-36

Query Match 62.6%; Score 33.8; DB 10; Length 52;
Best Local Similarity 94.6%; Pred. No. 0.01;
Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAATTAATACGACTCACTATAGGAGACCATTTGTG 38
|||
Db 2 AAATTAATACGACTCACTATAGGAGACCATTTGTG 38

RESULT 66

US-10-001-407-19
; Sequence 19, Application US/10001407
; Publication No. US2002017127A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Yeasing
; APPLICANT: Burrell, Terrie
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP117-03 UT
; CURRENT APPLICATION NUMBER: US/10/001,407
; CURRENT FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/242,620
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/280,058
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 58
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T7 promoter primer having a promoter sequence
; OTHER INFORMATION: appended at the 5' end of an HIV-2 complementary
; OTHER INFORMATION: primer sequence
US-10-001-407-19

Query Match 61.5%; Score 33.2; DB 6; Length 58;
Best Local Similarity 92.1%; Pred. No. 0.018;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCATTTGTG 38
|||
Db 1 GAAATTAATACGACTCACTATAGGAGACCATTTGTG 38

RESULT 67

US-09-765-555-66
; Sequence 66, Application US/09765555
; Publication No. US20030037355A1
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: Methods and compositions to modulate
; FILE REFERENCE: 27801-20014.40
; CURRENT APPLICATION NUMBER: US/09/765,555
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 09/620,897
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,468
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 5731
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: 2C7-SiD
US-09-765-555-66

Query Match	61.5%;	Score 33.2;	DB 3;	Length 5731;
Best Local Similarity	75.9%;	Pred. No. 0.046;		
Matches 41;	Conservative 0;	Mismatches 13;	Indels 0;	Gaps 0;
Qy	1	GAATTTAATACGACTCACTATAGGGAGACCAATTTGTCCAATATTCCCACTGC	54	
Db	858	GAATTTAATACGACTCACTATAGGGAGACCAAGCTGGCTAGCATGGCCGCTGC	911	

```

Query Match      61.1%; Score 33; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAAACGACTCACTATAGGGAGACCACA 33
    | | | | | | | | | | | | | | | | | |
Db 1 GAAATTAAACGACTCACTATAGGGAGACCACA 33
    | | | | | | | | | | | | | | | | | |

```

```

Query Match      61.1%; Score 33; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 33; Conservative 0; Mismatches 0; Indels 0;

Qy 1 GAAATTAAACGACTCACTATAGGGAGACCACA 33
Db 1 GAAATTAAACGACTCACTATAGGGAGACCACA 33

```

Query Match	61.1%	Score 33;	DB 3;	Length 33;
Best Local Similarity	100.0%	Pred. No. 0.019;		
Matches 33;	Conservative 0;	Mismatches 0;	Indels 0;	
Qy	1	GAATTTAATAGCACTCACTATAGGGAGACCACA	33	
Dy	1	GAATTTAATAGCACTCACTATAGGGAGACCACA	33	

Query Match 61.1%; Score 33; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 33; Conservative 0; Mismatches 0; Indels

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 72
US-10-425-975-4
; Sequence 4, Application US/10425975
; Publication No. US20030228574A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: T7 promoter
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-4

Query Match 61.1%; Score 33; DB 7; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 73
US-10-862-026-10
; Sequence 10, Application US/10862026
; Publication No. US20040224348A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/10/862,026
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: promoter
US-10-862-026-10

Query Match 61.1%; Score 33; DB 9; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.019;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 74
US-10-665-708-36
; Sequence 36, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAN, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: promoter
US-10-665-708-36

Query Match 61.1%; Score 33; DB 10; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 75
US-11-145-272-4
; Sequence 4, Application US/11145272
; Publication No. US20050227227A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences assoc
; FILE REFERENCE: GP114-04.DV2
; CURRENT APPLICATION NUMBER: US/11/145,272
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/425,975
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: T7 promoter
US-11-145-272-4

Query Match 61.1%; Score 33; DB 13; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 33; Conservative 0; Mismatches 0; Indels

Qy 1 GAAATTAATACGACTCACTATAGGGAGACCACA 33
|||

Db 1 GAAATTAATACGACTCACTATAGGGAGACCACA 33
|||

RESULT 76

```

US-10-651-563-9
; Sequence 9, Application US/10651563
; Publication No. US20040072992A1
; GENERAL INFORMATION:
; APPLICANT: Sachiko MACHIDA
; APPLICANT: Ken TOKUYASU
; APPLICANT: Shigeru MATSUNAGA
; APPLICANT: Yoshikiyo SAKAKIBARA
; APPLICANT: Masuko KOBORI
; APPLICANT: Zhesheng WEN
; TITLE OF INVENTION: Novel Peptide Capable of Specifically Acting on Biological Membranes
; FILE REFERENCE: NF002
; CURRENT APPLICATION NUMBER: US/10/651,563
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: 2002-253169
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 2003-21198
; PRIOR FILING DATE: 2003-01-29
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 39
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: primer
US-10-651-563-9

```

```
Query Match      61.1%; Score 33; DB 8; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 33: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 GAAATTAATACGACTCACTATAGGGAGACCACA 33
|||
Db 3 GAAATTAATACGACTCACTATAGGGAGACCACA 35

RESIII.T 77

```

US-09-953-321-15
; Sequence 15, Application US/09953321
; Patent No. US20020115083A1
; GENERAL INFORMATION:
; APPLICANT: PLUCKTHUN, ANDREAS
; APPLICANT: HANES, JOZEF
; APPLICANT: JERMUTUS, LUTZ
; TITLE OF INVENTION: NOVEL METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING
; FILE OF INVENTION: (POLY) PEPTIDES THAT INTERACT WITH TARGET MOLECULES
; FILE REFERENCE: PLUCK1/1 CON2
; CURRENT APPLICATION NUMBER: US/09/953,321
; PRIOR APPLICATION NUMBER: 2001-09-14
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:

```

```
US-11-142-790-3
; Publication No. US20030228574A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: INFERRING FUNCTION FROM SHOTGUN SEQUENCING DATA
; FILE REFERENCE: NEB-248-US
; CURRENT APPLICATION NUMBER: US/11/142,790
; PRIOR FILING DATE: 2005-06-01
; PRIOR APPLICATION NUMBER: 60/576,196
; PRIOR FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 42
; TYPE: DNA
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: T7 universal primer
US-11-142-790-3

Query Match          61.1%; Score 33; DB 16; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
    |||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 81
US-09-944-036-41
; Sequence 41, Application US/09944036
; Patent No. US20020055095A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; OTHER INFORMATION: target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-41

Query Match          61.1%; Score 33; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
    |||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 82
US-10-425-975-41
; Sequence 41, Application US/10425975
; Publication No. US2005022727A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated
; FILE REFERENCE: GP114-04.DV2
; CURRENT APPLICATION NUMBER: US/11/145,272
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/425,975
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/229,790
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for Reverse Transcriptase target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; OTHER INFORMATION:
```



```
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Protease target
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-37
```

```
Query Match 61.1%; Score 33; DB 3; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GAAATTAATACGACTCACTATAGGGAGACCACA 33
|||||
DB 1 GAAATTAATACGACTCACTATAGGGAGACCACA 33
```

```
RESULT 88
US-10-425-975-37
; Sequence 37, Application US/10425975
; Publication No. US20030228574A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Protease target
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-37
```

```
Query Match 61.1%; Score 33; DB 7; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GAAATTAATACGACTCACTATAGGGAGACCACA 33
|||||
DB 1 GAAATTAATACGACTCACTATAGGGAGACCACA 33
```

```
RESULT 89
US-11-145-272-37
; Sequence 37, Application US/11145272
; Publication No. US20050227227A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated
; FILE REFERENCE: GP114-04.DV2
; CURRENT APPLICATION NUMBER: US/11/145,272
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/425,975
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for Protease target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; OTHER INFORMATION:
US-11-145-272-37

Query Match 61.1%; Score 33; DB 13; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGGAGACCACA 33
|||||
DB 1 GAAATTAATACGACTCACTATAGGGAGACCACA 33

RESULT 90
US-09-944-036-44
; Sequence 44, Application US/09944036
; Patent No. US20020055095A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; OTHER INFORMATION: target sequence
```

```
; NAME/KEY: promoter
; LOCATION: (1)...(33)
US-09-944-036-44

Query Match      61.1%; Score 33; DB 3; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 91
US-10-425-975-44
; Sequence 44, Application US/10425975
; Publication No. US20030228574A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 44
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; OTHER INFORMATION: target sequence
; NAME/KEY: promoter
; LOCATION: (1)...(33)
US-10-425-975-44

Query Match      61.1%; Score 33; DB 7; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 92
US-11-145-272-44
; Sequence 44, Application US/11145272
; Publication No. US2005022727A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated
; FILE REFERENCE: GP114-04.DV2
; CURRENT APPLICATION NUMBER: US/11/145,272
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: US 10/425,975
; PRIOR FILING DATE: 2003-04-28

; NAME/KEY: promoter
; LOCATION: (1)...(33)
US-09-944-036-44

Query Match      61.1%; Score 33; DB 3; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 93
US-10-001-407-18
; Sequence 18, Application US/10001407
; Publication No. US20020177127A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Yeasing
; APPLICANT: Burrell, Terrie
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP117-03.UT
; CURRENT APPLICATION NUMBER: US/10/001,407
; CURRENT FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/242,620
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/280,058
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T7 promoter primer having a promoter sequence
; OTHER INFORMATION: appended at the 5' end of the sequence given as
; OTHER INFORMATION: SEQ ID NO:13
US-10-001-407-18

Query Match      61.1%; Score 33; DB 6; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 94
US-10-500-646-234
; Sequence 234, Application US/10500646
; Publication No. US20050069890A1
; GENERAL INFORMATION:
; APPLICANT: MABILAT, Claude
; APPLICANT: DESVARENNE, Sabine
; APPLICANT: BABOLA, Odile
; APPLICANT: LACROIX, Bruno
```

```
; APPLICANT: BELLO PIGEM, Natalia
; TITLE OF INVENTION: Method for the detection and/or identification of the original an
; FILE REFERENCE: 120162
; CURRENT APPLICATION NUMBER: US/10/500,646
; CURRENT FILING DATE: 2004-07-02
; PRIOR APPLICATION NUMBER: FR 0200265
; PRIOR FILING DATE: 2002-01-10
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 234
; LENGTH: 58
; TYPE: DNA
; ORGANISM: primer sequence CBHT7
US-10-500-646-234

Query Match          61.1%; Score 33; DB 10; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 95
US-09-738-972-1
; Sequence 1, Application US/09738972
; Patent No. US20020012918A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 59
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-738-972-1

Query Match          61.1%; Score 33; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
    |||||
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RESULT 96
US-09-738-972-11/c
; Sequence 11, Application US/09738972
; Patent No. US20020012918A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
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; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 59
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: probe
US-09-738-972-11

Query Match          61.1%; Score 33; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 59 GAAATTAATACGACTCACTATAGGAGACCACA 27

RESULT 97
US-10-862-026-1
; Sequence 1, Application US/10862026
; Publication No. US20040224348A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/10/862,026
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
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; TYPE: DNA
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; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-862-026-1

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Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 98
US-10-862-026-11/c
; Sequence 11, Application US/10862026
; Publication No. US20040224348A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/10/862,026
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
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; Sequence 5, Application US/09953321
; Patent No. US20020115083A1
; GENERAL INFORMATION:
; APPLICANT: HANES, JOZEF
; APPLICANT: JERMUTUS, LUTZ
; TITLE OF INVENTION: NOVEL METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING
; FILE REFERENCE: PLUCK/1 CON2
; CURRENT APPLICATION NUMBER: US/09/953,321
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/425,585
; NUMBER OF SEQ ID NOS: 15
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; LENGTH: 63
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US-09-953-321-5

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; Publication No. US20030073201A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics Corp.
; TITLE OF INVENTION: Method for Improving the Stability of Linear DNA in Cell-free in
; FILE REFERENCE: RDID 010490S
; CURRENT APPLICATION NUMBER: US/10/124,663
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 3
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; OTHER INFORMATION: sense primer
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OM nucleic - nucleic search, using sw model

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Title: US-10-665-708-11

Perfect score: 54

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Searched: 224314 seqs, 35277956 residues

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Listing first 300 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	33	61.1	654	US-10-953-688A-3	Sequence 3, Appli
6	33	61.1	8810	US-11-258-704-40	Sequence 40, Appli
7	33	61.1	8819	US-11-258-704-41	Sequence 41, Appli
8	30.8	57.0	2338	US-11-246-999-148	Sequence 148, App
9	30.2	55.9	3780	US-11-258-392-2	Sequence 2, Appli
10	30	55.6	42	US-11-283-332A-24	Sequence 24, Appli
11	30	55.6	3821	US-11-267-871-716	Sequence 716, App
12	30	55.6	5933	US-11-258-392-3	Sequence 3, Appli
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21	25	46.3	391	US-11-219-635-11	Sequence 11, Appli
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29	25	46.3	5502	7	US-11-301-554-785	Sequence 785, App
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	140	21.4	39.6	8165	7	US-11-024-545-64	Sequence 64, App	c	213	21	38.9	513	7	US-11-217-529-174584	Sequence 174584, A
	141	21.4	39.6	8165	7	US-11-251-466-40	Sequence 40, Appl	c	214	21	38.9	1926	7	US-11-217-529-82033	Sequence 82033, A
	142	21.4	39.6	8165	7	US-11-254-173-65	Sequence 65, Appl	215	20.8	38.5	98	7	US-11-260-844-43	Sequence 43, Appl	
	143	21.4	39.6	8165	7	US-11-264-784-118	Sequence 118, App	216	20.8	38.5	446	6	US-10-488-619-946	Sequence 946, App	
	144	21.4	39.6	8179	7	US-11-264-784-155	Sequence 155, App	c	217	20.8	1531	6	US-11-256-221-1	Sequence 1, Appl	
	145	21.4	39.6	8194	7	US-11-024-544A-128	Sequence 128, App	c	218	20.8	5487	6	US-10-473-173-27	Sequence 27, Appl	
	146	21.4	39.6	8194	7	US-11-024-545-56	Sequence 56, Appl	c	219	20.8	5487	6	US-10-505-928-120	Sequence 120, App	
	147	21.4	39.6	8194	7	US-11-190-750-111	Sequence 111, App	c	220	20.4	37.8	23	6	US-10-521-634-4	Sequence 4, Appl
	148	21.4	39.6	8194	7	US-11-251-466-30	Sequence 30, Appl	c	221	20.2	37.4	2298	6	US-10-505-928-354	Sequence 354, App
	149	21.4	39.6	8194	7	US-11-264-784-129	Sequence 129, App	c	222	20.2	37.4	2298	6	US-10-511-937-434	Sequence 434, App
	150	21.4	39.6	8196	7	US-11-024-544A-55	Sequence 55, Appl	c	223	20	37.0	20	7	US-11-223-738-8	Sequence 8, Appl
	151	21.4	39.6	8196	7	US-11-190-750-32	Sequence 32, Appl	224	20	37.0	20	7	US-11-273-937-12	Sequence 12, Appl	
	152	21.4	39.6	8196	7	US-11-264-784-156	Sequence 156, App	225	20	37.0	21	7	US-11-217-194-2	Sequence 2, Appl	
	153	21.4	39.6	8273	7	US-11-264-784-152	Sequence 152, App	226	20	37.0	22	6	US-10-508-063A-8	Sequence 8, Appl	
c	154	21.4	39.6	8411	7	US-11-251-466-52	Sequence 52, Appl	227	20	37.0	22	7	US-11-024-544A-154	Sequence 154, App	
	155	21.4	39.6	8411	7	US-11-264-784-139	Sequence 139, App	228	20	37.0	22	7	US-11-024-545-29	Sequence 29, App	
	156	21.4	39.6	8462	7	US-11-264-784-145	Sequence 145, App	229	20	37.0	22	7	US-11-185-301-18	Sequence 18, Appl	
	157	21.4	39.6	8502	7	US-11-264-784-120	Sequence 120, App	230	20	37.0	22	7	US-11-190-750-22	Sequence 22, Appl	
	158	21.4	39.6	8666	7	US-11-264-784-120	Sequence 120, App	231	20	37.0	22	7	US-11-254-173-17	Sequence 17, Appl	
	159	21.4	39.6	8666	7	US-11-024-544A-165	Sequence 165, App	232	20	37.0	22	7	US-11-264-784-258	Sequence 258, App	
	160	21.4	39.6	8953	7	US-11-185-301-10	Sequence 10, Appl	233	20	37.0	22	7	US-11-264-784-307	Sequence 307, App	
	161	21.4	39.6	8953	7	US-11-264-784-113	Sequence 113, App	234	20	37.0	36	6	US-10-537-581-1	Sequence 1, Appl	
	162	21.4	39.6	9239	7	US-11-254-173-68	Sequence 68, Appl	235	20	37.0	42	6	US-10-508-063A-10	Sequence 10, Appl	
	163	21.4	39.6	9239	7	US-11-264-784-143	Sequence 143, App	c	236	20	37.0	44	6	US-10-508-063A-6	Sequence 6, Appl
c	164	21.4	39.6	9685	7	US-11-226-605-88	Sequence 88, Appl	c	237	20	37.0	1106	6	US-10-196-749-535	Sequence 535, App
	165	21.4	39.6	10195	7	US-11-264-784-149	Sequence 149, App	238	20	37.0	1376	7	US-11-219-635-13	Sequence 13, Appl	
	166	21.4	39.6	10448	7	US-11-024-544A-129	Sequence 129, App	239	20	37.0	1376	7	US-11-219-635-17	Sequence 17, Appl	
	167	21.4	39.6	10448	7	US-11-190-750-112	Sequence 112, App	240	20	37.0	2797	7	US-11-181-115-17	Sequence 17, Appl	
	168	21.4	39.6	10448	7	US-11-264-784-123	Sequence 123, App								

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245 19.8 36.7 3249 7 US-11-217-529-81701
c 246 19.8 36.7 4356 7 US-11-217-529-2957
c 247 19.8 36.7 5524 6 US-10-473-173-51
c 248 19.6 36.3 1476 6 US-10-473-173-85
c 249 19.6 36.3 128361 6 US-10-505-928-151
c 250 19.4 35.9 95 7 US-11-150-778-46
c 251 19.4 35.9 138 7 US-11-217-529-81896
c 252 19.4 35.9 561 6 US-10-488-619-1361
c 253 19.4 35.9 1836 7 US-10-488-619-2840
c 254 19.4 35.9 1836 7 US-11-217-529-82281
c 255 19.2 35.6 1674 7 US-10-505-928-444
c 256 19 35.2 1674 7 US-11-217-529-5194
c 257 19 35.2 1674 7 US-11-263-057-22
c 258 19 35.2 706 6 US-10-522-171-7
c 259 19 35.2 706 6 US-10-488-619-1361
c 260 19 35.2 1098 7 US-11-217-529-82221
c 261 19 35.2 1167 7 US-11-217-529-78985
c 262 19 35.2 1245 7 US-11-217-529-78111
c 263 19 35.2 1301 6 US-10-505-928-279
c 264 19 35.2 394191 6 US-11-217-529-77878
c 265 18.8 34.8 1542 7 US-11-217-529-77984
c 266 18.8 34.8 1731 7 US-11-217-529-78208
c 267 18.8 34.8 1776 7 US-11-217-529-4802
c 268 18.8 34.8 1842 7 US-11-217-529-81292
c 269 18.8 34.8 50000 6 US-10-528-659-2
c 270 18.6 34.4 831 7 US-11-217-529-82708
c 271 18.6 34.4 1380 7 US-11-217-529-79862
c 272 18.6 34.4 1536 7 US-11-217-529-77398
c 273 18.6 34.4 2885 7 US-11-217-529-4885
c 274 18.6 34.4 4710 7 US-11-217-529-2497
c 275 18.6 34.4 7056 7 US-11-280-757-34
c 276 18.6 34.4 7931 7 US-11-183-218-29
c 277 18.6 34.4 151830 6 US-10-519-335-37
c 278 18.4 34.1 114 7 US-11-301-554-1764
c 279 18.4 34.1 432 7 US-11-217-529-80397
c 280 18.4 34.1 867 7 US-11-217-529-3540
c 281 18.4 34.1 999 7 US-11-217-529-77915
c 282 18.4 34.1 1293 1 US-09-949-925-33
c 283 18.4 34.1 2796 7 US-11-217-529-82728
c 284 18.4 34.1 3093 7 US-11-217-529-1218
c 285 18.4 34.1 3093 7 US-11-217-529-4214
c 286 18.4 34.1 4407 7 US-11-217-529-5983
c 287 18.4 34.1 97 7 US-11-260-844-54
c 288 18.2 33.7 1584 1 US-09-756-097B-101
c 289 18.2 33.7 1872 7 US-11-217-529-191177
c 290 18.2 33.7 2239 6 US-10-196-749-327
c 291 18.2 33.7 2339 7 US-11-101-316-109
c 292 18.2 33.7 2340 7 US-11-217-529-1807
c 293 18.2 33.7 2511 7 US-11-217-529-5222
c 294 18.2 33.7 2567 7 US-11-217-529-2499
c 295 18.2 33.7 4542 7 US-11-217-529-3362
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ALIGNMENTS

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RESULT 1
US-10-953-688A-5
; Sequence 5, Application US/10953688A
; Publication No. US20060099602A1
; GENERAL INFORMATION:
; APPLICANT: Precision System Science Co., Ltd
; APPLICANT: National Institute of Advanced Industrial Science and Technology
; TITLE OF INVENTION: Nucleic acid library and protein library
; FILE REFERENCE: PCT03-1004-US
; CURRENT APPLICATION NUMBER: US/10/953,688A
; PRIOR FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: JP 2002-095285
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Sequence 81701, A
Sequence 2957, Ap
Sequence 51, Appl
Sequence 85, Appl
Sequence 151, Appl
Sequence 46, Appl
Sequence 81896, A
Sequence 2840, Ap
Sequence 82281, A
Sequence 444, App
Sequence 5194, Ap
Sequence 22, Appl
Sequence 7, Appl
Sequence 1361, Ap
Sequence 82221, A
Sequence 78985, A
Sequence 78111, A
Sequence 279, App
Sequence 77878, A
Sequence 3, Appl
Sequence 77984, A
Sequence 78208, A
Sequence 4802, Ap
Sequence 81292, A
Sequence 3169, Ap
Sequence 2, Appl
Sequence 82708, A
Sequence 779862, A
Sequence 77398, A
Sequence 4885, Ap
Sequence 2497, Ap
Sequence 34, Appl
Sequence 29, Appl
Sequence 37, Appl
Sequence 1764, Ap
Sequence 80397, A
Sequence 3540, Ap
Sequence 77915, A
Sequence 33, Appl
Sequence 82728, A
Sequence 1218, Ap
Sequence 4214, Ap
Sequence 5983, Ap
Sequence 54, Appl
Sequence 173824, A
Sequence 77193, A
Sequence 166655, A
Sequence 75863, A
Sequence 101, App
Sequence 191177, A
Sequence 327, App
Sequence 109, App
Sequence 1807, App
Sequence 522, App
Sequence 2499, Ap
Sequence 3362, Ap
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; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 5
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNA comprising a sequence of
US-10-953-688A-5

Query Match 61.1%; Score 33; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|
Db 13 GAAATTAATACGACTCACTATAGGAGACCACA 45
|
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RESULT 2
US-10-953-688A-6
; Sequence 6, Application US/10953688A
; Publication No. US20060099602A1
; GENERAL INFORMATION:
; APPLICANT: Precision System Science Co., Ltd
; APPLICANT: National Institute of Advanced Industrial Science and Technology
; TITLE OF INVENTION: Nucleic acid library and protein library
; FILE REFERENCE: PCT03-1004-US
; CURRENT APPLICATION NUMBER: US/10/953,688A
; CURRENT FILING DATE: 2004-09-29
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: JP 2002-095285
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 6
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: upstream primer for 1st PCR
US-10-953-688A-6
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Query Match 61.1%; Score 33; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|
Db 13 GAAATTAATACGACTCACTATAGGAGACCACA 45
|
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RESULT 3
US-10-472-003-6
; Sequence 6, Application US/10472003
; Publication No. US20060099577A1
; GENERAL INFORMATION:
; APPLICANT: RiNA Netzwerk TNA-Technologien GmbH
; APPLICANT: Erdmann, Volker
; APPLICANT: Stiege, Wolfgang
; TITLE OF INVENTION: Method for Preparative Production of Long Nucleic Acids by PCR
; FILE REFERENCE: RNA/US/0308 / 00140/019001
; CURRENT APPLICATION NUMBER: US/10/472,003
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: DE 101 13 265
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: DE 101 51 071
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: DE 101 45 014
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 75
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; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Primer
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: (1)..(75)
US-10-472-003-6

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Query Match      61.1%; Score 33; DB 6; Length 75;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 33; Conservative 0; Mismatches 0; Indels
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Qy 1 GAAATTAATAGCACTCACTATTAGGAGACCACA 33
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Dp 1 GAAATTAATAGCACTCACTATTAGGAGACCACA 33

RESULT 4

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US-10-953-688A-2
; Sequence 2, Application US/10953688A
; Publication No. US20060099602A1
; GENERAL INFORMATION:
; APPLICANT: Precision System Science Co., Ltd
; APPLICANT: National Institute of Advanced Industrial Science and Technology
; TITLE OF INVENTION: Nucleic acid library and protein library
; FILE REFERENCE: PCT03-1004-US
; CURRENT APPLICATION NUMBER: US/10/953,688A
; CURRENT FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: JP 2002-095285
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 2
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (97)..(534)
; OTHER INFORMATION: Description of Artificial Sequence: His-labeled avidin
US-10-953-688A-2

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Query Match      61.1%; Score 33; DB 6; Length 651;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
13 GAAATTAATACGACTCACTATAGGAGACCACA 45
pb

RESULT 5

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US-10-953-688A-3
; Sequence 3, Application US/10953688A
; Publication No. US20060099602A1
; GENERAL INFORMATION:
; APPLICANT: Precision System Science Co., Ltd
; APPLICANT: National Institute of Advanced Industrial Science and Technology
; TITLE OF INVENTION: Nucleic acid library and protein library
; FILE REFERENCE: PCT03-1004-US
; CURRENT APPLICATION NUMBER: US/10/953,688A
; CURRENT FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: JP 2002-095285
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 3
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (97)..(537)
; OTHER INFORMATION: Description of Artificial Sequence: HA-labeled avidin g

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US-10-953-688A-3

Query Match 61.1%; Score 33; DB 6; Length 654;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGGAGACCACA 33
|||
13 GAAATTAATACGACTCACTATAGGGAGACCACA 45
Db

RESULT 6

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US-11-258-704-40
; Sequence 40, Application US/11258704
; Publication No. US20060101545A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Zhan-Bin
; APPLICANT: Stoop, Johan
; TITLE OF INVENTION: PM29 AND LEA3 PROMOTERS AND USE IN EXPRESSION OF TRANSGENIC GENES
; TITLE OF INVENTION: IN PLANTS
; FILE REFERENCE: BB-1551
; CURRENT APPLICATION NUMBER: US/11/258,704
; CURRENT FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/625,835
; PRIOR FILING DATE: 2004-11-08
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 40
; LENGTH: 8810
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid SH50
US-11-258-704-40

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Query Match 61.1%; Score 33; DB 7; Length 8810;
Best Local Similarity 100.0%; Pred. No. 7.1e-05;
Matches 33; Conservative 0; Mismatches 0; Indels

Qy 1 GAAATTAATACGACTCACTATAGGGAGACCACA 33
|||||
Db 5216 GAAATTAATACGACTCACTATAGGGAGACCACA 5248

RESULT 7

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US-11-258-704-41
; Sequence 41, Application US/11258704
; Publication No. US20060101545A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Zhan-Bin
; APPLICANT: Stoop, Johan
; TITLE OF INVENTION: PM29 AND LEA3 PROMOTERS AND USE IN EXPRESSION OF TRANSGENIC GENES
; TITLE OF INVENTION: IN PLANTS
; FILE REFERENCE: BB-1551
; CURRENT APPLICATION NUMBER: US/11/258,704
; CURRENT FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/625,835
; PRIOR FILING DATE: 2004-11-08
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 41
; LENGTH: 8819
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid SH58
US-11-258-704-41

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Query Match 61.1%; Score 33; DB 7; Length 8819;
Best Local Similarity 100.0%; Pred. No. 7.1e-05;
Matches 33; Conservative 0; Mismatches 0; Indels

QY 1 GAAATTAACGACTCACTATAGGGAGACCACA 33

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Db      6810 GAAATTAATACGACTCACTATAGGAGACCACA 6842
|||||
RESULT 8
US-11-246-999-148
; Sequence 148, Application US/11246999
; Publication No. US20060099622A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PF489P2
; CURRENT APPLICATION NUMBER: US/11/246,999
; CURRENT FILING DATE: 2005-10-11
; PRIOR APPLICATION NUMBER: US/09/984,130
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,792
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/836,353
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 148
; LENGTH: 2338
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (6)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (9)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (11)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (12)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (17)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (18)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (21)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (23)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (25)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
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; LOCATION: (26)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (27)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (28)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (29)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (30)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (31)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (32)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (33)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (34)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (37)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (38)
; OTHER INFORMATION: n equals a,t,g, or c
US-11-246-999-148

Query Match      57.0%; Score 30.8; DB 7; Length 2338;
Best Local Similarity 83.3%; Pred. No. 0.00038;
Matches 35; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      1 GAAATTAATACGACTCACTATAGGAGACCACATTGTGCAAT 42
|||||
Db      107 GAAATTAATACGACTCACTATAGGAGACCACAGCTTGATAT 148

RESULT 9
US-11-258-392-2
; Sequence 2, Application US/11258392
; Publication No. US20060099193A1
; GENERAL INFORMATION:
; APPLICANT: SUGAYA, IKUKO
; APPLICANT: SUGAYA, KIMINOBU
; TITLE OF INVENTION: METHODS AND MATERIALS FOR SUPPRESSING PAIN
; FILE REFERENCE: 10669-009
; CURRENT APPLICATION NUMBER: US/11/258,392
; CURRENT FILING DATE: 2005-10-24
; PRIOR APPLICATION NUMBER: 60/621,903
; PRIOR FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 2
; LENGTH: 3780
; TYPE: DNA
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Cloning vector sequence
US-11-258-392-2

Query Match          55.9%; Score 30.2; DB 7; Length 3780;
Best Local Similarity 91.4%; Pred. No. 0.00078;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTT 35
    |||||
Db 2778 GAAATTAATACGACTCACTATAGGAGACCGAAT 2812

RESULT 10
US-11-283-332A-24
; Sequence 24, Application US/11283332A
; Publication No. US20060099686A1
; GENERAL INFORMATION:
; APPLICANT: Scil Proteins GmbH
; APPLICANT: Fiedler, Markus
; APPLICANT: Fiedler, Ulrike
; APPLICANT: Rudolph, Rainer
; TITLE OF INVENTION: Generation of artificial binding proteins based on ubiquitin protein
; FILE REFERENCE: P17437
; CURRENT APPLICATION NUMBER: US/11/283,332A
; CURRENT FILING DATE: 2005-11-18
; PRIOR APPLICATION NUMBER: DE 103 24 447.6
; PRIOR FILING DATE: 2003-05-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially synthesized flanking oligonucleotide
US-11-283-332A-24

Query Match          55.6%; Score 30; DB 7; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
    |||||
Db 5 GAAATTAATACGACTCACTATAGGAGACC 34

RESULT 11
US-11-267-871-716
; Sequence 716, Application US/11267871
; Publication No. US20060094655A1
; GENERAL INFORMATION:
; APPLICANT: Guyon, Thierry
; APPLICANT: Borrelly, Gilles
; APPLICANT: Dittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: MODIFIED GROWTH HORMONES
; FILE REFERENCE: 17109-015001/925
; CURRENT APPLICATION NUMBER: US/11/267,871
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: 60/706,697
; PRIOR FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: 60/625,652
; PRIOR FILING DATE: 2004-11-04
; NUMBER OF SEQ ID NOS: 719
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 716
; LENGTH: 3821
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pNAUT hGH vector
```

```
US-11-267-871-716

Query Match          55.6%; Score 30; DB 7; Length 3821;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
    |||||
Db 480 GAAATTAATACGACTCACTATAGGAGACC 509

RESULT 12
US-11-258-392-3
; Sequence 3, Application US/11258392
; Publication No. US20060099193A1
; GENERAL INFORMATION:
; APPLICANT: SUGAYA, IKUKO
; APPLICANT: SUGAYA, KIMINOBU
; TITLE OF INVENTION: METHODS AND MATERIALS FOR SUPPRESSING PAIN
; FILE REFERENCE: 10669-009
; CURRENT APPLICATION NUMBER: US/11/258,392
; CURRENT FILING DATE: 2005-10-24
; PRIOR APPLICATION NUMBER: 60/621,903
; PRIOR FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 3
; LENGTH: 5933
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: cloning vector sequence
US-11-258-392-3

Query Match          55.6%; Score 30; DB 7; Length 5933;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
    |||||
Db 858 GAAATTAATACGACTCACTATAGGAGACC 887

RESULT 13
US-11-233-094-37
; Sequence 37, Application US/11233094
; Publication No. US20060094041A1
; GENERAL INFORMATION:
; APPLICANT: MARUYAMA, TAKAHIRO
; APPLICANT: ISHIGURO, TAKAHIRO
; APPLICANT: TAYA, TOSHIKI
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN
; FILE REFERENCE: 220081USO
; CURRENT APPLICATION NUMBER: US/11/233,094
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US/10/085,056
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2001-58143
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-11-233-094-37

Query Match          49.6%; Score 26.8; DB 7; Length 53;
Best Local Similarity 93.3%; Pred. No. 0.0053;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

QY 6 TTAATACGACTCACTATAGGAGACACACATT 35
|||||
Db 6 TTAATACGACTCACTATAGGAGACGCGCAT 35

RESULT 14
US-11-313-849-37
; Sequence 37, Application US/11313849
; Publication No. US20060099637A1
; GENERAL INFORMATION:
; APPLICANT: MARUYAMA, TAKAHIRO
; APPLICANT: TAYA, TOSHIKI
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN
; FILE REFERENCE: 220081U50
; CURRENT APPLICATION NUMBER: US/11/313,849
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US/10/085,056
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: JP 2001-58143
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-11-313-849-37

Query Match 49.6%; Score 26.8; DB 7; Length 53;
Best Local Similarity 93.3%; Pred. No. 0.0053; Mismatches 2; Indels 0; Gaps 0;

QY 6 TTAATACGACTCACTATAGGAGACACACATT 35
|||||
Db 6 TTAATACGACTCACTATAGGAGACGCGCAT 35

RESULT 15
US-11-260-844-35
; Sequence 35, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 97
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
US-11-260-844-35

Query Match 48.1%; Score 26; DB 7; Length 97;
Best Local Similarity 70.0%; Pred. No. 0.014; Mismatches 15; Indels 0; Gaps 0;

QY 5 TTAATACGACTCACTATAGGAGACACACATTGTGCAATATTTCCCACTGC 54
|||||
Db 8 TTAATACGACTCACTATAGGAGGAGCGGACAAATCTCCTTACCGC 57

RESULT 16
US-11-260-844-36
; Sequence 36, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 97
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
US-11-260-844-36

Query Match 48.1%; Score 26; DB 7; Length 97;
Best Local Similarity 70.0%; Pred. No. 0.014; Mismatches 15; Indels 0; Gaps 0;

QY 5 TTAATACGACTCACTATAGGAGACACACATTGTGCAATATTTCCCACTGC 54
|||||
Db 8 TTAATACGACTCACTATAGGAGGAGCGGACAAATCTCCTTACCGC 57

RESULT 17
US-11-260-844-39
; Sequence 39, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 95
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
US-11-260-844-39

Query Match 46.7%; Score 25.2; DB 7; Length 95;
Best Local Similarity 78.9%; Pred. No. 0.029; Mismatches 8; Indels 0; Gaps 0;

Oy	5 TTAATACGACTCACATATAGGAGACCACATTGTGCAAT	42
D6	6 TTAATACGACTCACATATAGGAGAGACGATCGGGGCAAT	43

RESULT 18

```

US-11-260-844-38
; Sequence 38, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 97
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
US-11-260-844-38

```

RESULT 19

```

US-11-260-844-41
; Sequence 41, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260, 844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 97
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
; NAME/KEY: misc_feature
; LOCATION: 54, 58, 79, 81, 83, 86, 90, 94
; OTHER INFORMATION: n = any of a, c, g, or t

```

US-11-260-844-41

Query Match 46.7%; Score 25.2; DB 7; Length 97;
Best Local Similarity 78.9%; Pred. No. 0.029;
Matches 30; Conservative 0; Mismatches 8; Indels

RESULT 20

```

US-10-472-003--7
; Sequence 7, Application US/10472003
; Publication No. US200609577A1
; GENERAL INFORMATION:
; APPLICANT: RINA Netzwerk TNA-Technologien GmbH
; APPLICANT: Merk, Helmut
; APPLICANT: Erdmann, Volker
; APPLICANT: Siege, Wolfgang
; TITLE OF INVENTION: Method for Preparative Production of Long Nucleic Acids by PCR
; FILE REFERENCE: RNA/US/0308 / 00140/019001
; CURRENT APPLICATION NUMBER: US/10/472,003
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: DE 101 13 265
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: DE 101 51 071
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: DE 101 45 014
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Primer
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: (1)..(47)
US-10-472-003--7

```

RESULT 21

```

US-11-219-635-11
/ Sequence 11, Application US/11219635
/ Publication No. US20060100218A1
/
/ GENERAL INFORMATION:
/ APPLICANT: IBRAHIM, PRABHA
/ APPLICANT: BREMER, RYAN
/ APPLICANT: GILLETTE, SAM
/ APPLICANT: CHO, HANNA
/ APPLICANT: NESPI, MARIKA
/ APPLICANT: MAMO, SHUMEYE
/ APPLICANT: ZHANG, CHAO
/ APPLICANT: ARTIS, DEAN R.
/ APPLICANT: LEE, BYUNGHUN
/ APPLICANT: ZUCKERMAN REBECCA
/
/ TITLE OF INVENTION: PDE4B INHIBITORS
/
/ FILE REFERENCE: 039363-1111
/ CURRENT APPLICATION NUMBER: US/11/219,635
/ CURRENT FILING DATE: 2005-09-02
/ PRIOR APPLICATION NUMBER: 60/607,407
/ PRIOR FILING DATE: 2004-09-03
/

```

; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 11
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (108)..(170)
US-11-219-635-11

Query Match 46.3%; Score 25; DB 7; Length 391;
Best Local Similarity 100.0%; Pred. No. 0.053; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGG 25
Db 16 GAAATTAATACGACTCACTATAGG 40

RESULT 22
US-11-245-473-14
; Sequence 14, Application US/11245473
; Publication No. US20060094085A1
; GENERAL INFORMATION:
; APPLICANT: Berry, Alan
; APPLICANT: Burlingame, Richard P.
; APPLICANT: Millis, James R.
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
; FILE REFERENCE: 3161-18-C1
; CURRENT APPLICATION NUMBER: US/11/245,473
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US/10/024,460
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,475
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,494
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; TYPE: DNA
; ORGANISM: Escherichia coli
US-11-245-473-14

Query Match 46.3%; Score 25; DB 7; Length 2184;
Best Local Similarity 100.0%; Pred. No. 0.09; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGG 25
Db 32 GAAATTAATACGACTCACTATAGG 56

RESULT 23
US-11-245-473-17
; Sequence 17, Application US/11245473
; Publication No. US20060094085A1
; GENERAL INFORMATION:
; APPLICANT: Berry, Alan
; APPLICANT: Burlingame, Richard P.
; APPLICANT: Millis, James R.
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
; FILE REFERENCE: 3161-18-C1
; CURRENT APPLICATION NUMBER: US/11/245,473
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US/10/024,460
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,475

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,494
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; TYPE: DNA
; ORGANISM: Escherichia coli
US-11-245-473-17

Query Match 46.3%; Score 25; DB 7; Length 2184;
Best Local Similarity 100.0%; Pred. No. 0.09; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGG 25
Db 32 GAAATTAATACGACTCACTATAGG 56

RESULT 24
US-11-245-473-20
; Sequence 20, Application US/11245473
; Publication No. US20060094085A1
; GENERAL INFORMATION:
; APPLICANT: Berry, Alan
; APPLICANT: Burlingame, Richard P.
; APPLICANT: Millis, James R.
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
; FILE REFERENCE: 3161-18-C1
; CURRENT APPLICATION NUMBER: US/11/245,473
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US/10/024,460
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,475
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,494
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; TYPE: DNA
; ORGANISM: Escherichia coli
US-11-245-473-20

Query Match 46.3%; Score 25; DB 7; Length 2184;
Best Local Similarity 100.0%; Pred. No. 0.09; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGG 25
Db 32 GAAATTAATACGACTCACTATAGG 56

RESULT 25
US-11-245-473-23
; Sequence 23, Application US/11245473
; Publication No. US20060094085A1
; GENERAL INFORMATION:
; APPLICANT: Berry, Alan
; APPLICANT: Burlingame, Richard P.
; APPLICANT: Millis, James R.
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
; FILE REFERENCE: 3161-18-C1
; CURRENT APPLICATION NUMBER: US/11/245,473
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US/10/024,460
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,475
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,494
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-14

```
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Escherichia coli
US-11-245-473-23

Query Match          46.3%; Score 25; DB 7; Length 2184;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGG 25
    |||||
Db 32 GAAATTAATACGACTCACTATAGG 56

RESULT 26
US-11-245-473-26
; Sequence 26, Application US/11245473
; Publication No. US20060094085A1
; GENERAL INFORMATION:
; APPLICANT: Berry, Alan
; APPLICANT: Burlingame, Richard P.
; APPLICANT: Millis, James R.
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
; FILE REFERENCE: 3161-18-C1
; CURRENT APPLICATION NUMBER: US/11/245,473
; CURRENT FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US/10/024,460
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,475
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,494
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Escherichia coli
US-11-245-473-26

Query Match          46.3%; Score 25; DB 7; Length 2184;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGG 25
    |||||
Db 32 GAAATTAATACGACTCACTATAGG 56

RESULT 27
US-11-245-473-29
; Sequence 29, Application US/11245473
; Publication No. US20060094085A1
; GENERAL INFORMATION:
; APPLICANT: Berry, Alan
; APPLICANT: Burlingame, Richard P.
; APPLICANT: Millis, James R.
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
; FILE REFERENCE: 3161-18-C1
; CURRENT APPLICATION NUMBER: US/11/245,473
; CURRENT FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US/10/024,460
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,475
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,494
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
```

```
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Escherichia coli
US-11-245-473-29

Query Match          46.3%; Score 25; DB 7; Length 2184;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGG 25
    |||||
Db 32 GAAATTAATACGACTCACTATAGG 56

RESULT 28
US-11-267-871-718/c
; Sequence 718, Application US/11267871
; Publication No. US20060094655A1
; GENERAL INFORMATION:
; APPLICANT: Guyon, Thierry
; APPLICANT: Borrelly, Gilles
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: MODIFIED GROWTH HORMONES
; FILE REFERENCE: 17109-015001/925
; CURRENT APPLICATION NUMBER: US/11/267,871
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: 60/706,697
; PRIOR FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: 60/625,652
; PRIOR FILING DATE: 2004-11-04
; NUMBER OF SEQ ID NOS: 719
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 718
; LENGTH: 5236
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pET - 24 vector
US-11-267-871-718

Query Match          46.3%; Score 25; DB 7; Length 5236;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGG 25
    |||||
Db 258 GAAATTAATACGACTCACTATAGG 234

RESULT 29
US-11-301-554-785
; Sequence 785, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
```

; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 785
; LENGTH: 5502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-301-554-785

Query Match 46.3%; Score 25; DB 7; Length 5502;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGG 25
Db 4979 GAAATTAATACGACTCACTATAGGG 5003

RESULT 30
US-11-301-554-784
; Sequence 784, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongcong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF LUNG CANCER
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13

; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 784
; LENGTH: 6353
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-301-554-784

Query Match 46.3%; Score 25; DB 7; Length 6353;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGG 25
Db 4979 GAAATTAATACGACTCACTATAGGG 5003

RESULT 31
US-11-196-366-3/c
; Sequence 3, Application US/11196366
; Publication No. US20060099710A1
; GENERAL INFORMATION:
; APPLICANT: DONNELLY, MARK I.
; APPLICANT: JOACHIMIAK, ANDRZEJ
; TITLE OF INVENTION: A VECTOR FOR IMPROVED IN VIVO PRODUCTION OF PROTEINS
; FILE REFERENCE: 21416-99616
; CURRENT APPLICATION NUMBER: US/11/196,366
; CURRENT FILING DATE: 2005-08-03
; PRIOR APPLICATION NUMBER: 60/626,800
; PRIOR FILING DATE: 2004-11-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 3
; LENGTH: 6441
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: pMCSG19 nucleotide sequence
US-11-196-366-3

Query Match 46.3%; Score 25; DB 7; Length 6441;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGG 25
Db 1536 GAAATTAATACGACTCACTATAGGG 1512

RESULT 32
US-11-245-473-13
; Sequence 13, Application US/11245473
; Publication No. US20060094085A1
; GENERAL INFORMATION:
; APPLICANT: Berry, Alan
; APPLICANT: Burlingame, Richard P.
; APPLICANT: Millis, James R.
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
; FILE REFERENCE: 3161-18-C1
; CURRENT APPLICATION NUMBER: US/11/245,473
; CURRENT FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US/10/024,460
; PRIOR FILING DATE: 2001-12-17

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,475
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,494
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-14
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 13
 ; LENGTH: 7408
 ; TYPE: DNA
 ; ORGANISM: Escherichia coli
 ; FEATURE:
 ; NAME/KEY: RBS
 ; LOCATION: (1240)..(1245)
 ; FEATURE:
 ; NAME/KEY: promoter
 ; LOCATION: (1185)..(1181)
 ; FEATURE:
 ; NAME/KEY: conflict
 ; LOCATION: (2509)..(2510)
 ; US-11-245-473-13

Query Match 46.3%; Score 25; DB 7; Length 7408;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GAATTAATACGACTCACTATAGG 25
 Db 1161 GAATTAATACGACTCACTATAGG 1185

RESULT 33
 US-11-233-094-39
 ; Sequence 39, Application US/11233094
 ; Publication No. US20060094041A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MARUYAMA, TAKAHIRO
 ; APPLICANT: ISHIGURO, TAKAHIRO
 ; APPLICANT: TAYA, TOSHIKI
 ; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN
 ; FILE REFERENCE: 220081US0
 ; CURRENT APPLICATION NUMBER: US/11/233,094
 ; CURRENT FILING DATE: 2005-09-23
 ; PRIOR APPLICATION NUMBER: US/10/085,056
 ; PRIOR FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: JP 2001-58143
 ; PRIOR FILING DATE: 2001-03-02
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 39
 ; LENGTH: 53
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic DNA
 ; US-11-233-094-39

Query Match 45.6%; Score 24.6; DB 7; Length 53;
 Best Local Similarity 87.1%; Pred. No. 0.042;
 Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 6 TAATACGACTCACTATAGGAGACCATG 36
 Db 6 TAATACGACTCACTATAGGAGATCATG 36

RESULT 34
 US-11-313-849-39
 ; Sequence 39, Application US/11313849
 ; Publication No. US20060099637A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MARUYAMA, TAKAHIRO
 ; APPLICANT: ISHIGURO, TAKAHIRO
 ; APPLICANT: TAYA, TOSHIKI

; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN
 ; FILE REFERENCE: 220081US0
 ; CURRENT APPLICATION NUMBER: US/11/313,849
 ; CURRENT FILING DATE: 2005-12-22
 ; PRIOR APPLICATION NUMBER: US/10/085,056
 ; PRIOR FILING DATE: 2002-03-01
 ; PRIOR APPLICATION NUMBER: JP 2001-58143
 ; PRIOR FILING DATE: 2001-03-02
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 39
 ; LENGTH: 53
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic DNA
 ; US-11-313-849-39

Query Match 45.6%; Score 24.6; DB 7; Length 53;
 Best Local Similarity 87.1%; Pred. No. 0.042;
 Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 6 TAATACGACTCACTATAGGAGACCATG 36
 Db 6 TAATACGACTCACTATAGGAGATCATG 36

RESULT 35
 US-11-233-094-40
 ; Sequence 40, Application US/11233094
 ; Publication No. US20060094041A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MARUYAMA, TAKAHIRO
 ; APPLICANT: ISHIGURO, TAKAHIRO
 ; APPLICANT: TAYA, TOSHIKI
 ; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN
 ; FILE REFERENCE: 220081US0
 ; CURRENT APPLICATION NUMBER: US/11/233,094
 ; CURRENT FILING DATE: 2005-09-23
 ; PRIOR APPLICATION NUMBER: US/10/085,056
 ; PRIOR FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: JP 2001-58143
 ; PRIOR FILING DATE: 2001-03-02
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 40
 ; LENGTH: 53
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic DNA
 ; US-11-233-094-40

Query Match 44.8%; Score 24.2; DB 7; Length 53;
 Best Local Similarity 89.7%; Pred. No. 0.062;
 Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 6 TAATACGACTCACTATAGGAGACCAT 34
 Db 6 TAATACGACTCACTATAGGAGAGTATAT 34

RESULT 36
 US-11-233-094-41
 ; Sequence 41, Application US/11233094
 ; Publication No. US20060094041A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MARUYAMA, TAKAHIRO
 ; APPLICANT: ISHIGURO, TAKAHIRO
 ; APPLICANT: TAYA, TOSHIKI
 ; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN
 ; FILE REFERENCE: 220081US0
 ; CURRENT APPLICATION NUMBER: US/11/233,094

; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US/10/085,056
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2001-58143
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; TYPE: DNA
; LENGTH: 53
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-11-233-094-41

Query Match 44.8%; Score 24.2; DB 7; Length 53;
Best Local Similarity 89.7%; Pred. No. 0.062;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 TAATACGACTCACTATAGGAGACCACAT 34
|||||
DB 6 TAATACGACTCACTATAGGAGAGTATAT 34
|||||

RESULT 37
US-11-313-849-40
; Sequence 40, Application US/11313849
; Publication No. US20060099637A1
; GENERAL INFORMATION:
; APPLICANT: MARUYAMA, TAKAHIRO
; APPLICANT: ISHIGURO, TAKAHIRO
; APPLICANT: TAYA, TOSHIKI
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN
; FILE REFERENCE: 220081USO
; CURRENT APPLICATION NUMBER: US/11/313,849
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/085,056
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: JP 2001-58143
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-11-313-849-40

Query Match 44.8%; Score 24.2; DB 7; Length 53;
Best Local Similarity 89.7%; Pred. No. 0.062;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 TAATACGACTCACTATAGGAGACCACAT 34
|||||
DB 6 TAATACGACTCACTATAGGAGAGTATAT 34
|||||

RESULT 38
US-11-313-849-41
; Sequence 41, Application US/11313849
; Publication No. US20060099637A1
; GENERAL INFORMATION:
; APPLICANT: MARUYAMA, TAKAHIRO
; APPLICANT: ISHIGURO, TAKAHIRO
; APPLICANT: TAYA, TOSHIKI
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN
; FILE REFERENCE: 220081USO
; CURRENT APPLICATION NUMBER: US/11/313,849
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/085,056
; PRIOR FILING DATE: 2002-03-01

; PRIOR APPLICATION NUMBER: JP 2001-58143
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-11-313-849-41

Query Match 44.8%; Score 24.2; DB 7; Length 53;
Best Local Similarity 89.7%; Pred. No. 0.062;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 TAATACGACTCACTATAGGAGACCACAT 34
|||||
DB 6 TAATACGACTCACTATAGGAGAGTATAT 34
|||||

RESULT 39
US-11-233-094-44
; Sequence 44, Application US/11233094
; Publication No. US20060094041A1
; GENERAL INFORMATION:
; APPLICANT: MARUYAMA, TAKAHIRO
; APPLICANT: ISHIGURO, TAKAHIRO
; APPLICANT: TAYA, TOSHIKI
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN
; FILE REFERENCE: 220081USO
; CURRENT APPLICATION NUMBER: US/11/233,094
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US/10/085,056
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2001-58143
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-11-233-094-44

Query Match 44.4%; Score 24; DB 7; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TAATACGACTCACTATAGGAGAC 29
|||||
DB 6 TAATACGACTCACTATAGGAGAC 29
|||||

RESULT 40
US-11-313-849-44
; Sequence 44, Application US/11313849
; Publication No. US20060099637A1
; GENERAL INFORMATION:
; APPLICANT: MARUYAMA, TAKAHIRO
; APPLICANT: ISHIGURO, TAKAHIRO
; APPLICANT: TAYA, TOSHIKI
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN
; FILE REFERENCE: 220081USO
; CURRENT APPLICATION NUMBER: US/11/313,849
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/085,056
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: JP 2001-58143
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 44

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-11-313-849-44
```

```
Query Match      44.4%; Score 24; DB 7; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 6 TAATACGACTCACTATAGGGAGAC 29
    |||||
Db 6 TAATACGACTCACTATAGGGAGAC 29
```

RESULT 41

```
US-11-267-871-719
```

```
; Sequence 719, Application US/11267871
; Publication No. US20060094655A1
; GENERAL INFORMATION:
; APPLICANT: Guyon, Thierry
; APPLICANT: Borrelly, Gilles
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: MODIFIED GROWTH HORMONES
; FILE REFERENCE: 17109-015001/925
; CURRENT APPLICATION NUMBER: US/11/267,871
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: 60/705,697
; PRIOR FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: 60/625,652
; PRIOR FILING DATE: 2004-11-04
; NUMBER OF SEQ ID NOS: 719
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 719
; LENGTH: 10574
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pET24Naut-hGH Plasmid
```

```
US-11-267-871-719
```

```
Query Match      44.4%; Score 24; DB 7; Length 10574;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2 AAATTAATACGACTCACTATAGGG 25
    |||||
Db 9001 AAATTAATACGACTCACTATAGGG 9024
```

RESULT 42

```
US-11-260-844-59
```

```
; Sequence 59, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
```

```
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 59
; LENGTH: 95
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
US-11-260-844-59
```

```
Query Match      44.1%; Score 23.8; DB 7; Length 95;
Best Local Similarity 92.6%; Pred. No. 0.11;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 5 TTAATACGACTCACTATAGGGAGACCA 31
    |||||
Db 8 TTAATACGACTCACTATAGGGAGCGA 34
```

RESULT 43

```
US-11-260-844-40
```

```
; Sequence 40, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 97
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1, 3, 6..8, 12, 15, 21, 31, 32, 34, 37, 57, 58, 62, 68, 69
; OTHER INFORMATION: n = any of a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 75, 78
; OTHER INFORMATION: n = any of a, c, g, or t
US-11-260-844-40
```

```
Query Match      44.1%; Score 23.8; DB 7; Length 97;
Best Local Similarity 62.2%; Pred. No. 0.11;
Matches 28; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
```

```
Qy 2 AAATTAATACGACTCACTATAGGGAGACCAATTGTGCAATATTC 46
    |||||
Db 5 ANNNTAANGCNACTCANTATAGGGAGNNCNCATNCGGCAATGTCC 49
```

RESULT 44

```
US-11-233-094-42
```

```
; Sequence 42, Application US/11233094
; Publication No. US20060094041A1
; GENERAL INFORMATION:
; APPLICANT: MARUYAMA, TAKAHIRO
; APPLICANT: ISHIGURO, TAKAHIRO
; APPLICANT: TAYA, TOSHIKI
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN
; FILE REFERENCE: 220081USO
```

; CURRENT APPLICATION NUMBER: US/11/233,094
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US/10/085,056
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2001-58143
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-11-233-094-42

Query Match 43.3%; Score 23.4; DB 7; Length 53;
Best Local Similarity 96.0%; Pred. No. 0.13; Mismatches 0; Indels 1; Gaps 0;

QY 6 TAATACGACTCACTATAGGAGACC 30
|||||
DB 6 TAATACGACTCACTATAGGAGAAC 30

RESULT 45
US-11-313-849-42
; Sequence 42, Application US/11313849
; Publication No. US20060099637A1
; GENERAL INFORMATION:
; APPLICANT: MARUYAMA, TAKAHIRO
; APPLICANT: ISHIGURO, TAKAHIRO
; APPLICANT: TAYA, TOSHIKI
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN
; FILE REFERENCE: 220081U0
; CURRENT APPLICATION NUMBER: US/11/313,849
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/085,056
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: JP 2001-58143
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-11-313-849-42

Query Match 43.3%; Score 23.4; DB 7; Length 53;
Best Local Similarity 96.0%; Pred. No. 0.13; Mismatches 0; Indels 1; Gaps 0;

QY 6 TAATACGACTCACTATAGGAGACC 30
|||||
DB 6 TAATACGACTCACTATAGGAGAAC 30

RESULT 46
US-10-541-993-4/c
; Sequence 4, Application US/10541993
; Publication No. US20060099670A1
; GENERAL INFORMATION:
; APPLICANT: Matuschek, Markus
; APPLICANT: Heinekamp, Thorsten
; APPLICANT: Schmidt, Andre
; APPLICANT: Brakhage, Axel
; TITLE OF INVENTION: Method for the genetic modification of organisms of the genus
; TITLE OF INVENTION: Blakesles, corresponding organisms, and the use of the same
; FILE REFERENCE: 13311-00010-US
; CURRENT APPLICATION NUMBER: US/10/541,993

; CURRENT FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: PCT/EP2004/000100
; PRIOR FILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: DE 103 00 649.4
; PRIOR FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: DE 103 41 272.7
; PRIOR FILING DATE: 2003-09-08
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 11611
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Vector
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (227)..(227)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (318)..(318)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (526)..(526)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8946)..(8946)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10028)..(10028)
; OTHER INFORMATION: n is a, c, g, or t
US-10-541-993-4

Query Match 43.3%; Score 23.4; DB 6; Length 11611;
Best Local Similarity 67.3%; Pred. No. 0.68; Mismatches 33; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 6 TAATACGACTCACTATAGGAGACCACATTTGTGCATATATTCCTCCACTGC 54
|||||
DB 8291 TAATACGACTCACTATAGGATCCTTTAGTAGGGTTAATTGGCGCCG 8243

RESULT 47
US-11-193-682-4
; Sequence 4, Application US/11193682
; Publication No. US20060094110A1
; GENERAL INFORMATION:
; APPLICANT: MCGARRITY, Gerard J.
; APPLICANT: GARCIA-BLANCO, Mariano
; TITLE OF INVENTION: USE OF SPLICEOSOME MEDIATED RNA TRANS-SPLICING FOR IMMUNOTHERAPY
; FILE REFERENCE: 027705.00102
; CURRENT APPLICATION NUMBER: US/11/193,682
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: US 60/592,607
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: unable to identify
US-11-193-682-4

Query Match 42.6%; Score 23; DB 7; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.15; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TAATACGACTCACTATAGGGAGA 28
|||||
Db 1 TAATACGACTCACTATAGGGAGA 23

RESULT 48
US-11-260-844-17
; Sequence 17, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-11-260-844-17

Query Match 42.6%; Score 23; DB 7; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTATACGACTCACTATAGGGAG 27
|||||
Db 8 TTATACGACTCACTATAGGGAG 30

RESULT 49
US-11-233-094-36
; Sequence 36, Application US/11233094
; Publication No. US20060094041A1
; GENERAL INFORMATION:
; APPLICANT: MARYAMA, TAKAHIRO
; APPLICANT: ISHIGURO, TAKAHIRO
; APPLICANT: TAYA, TOSHIKI
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN
; FILE REFERENCE: 220081US0
; CURRENT APPLICATION NUMBER: US/11/233,094
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US/10/085,056
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2001-58143
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-11-233-094-36

Query Match 42.6%; Score 23; DB 7; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TAATACGACTCACTATAGGGAGA 28

Db 6 TAATACGACTCACTATAGGGAGA 28
|||||

RESULT 50
US-11-233-094-38
; Sequence 38, Application US/11233094
; Publication No. US20060094041A1
; GENERAL INFORMATION:
; APPLICANT: MARYAMA, TAKAHIRO
; APPLICANT: ISHIGURO, TAKAHIRO
; APPLICANT: TAYA, TOSHIKI
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN
; FILE REFERENCE: 220081US0
; CURRENT APPLICATION NUMBER: US/11/233,094
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US/10/085,056
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2001-58143
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-11-233-094-38

Query Match 42.6%; Score 23; DB 7; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TAATACGACTCACTATAGGGAGA 28
|||||
Db 6 TAATACGACTCACTATAGGGAGA 28

RESULT 51
US-11-233-094-43
; Sequence 43, Application US/11233094
; Publication No. US20060094041A1
; GENERAL INFORMATION:
; APPLICANT: MARYAMA, TAKAHIRO
; APPLICANT: ISHIGURO, TAKAHIRO
; APPLICANT: TAYA, TOSHIKI
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN
; FILE REFERENCE: 220081US0
; CURRENT APPLICATION NUMBER: US/11/233,094
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US/10/085,056
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2001-58143
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-11-233-094-43

Query Match 42.6%; Score 23; DB 7; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TAATACGACTCACTATAGGGAGA 28
|||||
Db 6 TAATACGACTCACTATAGGGAGA 28

```
RESULT 52
US-11-313-849-36
; Sequence 36, Application US/11313849
; Publication No. US20060099637A1
; GENERAL INFORMATION:
; APPLICANT: MARIYAMA, TAKAHIRO
; APPLICANT: ISHIGURO, TAKAHIRO
; APPLICANT: TAYA, TOSHIKI
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN
; FILE REFERENCE: 220081US0
; CURRENT APPLICATION NUMBER: US/11/313,849
; PRIOR FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/085,056
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: JP 2001-58143
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-11-313-849-36

Query Match          42.6%; Score 23; DB 7; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TAATACGACTCACTATAGGAGA 28
   |||||
DB 6 TAATACGACTCACTATAGGAGA 28

RESULT 53
US-11-313-849-38
; Sequence 38, Application US/11313849
; Publication No. US20060099637A1
; GENERAL INFORMATION:
; APPLICANT: MARIYAMA, TAKAHIRO
; APPLICANT: ISHIGURO, TAKAHIRO
; APPLICANT: TAYA, TOSHIKI
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN
; FILE REFERENCE: 220081US0
; CURRENT APPLICATION NUMBER: US/11/313,849
; PRIOR FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/085,056
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: JP 2001-58143
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-11-313-849-38

Query Match          42.6%; Score 23; DB 7; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TAATACGACTCACTATAGGAGA 28
   |||||
DB 6 TAATACGACTCACTATAGGAGA 28

RESULT 54
US-11-313-849-43
; Sequence 43, Application US/11313849
; Publication No. US20060099637A1
; GENERAL INFORMATION:
; APPLICANT: MARIYAMA, TAKAHIRO
; APPLICANT: ISHIGURO, TAKAHIRO
; APPLICANT: TAYA, TOSHIKI
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN
; FILE REFERENCE: 220081US0
; CURRENT APPLICATION NUMBER: US/11/313,849
; PRIOR FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/085,056
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: JP 2001-58143
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-11-313-849-43

Query Match          42.6%; Score 23; DB 7; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TAATACGACTCACTATAGGAGA 28
   |||||
DB 6 TAATACGACTCACTATAGGAGA 28

RESULT 55
US-11-260-844-57
; Sequence 57, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 95
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Apramer
US-11-260-844-57

Query Match          42.6%; Score 23; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTAATACGACTCACTATAGGAG 27
   |||||
DB 8 TTAATACGACTCACTATAGGAG 30

RESULT 56
US-11-260-844-24
; Sequence 24, Application US/11260844
```

```
; Sequence 43, Application US/11313849
; Publication No. US20060099637A1
; GENERAL INFORMATION:
; APPLICANT: MARIYAMA, TAKAHIRO
; APPLICANT: ISHIGURO, TAKAHIRO
; APPLICANT: TAYA, TOSHIKI
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN
; FILE REFERENCE: 220081US0
; CURRENT APPLICATION NUMBER: US/11/313,849
; PRIOR FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/085,056
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: JP 2001-58143
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-11-313-849-43

Query Match          42.6%; Score 23; DB 7; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TAATACGACTCACTATAGGAGA 28
   |||||
DB 6 TAATACGACTCACTATAGGAGA 28

RESULT 55
US-11-260-844-57
; Sequence 57, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 95
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Apramer
US-11-260-844-57

Query Match          42.6%; Score 23; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTAATACGACTCACTATAGGAG 27
   |||||
DB 8 TTAATACGACTCACTATAGGAG 30

RESULT 56
US-11-260-844-24
; Sequence 24, Application US/11260844
```

```
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR FILING DATE: 1999-03-25
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 96
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
US-11-260-844-24
```

```
Query Match 42.6%; Score 23; DB 7; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 5 TTAATACGACTCACTATAGGGAG 27
|||||
DB 8 TTAATACGACTCACTATAGGGAG 30
```

RESULT 57

```
US-11-260-844-34
; Sequence 34, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR FILING DATE: 1999-03-25
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 96
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
US-11-260-844-34
```

```
Query Match 42.6%; Score 23; DB 7; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 5 TTAATACGACTCACTATAGGGAG 27
|||||
DB 7 TTAATACGACTCACTATAGGGAG 29
```

RESULT 58

```
US-11-260-844-37
```

```
; Sequence 37, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR FILING DATE: 1999-03-25
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 96
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
US-11-260-844-37
```

```
Query Match 42.6%; Score 23; DB 7; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 5 TTAATACGACTCACTATAGGGAG 27
|||||
DB 8 TTAATACGACTCACTATAGGGAG 30
```

RESULT 59

```
US-11-260-844-52
; Sequence 52, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR FILING DATE: 1999-03-25
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 96
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
US-11-260-844-52
```

```
Query Match 42.6%; Score 23; DB 7; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 5 TTAATACGACTCACTATAGGGAG 27
|||||
DB 8 TTAATACGACTCACTATAGGGAG 30
```

RESULT 60

US-11-260-844-25
; Sequence 25, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 97
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
US-11-260-844-25

Query Match 42.6%; Score 23; DB 7; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTAATACGACTCACTATAGGAG 27
|||||
DB 8 TTAATACGACTCACTATAGGAG 30

RESULT 61
US-11-260-844-27
; Sequence 27, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 97
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
US-11-260-844-27

Query Match 42.6%; Score 23; DB 7; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTAATACGACTCACTATAGGAG 27
|||||
DB 8 TTAATACGACTCACTATAGGAG 30

RESULT 62
US-11-260-844-28
; Sequence 28, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 97
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
US-11-260-844-28

Query Match 42.6%; Score 23; DB 7; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTAATACGACTCACTATAGGAG 27
|||||
DB 8 TTAATACGACTCACTATAGGAG 30

RESULT 63
US-11-260-844-29
; Sequence 29, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 97
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
US-11-260-844-29

Query Match 42.6%; Score 23; DB 7; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTAATACGACTCACTATAGGAG 27
|||||
DB 8 TTAATACGACTCACTATAGGAG 30

RESULT 64
 US-11-260-844-30
 ; Sequence 30, Application US/11260844
 ; Publication No. US20060093602A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Life, Paul F
 ; APPLICANT: Rees, Edward S
 ; APPLICANT: Rhodes, Andrew D
 ; TITLE OF INVENTION: Oncostatin M Antagonists
 ; FILE REFERENCE: 1430-282 / PG 3728US
 ; CURRENT APPLICATION NUMBER: US/11/260,844
 ; CURRENT FILING DATE: 2005-10-27
 ; PRIOR APPLICATION NUMBER: US/10/442,289
 ; PRIOR FILING DATE: 2003-05-21
 ; PRIOR APPLICATION NUMBER: 09/276,147
 ; PRIOR FILING DATE: 1999-03-25
 ; PRIOR APPLICATION NUMBER: GB 9806530.3
 ; PRIOR FILING DATE: 1998-03-26
 ; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 30
 ; LENGTH: 97
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
 US-11-260-844-30

Query Match 42.6%; Score 23; DB 7; Length 97;
 Best Local Similarity 100.0%; Pred. No. 0.23;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTAATACGACTCACTATAGGGAG 27
 |||||
 Db 8 TTAATACGACTCACTATAGGGAG 30

RESULT 65
 US-11-260-844-42
 ; Sequence 42, Application US/11260844
 ; Publication No. US20060093602A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Life, Paul F
 ; APPLICANT: Rees, Edward S
 ; APPLICANT: Rhodes, Andrew D
 ; TITLE OF INVENTION: Oncostatin M Antagonists
 ; FILE REFERENCE: 1430-282 / PG 3728US
 ; CURRENT APPLICATION NUMBER: US/11/260,844
 ; CURRENT FILING DATE: 2005-10-27
 ; PRIOR APPLICATION NUMBER: US/10/442,289
 ; PRIOR FILING DATE: 2003-05-21
 ; PRIOR APPLICATION NUMBER: 09/276,147
 ; PRIOR FILING DATE: 1999-03-25
 ; PRIOR APPLICATION NUMBER: GB 9806530.3
 ; PRIOR FILING DATE: 1998-03-26
 ; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 42
 ; LENGTH: 97
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
 ; NAME/KEY: misc feature
 ; LOCATION: 41..43, 48, 50..52, 54, 55, 57, 58, 60, 65, 66, 76
 ; OTHER INFORMATION: n = any of a, c, g, or t
 US-11-260-844-42

Query Match 42.6%; Score 23; DB 7; Length 97;
 Best Local Similarity 100.0%; Pred. No. 0.23;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTAATACGACTCACTATAGGGAG 27
 |||||
 Db 8 TTAATACGACTCACTATAGGGAG 30

RESULT 66
 US-11-260-844-44
 ; Sequence 44, Application US/11260844
 ; Publication No. US20060093602A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Life, Paul F
 ; APPLICANT: Rees, Edward S
 ; APPLICANT: Rhodes, Andrew D
 ; TITLE OF INVENTION: Oncostatin M Antagonists
 ; FILE REFERENCE: 1430-282 / PG 3728US
 ; CURRENT APPLICATION NUMBER: US/11/260,844
 ; CURRENT FILING DATE: 2005-10-27
 ; PRIOR APPLICATION NUMBER: US/10/442,289
 ; PRIOR FILING DATE: 2003-05-21
 ; PRIOR APPLICATION NUMBER: 09/276,147
 ; PRIOR FILING DATE: 1999-03-25
 ; PRIOR APPLICATION NUMBER: GB 9806530.3
 ; PRIOR FILING DATE: 1998-03-26
 ; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 44
 ; LENGTH: 97
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
 US-11-260-844-44

Query Match 42.6%; Score 23; DB 7; Length 97;
 Best Local Similarity 100.0%; Pred. No. 0.23;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTAATACGACTCACTATAGGGAG 27
 |||||
 Db 8 TTAATACGACTCACTATAGGGAG 30

RESULT 67
 US-11-260-844-45
 ; Sequence 45, Application US/11260844
 ; Publication No. US20060093602A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Life, Paul F
 ; APPLICANT: Rees, Edward S
 ; APPLICANT: Rhodes, Andrew D
 ; TITLE OF INVENTION: Oncostatin M Antagonists
 ; FILE REFERENCE: 1430-282 / PG 3728US
 ; CURRENT APPLICATION NUMBER: US/11/260,844
 ; CURRENT FILING DATE: 2005-10-27
 ; PRIOR APPLICATION NUMBER: US/10/442,289
 ; PRIOR FILING DATE: 2003-05-21
 ; PRIOR APPLICATION NUMBER: 09/276,147
 ; PRIOR FILING DATE: 1999-03-25
 ; PRIOR APPLICATION NUMBER: GB 9806530.3
 ; PRIOR FILING DATE: 1998-03-26
 ; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 45
 ; LENGTH: 97
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
 US-11-260-844-45

Query Match 42.6%; Score 23; DB 7; Length 97;
 Best Local Similarity 100.0%; Pred. No. 0.23;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTAATACGACTCACTATAGGAG 27
Db 8 TTAATACGACTCACTATAGGAG 30

RESULT 68

US-11-260-844-46
; Sequence 46, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 97
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
US-11-260-844-46

Query Match 42.6%; Score 23; DB 7; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTAATACGACTCACTATAGGAG 27
Db 8 TTAATACGACTCACTATAGGAG 30

RESULT 69

US-11-260-844-49
; Sequence 49, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 97
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
; NAME/KEY: misc_feature
; LOCATION: 45, 49, 52, 54, 55, 67, 72..75, 81, 83, 85, 97

; OTHER INFORMATION: n = any of a, c, g, or t
US-11-260-844-49

Query Match 42.6%; Score 23; DB 7; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTAATACGACTCACTATAGGAG 27
Db 8 TTAATACGACTCACTATAGGAG 30

RESULT 70

US-11-260-844-50
; Sequence 50, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 97
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
US-11-260-844-50

Query Match 42.6%; Score 23; DB 7; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTAATACGACTCACTATAGGAG 27
Db 8 TTAATACGACTCACTATAGGAG 30

RESULT 71

US-11-260-844-51
; Sequence 51, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 97
; TYPE: DNA
; ORGANISM: Artificial Sequence

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
US-11-260-844-51

Query Match      42.6%; Score 23; DB 7; Length 97;
Best Local Similarity 100.0%; Pred.No. 0.23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTAATACGACTCACTATAGGAG 27
Db 8 TTAATACGACTCACTATAGGAG 30

RESULT 72
US-11-260-844-53
; Sequence 53, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 97
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
; NAME/KEY: misc_feature
; LOCATION: 45, 48, 50, 57, 59, 60, 74, 80, 84, 94, 96
; OTHER INFORMATION: n = any of a, c, g, or t
US-11-260-844-53

Query Match      42.6%; Score 23; DB 7; Length 97;
Best Local Similarity 100.0%; Pred.No. 0.23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTAATACGACTCACTATAGGAG 27
Db 8 TTAATACGACTCACTATAGGAG 30

RESULT 73
US-11-260-844-55
; Sequence 55, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 97
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
US-11-260-844-55

Query Match      42.6%; Score 23; DB 7; Length 97;
Best Local Similarity 100.0%; Pred.No. 0.23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTAATACGACTCACTATAGGAG 27
Db 8 TTAATACGACTCACTATAGGAG 30

RESULT 74
US-11-260-844-56
; Sequence 56, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 97
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
US-11-260-844-56

Query Match      42.6%; Score 23; DB 7; Length 97;
Best Local Similarity 100.0%; Pred.No. 0.23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTAATACGACTCACTATAGGAG 27
Db 8 TTAATACGACTCACTATAGGAG 30

RESULT 75
US-11-260-844-58
; Sequence 58, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
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; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 97
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
US-11-260-844-58

Query Match 42.6%; Score 23; DB 7; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TTAATACGACTCACTATAGGAG 27
|||||
Db 8 TTAATACGACTCACTATAGGAG 30

RESULT 76

US-11-260-844-60
; Sequence 60, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 97
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
US-11-260-844-60

Query Match 42.6%; Score 23; DB 7; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TTAATACGACTCACTATAGGAG 27
|||||
Db 8 TTAATACGACTCACTATAGGAG 30

RESULT 77

US-11-260-844-26
; Sequence 26, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3

; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 98
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
US-11-260-844-26

Query Match 42.6%; Score 23; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TTAATACGACTCACTATAGGAG 27
|||||
Db 8 TTAATACGACTCACTATAGGAG 30

RESULT 78

US-11-260-844-33
; Sequence 33, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 98
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
US-11-260-844-33

Query Match 42.6%; Score 23; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TTAATACGACTCACTATAGGAG 27
|||||
Db 8 TTAATACGACTCACTATAGGAG 30

RESULT 79

US-11-260-844-61
; Sequence 61, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27

; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 98
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
; NAME/KEY: misc_feature
; LOCATION: 42, 46, 54..56, 58, 59, 62, 72, 79, 80
; OTHER INFORMATION: n = any of a, c, g, or t
US-11-260-844-61

Query Match 42.6%; Score 23; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTAATACGACTCACTATAGGGAG 27
|||||
Db 8 TTAATACGACTCACTATAGGGAG 30

RESULT 80
US-11-260-844-19
; Sequence 19, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostratin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 105
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-11-260-844-19

Query Match 42.6%; Score 23; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTAATACGACTCACTATAGGGAG 27
|||||
Db 8 TTAATACGACTCACTATAGGGAG 30

RESULT 81
US-11-217-529-78404
; Sequence 78404, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO

; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78404
; LENGTH: 1701
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78404

Query Match 42.6%; Score 23; DB 7; Length 1701;
Best Local Similarity 68.1%; Pred. No. 0.55; Indels 0; Gaps 0;
Matches 32; Conservative 0; Mismatches 15;

Qy 4 ATTAATACGACTCACTATAGGGAGACCAACATTTGTGCAATATTTCCCA 50
|||||
Db 948 AATAATAGGATTGAAGAGCGGTACATCATCATGATGCAATATTTTCCA 994

RESULT 82
US-10-511-937-3082
; Sequence 3082, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3082
; LENGTH: 63
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-3082

Query Match 41.5%; Score 22.4; DB 6; Length 63;
Best Local Similarity 95.8%; Pred. No. 0.36;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 TAATACGACTCACTATAGGGAGAC 29
|||||
Db 14 TAATACGACTCACTATAGGGAGC 37

RESULT 83
US-10-511-937-3105
; Sequence 3105, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:

APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 50661200104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3105
LENGTH: 63
TYPE: DNA
ORGANISM: Homo sapiens
US-10-511-937-3105

Query Match 41.5%; Score 22.4; DB 6; Length 63;
Best Local Similarity 95.8%; Pred. No. 0.36; Mismatches 0; Indels 1; Gaps 0;
Matches 23; Conservative 0;

Qy 6 TAATACGACTCACTATAGGGAGAC 29
Db 14 TAATACGACTCACTATAGGGAGGC 37

RESULT 84
US-10-524-399-1
Sequence 1, Application US/10524399
Publication No. US20060099591A1
GENERAL INFORMATION:
APPLICANT: KRAUSE, Andreas
APPLICANT: NIESE, Detlef
APPLICANT: RAULF, Friedrich
APPLICANT: SCHERER, Andreas
TITLE OF INVENTION: Diagnosis of chronic rejection
FILE REFERENCE: 4-32608A
CURRENT APPLICATION NUMBER: US/10/524,399
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: US 60/405,225
PRIOR FILING DATE: 2002-08-22
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 63
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Primer sequence
US-10-524-399-1

Query Match 41.5%; Score 22.4; DB 6; Length 63;
Best Local Similarity 95.8%; Pred. No. 0.36; Mismatches 0; Indels 1; Gaps 0;
Matches 23; Conservative 0;

Qy 6 TAATACGACTCACTATAGGGAGAC 29
Db 14 TAATACGACTCACTATAGGGAGGC 37

RESULT 85
US-11-217-529-2644
Sequence 2644, Application US/11217529

Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 2644
LENGTH: 3915
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
NAME/KEY: modified base
LOCATION: (73)..(122)
FEATURE:
OTHER INFORMATION: a, c, g, t, unknown, or other
NAME/KEY: modified base
LOCATION: (1668)..(1721)
OTHER INFORMATION: a, c, g, t, unknown, or other
US-11-217-529-2644

Query Match 41.5%; Score 22.4; DB 7; Length 3915;
Best Local Similarity 66.7%; Pred. No. 1.3; Mismatches 32; Conservative 0; Indels 16; Gaps 0;

Qy 1 GAAATTATACGACTCACTATAGGAGACCATATGTCATATCC 48
Db 3466 GAAAGCAATACGAGTCATTAATAGTAAGAACAAAGATTCAGTTTACC 3513

RESULT 86
US-10-900-453-1
Sequence 1, Application US/10900453
Publication No. US20060099601A1
GENERAL INFORMATION:
APPLICANT: RABBANI, ELAZAR
APPLICANT: STAVRIANOPOULOS, JANNIS G.
APPLICANT: DONEGAN, JAMES J.
APPLICANT: COLEMAN, JACK
TITLE OF INVENTION: DETECTION AND QUANTIFICATION PROCESS FOR NUCLEIC
ACIDS IN LIBRARY
FILE REFERENCE: EN2-60 (D2)
CURRENT APPLICATION NUMBER: US/10/900,453
CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: 09/896,897
PRIOR FILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 1
LENGTH: 44
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Bacteriophage
T7 Promoter with a C9 3' Tail
US-10-900-453-1

Query Match 41.1%; Score 22.2; DB 6; Length 44;
Best Local Similarity 88.9%; Pred. No. 0.39; Mismatches 24; Conservative 0; Indels 3; Gaps 0;

Qy 6 TAATACGACTCACTATAGGAGAC 32
Db 14 TAATACGACTCACTATAGGATCCCC 40

RESULT 87

```

US-11-260-844-47
; Sequence 47, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 96
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
US-11-260-844-47

```

Query Match 41.1%; Score 22.2; DB 7; Length 96;
Best Local Similarity 88.9%; Pred. No. 0.49;
Matches 24; Conservative 0; Mismatches 3; Indels 0

Qy 1 GAAATTAATACGACTCACTATAGGAG 27
|||
Db 3 GAAGCTTATACGACTCACTATAGGAG 29

RESULT 88

```

US-11-260-844-22
; Sequence 22, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
US-11-260-844-22

```

Query Match 40.7%; Score 22; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 22; Conservative 0; Mismatches 0; Indels

Qy 6 TAATACGACTCACTATAGGAG 27

RESULT 91

db 1 TAA TAC GACTCACTATAGGGAG 22

RESULT 89

```

US-10-489-071--65
; Sequence 65, Application US/10489071
; Publication No. US2006094672A1
; GENERAL INFORMATION:
; APPLICANT: PASQUALINE ET AL.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF TARGETING PEPTIDES AGAINST
; FILE REFERENCE: UTSC-856US
; CURRENT APPLICATION NUMBER: US/10/489,071
; CURRENT FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: PCT/US02/27836
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-489-071--65

```

Query Match 40.7%; Score 22; DB 6; Length 43;
Best Local Similarity 73.7%; Pred. No. 0.46;
Matches 28; Conservative 0; Mismatches 10; Indels

Qy 6 TAATAGGACTCACTATAGGAGACCACTGTGCAATA 43
|||||
Db 1 TAATAGGACTCACTATAGGCAAGCTGATAAACCGATA 38
|||||

RESULT 90

```

US-11-260-844-20
; Sequence 20, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 89
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-11-260-844-20

```

Query Match 40.7%; Score 22; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 22; Conservative 0; Mismatches 0; Indels

Qy 6 TAATACGACTCACTATAGGGAG 27
|||
Db 1 TAATACGACTCACTATAGGGAG 22

```
US-11-217-529-173696/c
; Sequence 173696, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 173696
; LENGTH: 252
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-173696

Query Match      40.4%; Score 21.8; DB 7; Length 252;
Best Local Similarity 92.0%; Pred. No. 0.96;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 TAATACGACTCACTATAGGAGACC 30
Db 241 TAATACGACTCACTATAGGATCCC 217

RESULT 92
US-11-270-287-1/c
; Sequence 1, Application US/11270287
; Publication No. US20060099627A1
; GENERAL INFORMATION:
; APPLICANT: Kara, Anna K.
; APPLICANT: Ting, Robert C.
; APPLICANT: Tham, Jill M.
; APPLICANT: Nelson, James S.
; APPLICANT: Tan, Theresa M.
; TITLE OF INVENTION: Diagnosis of Parasites
; FILE REFERENCE: 64-99
; CURRENT APPLICATION NUMBER: US/11/270,287
; CURRENT FILING DATE: 2005-11-09
; PRIOR APPLICATION NUMBER: US/09/369,992
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: PCT/IB98/00212
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: AU P09481/97
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: AU P09329/97
; PRIOR FILING DATE: 1997-04-21
; PRIOR APPLICATION NUMBER: AU P04953/97
; PRIOR FILING DATE: 1997-02-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 5849
; TYPE: DNA
; ORGANISM: Plasmodium berghei
US-11-270-287-1

Query Match      40.0%; Score 21.6; DB 7; Length 5849;
Best Local Similarity 63.5%; Pred. No. 3;
Matches 33; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 3 AATTAATACGACTCACTATAGGAGACCACCATTTGCAATATTTCCCACTGC 54
Db 4581 AAGAAATATTATTTATCAAGCTTACGCTCATTTGTAATAATTTCTCACTGC 4530
```

```
RESULT 93
US-11-260-844-48
; Sequence 48, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 98
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
US-11-260-844-48

Query Match      39.6%; Score 21.4; DB 7; Length 98;
Best Local Similarity 66.0%; Pred. No. 1.1;
Matches 31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 5 TTAATACGACTCACTATAGGAGACCACCATTTGCAATATTTCCCAAC 51
Db 8 TTAATACGACTCACTATAGGAGGAGCGATCGGTTTAACCTCCCAAC 54

RESULT 94
US-10-980-856-34
; Sequence 34, Application US/10980856
; Publication No. US20060094026A1
; GENERAL INFORMATION:
; APPLICANT: LIU, JUWEN
; APPLICANT: LIU, YI
; TITLE OF INVENTION: NUCLEIC ACID ENZYME LIGHT-UP SENSOR UTILIZING INVASIVE DNA
; FILE REFERENCE: ILL05-052-US
; CURRENT APPLICATION NUMBER: US/10/980,856
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34
; LENGTH: 105
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic polynucleotide sequence
US-10-980-856-34

Query Match      39.6%; Score 21.4; DB 6; Length 105;
Best Local Similarity 95.7%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 TAATACGACTCACTATAGGAGGA 28
Db 12 TAATACGACTCACTATAGGAAGA 34

RESULT 95
US-10-980-856-35
; Sequence 35, Application US/10980856
; Publication No. US20060094026A1
; GENERAL INFORMATION:
```



```
; APPLICANT: LU, YI
; APPLICANT: LIU JUWEN
; TITLE OF INVENTION: NUCLEIC ACID ENZYME LIGHT-UP SENSOR UTILIZING INVASIVE DNA
; FILE REFERENCE: IL05-052-US
; CURRENT APPLICATION NUMBER: US/10/980,856
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
; LENGTH: 107
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic polynucleotide sequence
US-10-980-856-35

Query Match          39.6%; Score 21.4; DB 6; Length 107;
Best Local Similarity 95.7%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 TAATACGACTCACTATAGGAGGA 28
Db      12 TAATACGACTCACTATAGGAAGA 34

RESULT 96
US-11-529-5480
; Sequence 5480, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5480
; LENGTH: 222
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-529-5480

Query Match          39.6%; Score 21.4; DB 7; Length 222;
Best Local Similarity 80.6%; Pred. No. 1.4;
Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      6 TAATACGACTCACTATAGGAGACCACTTG 36
Db      11 TAATACGACTCACTACAGGGATCAACACTG 41

RESULT 97
US-11-265-954-5/c
; Sequence 5, Application US/11265954
; Publication No. US20060094052A1
; GENERAL INFORMATION:
; APPLICANT: Kelman, zvi
; APPLICANT: Shin, Jae-Ho
; TITLE OF INVENTION: PCR-BASED SUBSTRATE PREPARATION FOR HELICASE ASSAYS
; FILE REFERENCE: 4115-210
; CURRENT APPLICATION NUMBER: US/11/265,954
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: US 60/624,571
; PRIOR FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 5
```

```
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 226
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-265-954-5

Query Match          39.6%; Score 21.4; DB 7; Length 226;
Best Local Similarity 95.7%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 TAATACGACTCACTATAGGAGGA 28
Db      201 TAATACGACTCACTATAGGGCGA 179

RESULT 98
US-11-245-514-10
; Sequence 10, Application US/11245514
; Publication No. US20060099621A1
; GENERAL INFORMATION:
; APPLICANT: Schuetz, Ekkehard
; APPLICANT: Iakoubov, Leonid
; APPLICANT: Urnovitz, Howard
; APPLICANT: Chronix Biomedical
; TITLE OF INVENTION: Detection of Nucleic Acids to Assess Risk for
; TITLE OF INVENTION: Creutzfeldt-Jakob Disease
; FILE REFERENCE: 018651-000810US
; CURRENT APPLICATION NUMBER: US/11/245,514
; CURRENT FILING DATE: 2005-10-07
; PRIOR APPLICATION NUMBER: US 60/616,726
; PRIOR FILING DATE: 2004-10-07
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 320
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence 2
; OTHER INFORMATION: present in presumptive Creutzfeldt-Jakob Disease
; OTHER INFORMATION: (CJD) derived from PCR products using primers
; OTHER INFORMATION: 75P/83R
US-11-245-514-10

Query Match          39.6%; Score 21.4; DB 7; Length 320;
Best Local Similarity 95.7%; Pred. No. 1.5;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 TAATACGACTCACTATAGGAGGA 28
Db      24 TAATACGACTCACTATAGGGCGA 46

RESULT 99
US-09-949-925-25/c
; Sequence 25, Application US/09949925
; Publication No. US20060099575A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2023P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
```

;; PRIOR FILING DATE: 1998-01-30
;; PRIOR APPLICATION NUMBER: US 60/073,165
;; PRIOR FILING DATE: 1998-01-30
;; PRIOR APPLICATION NUMBER: US 60/073,164
;; PRIOR FILING DATE: 1998-01-30
;; PRIOR APPLICATION NUMBER: US 60/073,167
;; PRIOR FILING DATE: 1998-01-30
;; PRIOR APPLICATION NUMBER: US 60/073,162
;; PRIOR FILING DATE: 1998-01-30
;; PRIOR APPLICATION NUMBER: US 60/073,161
;; PRIOR FILING DATE: 1998-01-30
;; PRIOR APPLICATION NUMBER: US 60/073,170
;; PRIOR FILING DATE: 1998-01-30
;; NUMBER OF SEQ ID NOS: 298
;; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 1076
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (910)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (912)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (958)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1038)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-949-925-25

Query Match 39.6%; Score 21.4; DB 1; Length 1076;

Best Local Similarity 95.7%; Pred. No. 2.2; Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TAATACGACTCACTATAGGGAGA 28
|||
DB 800 TAATACGACTCACTATAGGGCGA 778

RESULT 100

US-11-315-766-11/c
; Sequence 11, Application US/11315766
; Publication No. US20060101544A1
; GENERAL INFORMATION:
; APPLICANT: Butler, Karlene H.
; APPLICANT: Cahoon, Edgar B.
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Hall, Sarah E.
; TITLE OF INVENTION: Phospholipid:diacylglycerol Acetyltransferases
; FILE REFERENCE: BB1486 US NA
; CURRENT APPLICATION NUMBER: US/11/315,766
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/321,802
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 11
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Vernonia mespilifolia
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1471)
; OTHER INFORMATION: n = a, c, g or t
US-11-315-766-11

Query Match 39.6%; Score 21.4; DB 7; Length 1475;

Best Local Similarity 95.7%; Pred. No. 2.4;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 TAATACGACTCACTATAGGGAGA 28
|||
DB 1456 TAATACGACTCACTATAGGGCGA 1434

Search completed: May 19, 2006, 05:38:15
Job time : 35.506 secs

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 02:23:06 ; Search time 873.946 Seconds
(without alignments)
1829.273 Million cell updates/sec

Title: US-10-665-708-21

Perfect score: 25
Sequence: 1 gcaagtcgaacggaaggccttctg 25

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database :

GenEmbl.*
1: gb_env.*
2: gb_pat.*
3: gb_ph.*
4: gb_pl.*
5: gb_pr.*
6: gb_ro.*
7: gb_sts.*
8: gb_sy.*
9: gb_un.*
10: gb_vi.*
11: gb_ov.*
12: gb_hcg.*
13: gb_in.*
14: gb_on.*
15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	25	100.0	25	2	AR438653 Sequence
2	25	100.0	25	2	AX166855 Sequence
3	25	100.0	541	15	AF547926
4	25	100.0	1456	15	MCAD16S
5	25	100.0	1459	15	MCO16S
6	24	96.0	24	2	AR438654
7	24	96.0	24	2	AX166856
8	24	96.0	1460	15	MSGRGDSB
9	24	96.0	1479	15	MSGRGDSB
10	23.4	93.6	268	15	MSGR16S
11	23.4	93.6	293	1	MSF404591
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15	23.4	93.6	394	1	AY395154
16	23.4	93.6	395	1	AY43901
17	23.4	93.6	395	1	AY395151
18	23.4	93.6	396	1	BSSMKN14

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24	23.4	93.6	411	15	DQ063199
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32	23.4	93.6	423	15	AY673206
33	23.4	93.6	423	15	AY673207
34	23.4	93.6	424	15	DQ063156
35	23.4	93.6	424	15	AY673287
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55	23.4	93.6	444	15	AY306205
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72	23.4	93.6	473	1	AY043719
73	23.4	93.6	474	1	DQ136108
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75	23.4	93.6	476	15	AY559492
76	23.4	93.6	478	1	AY251205
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91	23.4	93.6	500	15	AY215218

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AY234665	Bacterium
AY792017	Mycobacte
X78654	Bacterium s
DQ063154	Actinobac
DQ063199	Actinobac
AY792013	Mycobacte
AM085786	Unculture
AM085788	Unculture
AY673261	Mycobacte
AM085770	Unculture
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AY673205	Mycobacte
AY673206	Mycobacte
AY673207	Mycobacte
DQ063156	Actinobac
AY673287	Streptosp
AY394635	Unculture
AY673136	Mycobacte
AB106918	Gram-posi
DQ063058	Actinobac
AJ786822	Mycobacte
AY673202	Mycobacte
AB106919	Gram-posi
AF078232	Grassland
AY673198	Mycobacte
AY673266	Mycobacte
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DQ063046	Actinobac
AY673199	Mycobacte
AY673304	Mycobacte
AF078419	Grassland
AB232370	Mycobacte
AY306201	Mycobacte
AY306205	Mycobacte
AB106917	Gram-posi
DQ067466	Mycobacte
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MSP16SR	
AY358002	Actinobac
AJ746062	Mycobacte
AY358001	Actinobac
AJ609008	Unculture
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DQ142672	Mycobacte
DQ067465	Mycobacte
AY524839	Mycobacte
DQ154332	Soil bact
AY043719	Unculture
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AY559492	Mycobacte
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AY943206	Mycobacte
DQ154344	Unculture
AY215287	Mycobacte
AY215324	Mycobacte
AY215336	Mycobacte
DQ154566	Unculture
DQ154328	Soil bact
AY215236	Mycobacte
UF0233561	unculture
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AF498661	Mycobacte
AY162027	Mycobacte
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95	23.4	93.6	500	15	AV215237	Mycobacte	168	23.4	93.6	540	15	AF547964	Mycobacte
96	23.4	93.6	500	15	AV215245	Mycobacte	169	23.4	93.6	540	15	AF547972	Mycobacte
97	23.4	93.6	500	15	AV215247	Mycobacte	170	23.4	93.6	540	15	AF547981	Mycobacte
98	23.4	93.6	500	15	AV215251	Mycobacte	171	23.4	93.6	540	15	AV438068	Mycobacte
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100	23.4	93.6	500	15	AV215266	Mycobacte	173	23.4	93.6	540	15	AV438077	Mycobacte
101	23.4	93.6	500	15	AV215280	Mycobacte	174	23.4	93.6	541	15	AF547943	Mycobacte
102	23.4	93.6	500	15	AV215285	Mycobacte	175	23.4	93.6	541	15	AV438067	Mycobacte
103	23.4	93.6	500	15	AV215286	Mycobacte	176	23.4	93.6	542	15	AF547897	Mycobacte
104	23.4	93.6	500	15	AV215288	Mycobacte	177	23.4	93.6	542	15	AF547917	Mycobacte
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106	23.4	93.6	500	15	AV215290	Mycobacte	179	23.4	93.6	542	15	AF547980	Mycobacte
107	23.4	93.6	500	15	AV215291	Mycobacte	180	23.4	93.6	542	15	AV438079	Mycobacte
108	23.4	93.6	500	15	AV215292	Mycobacte	181	23.4	93.6	551	1	AV725804	Unculture
109	23.4	93.6	500	15	AV215293	Mycobacte	182	23.4	93.6	552	15	AV438073	Mycobacte
110	23.4	93.6	500	15	AV215304	Mycobacte	183	23.4	93.6	552	15	AV438074	Mycobacte
111	23.4	93.6	500	15	AV215316	Mycobacte	184	23.4	93.6	552	15	AV367021	Mycobacte
112	23.4	93.6	500	15	AV215320	Mycobacte	185	23.4	93.6	576	15	AV367021	Mycobacte
113	23.4	93.6	500	15	AV215323	Mycobacte	186	23.4	93.6	588	15	AJ627393	Unculture
114	23.4	93.6	500	15	AV215331	Mycobacte	187	23.4	93.6	611	1	DQ149896	Unculture
115	23.4	93.6	500	15	AV215346	Mycobacte	188	23.4	93.6	616	1	AY242618	Unculture
116	23.4	93.6	500	15	AV215348	Mycobacte	189	23.4	93.6	619	1	AY242619	Unculture
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118	23.4	93.6	501	15	AF498655	Mycobacte	191	23.4	93.6	629	1	DQ149916	Unculture
119	23.4	93.6	501	15	AV112744	Mycobacte	192	23.4	93.6	631	1	AY307880	Unculture
120	23.4	93.6	501	15	AV215219	Mycobacte	193	23.4	93.6	636	1	DQ149894	Unculture
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122	23.4	93.6	501	15	AV215229	Mycobacte	195	23.4	93.6	676	15	AV368530	Mycobacte
123	23.4	93.6	501	15	AV215238	Mycobacte	196	23.4	93.6	685	1	AY881659	Unculture
124	23.4	93.6	501	15	AV215370	Mycobacte	197	23.4	93.6	737	1	AY154573	Unculture
125	23.4	93.6	503	15	AV215227	Mycobacte	198	23.4	93.6	740	1	AF145831	Metal-con
126	23.4	93.6	503	15	AV215249	Mycobacte	199	23.4	93.6	749	15	AJ784807	Mycobacte
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128	23.4	93.6	508	15	AV148214	Mycobacte	201	23.4	93.6	761	15	AJ746076	Mycobacte
129	23.4	93.6	509	15	AV215212	Mycobacte	202	23.4	93.6	773	15	AJ746072	Mycobacte
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131	23.4	93.6	512	15	AV215272	Mycobacte	204	23.4	93.6	810	15	AJ746058	Mycobacte
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134	23.4	93.6	513	15	AV215273	Mycobacte	207	23.4	93.6	815	15	AJ746064	Mycobacte
135	23.4	93.6	514	15	AV215276	Mycobacte	208	23.4	93.6	815	1	AY154519	Unculture
136	23.4	93.6	519	15	MSU19366	Mycobacteri	209	23.4	93.6	817	15	AJ746069	Mycobacte
137	23.4	93.6	519	15	AJ746067	Mycobacte	210	23.4	93.6	824	15	AJ746060	Mycobacte
138	23.4	93.6	530	1	AY725810	Unculture	211	23.4	93.6	828	15	AJ746061	Mycobacte
139	23.4	93.6	530	15	AY039507	Soil bact	212	23.4	93.6	828	15	AJ746073	Mycobacte
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141	23.4	93.6	534	15	MFO416908	Mycobacte	214	23.4	93.6	878	15	AY429701	Mycobacte
142	23.4	93.6	535	1	AY148216	Unculture	215	23.4	93.6	893	1	AY494645	Unculture
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149	23.4	93.6	540	15	AF547912	Mycobacte	222	23.4	93.6	1019	15	AY163339	Mycobacte
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154	23.4	93.6	540	15	AF547924	Mycobacte	227	23.4	93.6	1276	15	MFO416915	Mycobacte
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156	23.4	93.6	540	15	AF547929	Mycobacte	229	23.4	93.6	1325	15	DQ083240	Mycobacte
157	23.4	93.6	540	15	AF547936	Mycobacte	230	23.4	93.6	1331	15	AF054278	Mycobacte
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163	23.4	93.6	540	15	AF547955	Mycobacte	236	23.4	93.6	1374	1	AY897827	Unculture
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260 23.4 93.6 1424 15 MCRO10165 Mycobacteri
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262 23.4 93.6 1425 15 X5592 M.farcinoge
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ALIGNMENTS

RESULT 1
AR438653
LOCUS AR438653 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 21 from patent US 6664081.
ACCESSION AR438653

VERSION AR438653.1 GI:42663577
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and Rodriguez,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: US 6664081-A 21 16-DEC-2003;
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCAAGTCGACGGAAGGCGCTTTCG 25
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Db 1 GCAAGTCGACGGAAGGCGCTTTCG 25
RESULT 2
LOCUS AX166855 25 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 21 from Patent WO0144510.
ACCESSION AX166855
VERSION AX166855.1 GI:14596458
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and Rodriguez,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: WO 0144510-A 21 21-JUN-2001;
Gen-Probe Incorporated (US); Biomerieux S.A. (FR)
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Best Local Similarity 100.0%; Pred.No. 2.9e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCAAGTCGACGGAAGGCGCTTTCG 25
|||||
Db 1 GCAAGTCGACGGAAGGCGCTTTCG 25
RESULT 3
LOCUS AF547926 541 bp DNA linear BCT 24-JAN-2006
DEFINITION Mycobacterium gadium strain CIP 105388 16S ribosomal RNA gene, partial sequence.
ACCESSION AF547926
VERSION AF547926.1 GI:27337350
KEYWORDS
SOURCE Mycobacterium gadium
ORGANISM Mycobacterium gadium
REFERENCE 1 (bases 1 to 541)
AUTHORS Devulder,G., de Montclos,M.P. and Flandrois,J.P.

TITLE A multigene approach to phylogenetic analysis using the genus
Mycobacterium as a model
JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBMED 15653890
REFERENCE 2 (bases 1 to 541)
AUTHORS Devulder,G., Pichat,C. and Flandrois,J.P.
TITLE Direct Submission
JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
FEATURES
source
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/organism="Mycobacterium gadium"
/mol_type="genomic DNA"
/strain="CIP 105388"
/db_xref="taxon:1794"
/note="type strain of Mycobacterium gadium"
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCAAGTCGACGGAAGGCCTTTCG 25
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Db 14 GCAAGTCGACGGAAGGCCTTTCG 38
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RESULT 4
MGAD16S
LOCUS MGAD16S 1456 bp DNA linear BCT 06-JUN-2003
DEFINITION M.gadium 16S ribosomal RNA, part.
ACCESSION X55594
VERSION X55594.1 GI:44291
KEYWORDS 16S ribosomal RNA.
SOURCE Mycobacterium gadium
ORGANISM Mycobacterium gadium
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 1456)
AUTHORS Pitulle,C., Dorsch,M., Kazda,J., Wolters,J. and Stackebrandt,E.
TITLE Phylogeny of rapidly growing members of the genus Mycobacterium
JOURNAL Int. J. Syst. Bacteriol. 42 (3), 337-343 (1992)
PUBMED 1380284
REFERENCE 2 (bases 1 to 1456)
AUTHORS Wolters,J.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-1990) Wolters J., Institut fuer Allgemeine
Mikrobiologie der Universitaet, Biologiezentrum, Am Botanischen
Garten 1-9, 2300 Kiel 1
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source
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/strain="ATCC 27726"
/db_xref="taxon:1794"
1. .>1456
/product="16S ribosomal RNA"
rRNA
ORIGIN
Query Match 100.0%; Score 25; DB 15; Length 1456;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCAAGTCGACGGAAGGCCTTTCG 25
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Db 58 GCAAGTCGACGGAAGGCCTTTCG 82
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RESULT 5
MCO16S
LOCUS MCO16S 1459 bp DNA linear BCT 11-JUN-2003
DEFINITION Mycobacterium cookii partial 16S rRNA.
ACCESSION X53896
VERSION X53896.1 GI:44201
KEYWORDS 16S ribosomal RNA; ribosomal RNA.
SOURCE Mycobacterium cookii
ORGANISM Mycobacterium cookii
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 1225)
AUTHORS Kazda,J., Stackebrandt,E., Smida,J., Minnikin,D.E., Daffe,M.,
Parlett,J.H. and Pitulle,C.
TITLE Mycobacterium cookii sp. nov.
JOURNAL Int. J. Syst. Bacteriol. 40 (3), 217-223 (1990)
PUBMED 1697763
REFERENCE 2 (bases 1 to 1459)
AUTHORS Stackebrandt,E.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-1990) Stackebrandt E
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/organism="Mycobacterium cookii"
/mol_type="genomic DNA"
/strain="ATCC 49103 (T) = NZ2."
/db_xref="taxon:1775"
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/product="16S ribosomal RNA"
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Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCAAGTCGACGGAAGGCCTTTCG 25
|||||
Db 58 GCAAGTCGACGGAAGGCCTTTCG 82
|||||
RESULT 6
AR438654
LOCUS AR438654 24 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 22 from patent US 6664081.
ACCESSION AR438654
VERSION AR438654.1 GI:42663578
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
Rodrigue,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: US 6664081-A 22 16-DEC-2003;
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA
FEATURES
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/organism="unknown"
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ORIGIN
Query Match 96.0%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 CAAGTCGAACGGAAGGCCTTTCG 25
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Db 1 CAAGTCGAACGGAAGGCCTTTCG 24
|||||
RESULT 7
AX166856
LOCUS AX166856 24 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 22 from Patent WO0144510.

LOCUS MCO16S 1459 bp DNA linear BCT 11-JUN-2003
DEFINITION Mycobacterium cookii partial 16S rRNA.
ACCESSION X53896
VERSION X53896.1 GI:44201
KEYWORDS 16S ribosomal RNA; ribosomal RNA.
SOURCE Mycobacterium cookii
ORGANISM Mycobacterium cookii
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 1225)
AUTHORS Kazda,J., Stackebrandt,E., Smida,J., Minnikin,D.E., Daffe,M.,
Parlett,J.H. and Pitulle,C.
TITLE Mycobacterium cookii sp. nov.
JOURNAL Int. J. Syst. Bacteriol. 40 (3), 217-223 (1990)
PUBMED 1697763
REFERENCE 2 (bases 1 to 1459)
AUTHORS Stackebrandt,E.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-1990) Stackebrandt E
FEATURES
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1. .1459
/organism="Mycobacterium cookii"
/mol_type="genomic DNA"
/strain="ATCC 49103 (T) = NZ2."
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1. .>1459
/product="16S ribosomal RNA"
rRNA
ORIGIN
Query Match 100.0%; Score 25; DB 15; Length 1459;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCAAGTCGACGGAAGGCCTTTCG 25
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Db 58 GCAAGTCGACGGAAGGCCTTTCG 82
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RESULT 6
AR438654
LOCUS AR438654 24 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 22 from patent US 6664081.
ACCESSION AR438654
VERSION AR438654.1 GI:42663578
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
Rodrigue,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: US 6664081-A 22 16-DEC-2003;
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA
FEATURES
source
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/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 96.0%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 CAAGTCGAACGGAAGGCCTTTCG 25
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Db 1 CAAGTCGAACGGAAGGCCTTTCG 24
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RESULT 7
AX166856
LOCUS AX166856 24 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 22 from Patent WO0144510.

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ACCESSION  AX166856
VERSION     AX166856.1  GI:14596459
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.

REFERENCE   1
AUTHORS    Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
            Rodrigue,M.
TITLE      Nucleic acid amplification and detection of mycobacterium species
JOURNAL    Patent: WO 0144510-A 22 JUN-2001;
            Gen-Probe incorporated (US) ; Biomerieux S.A. (FR)
FEATURES   Location/Qualifiers
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             /note="primer oligonucleotide"

ORIGIN
Query Match      96.0%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2  CAAAGTCGAAACGGAAGGCGCTTTTCG 25
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DB   1  CAAAGTCGAAACGGAAGGCGCTTTTCG 24

RESULT 8
MSGRGD5A  MSRGD5A 1460 bp DNA linear BCT 21-SEP-1993
LOCUS     Mycobacterium celatum 16S ribosomal RNA gene.
DEFINITION
ACCESSION L08169
VERSION   L08169.1 GI:293249
KEYWORDS  16S ribosomal RNA.
SOURCE    Mycobacterium celatum
ORGANISM  Mycobacterium celatum
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE   1 (bases 1 to 1460)
AUTHORS    Butler,W.R., O'Connor,S.P., Yakus,M.A., Smithwick,R.W.,
            Plikaytis,B.B., Moss,C.W., Floyd,M.M., Woodley,C.L., Kilburn,J.O.,
            Vadney,F.S. and Gross,W.M.
TITLE      Mycobacterium celatum sp. nov
JOURNAL    Int. J. Syst. Bacteriol. 43 (3), 539-548 (1993)
PUBMED    8102246
COMMENT    Original source text: Mycobacterium celatum (library: ATCC 51131)
            DNA.

FEATURES   Location/Qualifiers
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             /db_xref="taxon:28045"
             /tissue_lib="ATCC 51131"
             <1..>1460
             /product="16S ribosomal RNA"
             /note="putative"

rRNA

ORIGIN
Query Match      96.0%; Score 24; DB 15; Length 1460;
Best Local Similarity 96.0%; Pred. No. 2.3e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1  GCAAGTCGAACGGAAGGCGCTTTTCG 25
      |||||
DB   8  GCAAGTCGAACGGAAGGCGCTTTTCG 32

RESULT 9
MSGRGD5B  MSGRGD5B 1479 bp DNA linear BCT 21-SEP-1993
LOCUS     Mycobacterium celatum 16S ribosomal RNA gene.
DEFINITION
ACCESSION L08170
VERSION   L08170.1 GI:293250
KEYWORDS  16S ribosomal RNA.
SOURCE    Mycobacterium celatum
ORGANISM  Mycobacterium celatum
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE   1 (bases 1 to 1479)
AUTHORS    Butler,W.R., O'Connor,S.P., Yakus,M.A., Smithwick,R.W.,
            Plikaytis,B.B., Moss,C.W., Floyd,M.M., Woodley,C.L., Kilburn,J.O.,
            Vadney,F.S. and Gross,W.M.
TITLE      Mycobacterium celatum sp. nov
JOURNAL    Int. J. Syst. Bacteriol. 43 (3), 539-548 (1993)
PUBMED    8102246
COMMENT    Original source text: Mycobacterium celatum (library: ATCC 51130)
            DNA.

FEATURES   Location/Qualifiers
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             <1..>1479
             /product="16S ribosomal RNA"
             /note="putative"

rRNA

ORIGIN
Query Match      96.0%; Score 24; DB 15; Length 1479;
Best Local Similarity 96.0%; Pred. No. 2.3e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1  GCAAGTCGAACGGAAGGCGCTTTTCG 25
      |||||
DB   29  GCAAGTCGAACGGAAGGCGCTTTTCG 53

RESULT 10
MSGRR16S  MSGRR16S 268 bp rRNA linear BCT 27-APR-1993
LOCUS     Mycobacterium kansasii 16S ribosomal RNA.
DEFINITION
ACCESSION M95469
VERSION   M95469.1 GI:175317
KEYWORDS  16S ribosomal RNA.
SOURCE    Mycobacterium kansasii
ORGANISM  Mycobacterium kansasii
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE   1 (bases 1 to 268)
AUTHORS    Ross,B.C., Jackson,K., Yang,M., Sievers,A. and Dwyer,B.
TITLE      Identification of a genetically distinct sub-species of
            Mycobacterium kansasii
JOURNAL    Unpublished (1992)
PUBMED
COMMENT    Original source text: Mycobacterium kansasii rRNA.
            Location/Qualifiers
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             /db_xref="taxon:1768"
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gene
rRNA

ORIGIN
Query Match      93.6%; Score 23.4; DB 15; Length 268;
Best Local Similarity 96.0%; Pred. No. 5.9e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1  GCAAGTCGAACGGAAGGCGCTTTTCG 25
      |||||
DB   38  GCAAGTCGAACGGAAGGCGCTTTTCG 62

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RESULT 11
LOCUS MSP404591 293 bp DNA linear ENV 06-JUN-2003
DEFINITION Uncultured Mycobacterium MB1 partial 16S rRNA gene.
ACCESSION AJ404591
VERSION AJ404591.1 GI:8926769
KEYWORDS 16S ribosomal RNA; 16S rRNA gene.
SOURCE uncultured Mycobacterium MB1
ORGANISM uncultured Mycobacterium MB1
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental
samples.
REFERENCE 1
AUTHORS Kempell,K.E., Cox,C.J., Hurlle,M., Wong,A., Wilkie,S.,
Zanders,E.D., Gaston,J. and Crowe,J.
TITLE Reverse Transcriptase-Polymerase Chain Reaction of Bacterial rRNA
for Detection and Characterisation of Bacterial Species in
Arthritis Synovial Tissue
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 293)
AUTHORS Cox,C.J.
TITLE Direct Submission
JOURNAL Submitted (05-JUN-2000) Cox C.J., Cancer Research, Sanger Centre,
Wellcome Trust Genome Campus, Hinxton Hall, Hinxton,
Cambridgeshire, CB10 1SA, UNITED KINGDOM
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/mol_type="genomic DNA"
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/tissue_type="Synovium"
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/gene="16S rRNA"
/product="16S ribosomal RNA"

gene
rRNA

ORIGIN
Query Match 93.6%; Score 23.4; DB 1; Length 293;
Best Local Similarity 96.0%; Pred. No. 5.7e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCCTTCG 25
Db 20 GCAAGTCGACGGAAGGCCCTTCG 44

RESULT 12
LOCUS MF16SRRN 316 bp DNA linear BCT 14-NOV-1996
DEFINITION M.Fortuitum 16S rRNA gene, partial.
ACCESSION Y09325
VERSION Y09325.1 GI:1669698
KEYWORDS 16S ribosomal RNA; rrr gene.
SOURCE Mycobacterium fortuitum
ORGANISM Mycobacterium fortuitum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1
AUTHORS De Smet,K., Kampmann,B., Marshall,B., Kroll,S. and Levin,M.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 316)
AUTHORS De Smet,K.A.L.
TITLE Direct Submission
JOURNAL Submitted (08-NOV-1996) K.A.L. De Smet, Imperial College Medical
School at St Marys, Medical Microbiology, Norfolk Place, London, W2
1PG, UK
FEATURES
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/mol_type="genomic DNA"

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gene
rRNA

ORIGIN
Query Match 93.6%; Score 23.4; DB 15; Length 316;
Best Local Similarity 96.0%; Pred. No. 5.6e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCCTTCG 25
Db 45 GCAAGTCGACGGAAGGCCCTTCG 69

RESULT 13
LOCUS AY395145 388 bp DNA linear ENV 07-SEP-2004
DEFINITION Uncultured bacterium clone D29ST 16S ribosomal RNA gene, partial
sequence.
ACCESSION AY395145
VERSION AY395145.1 GI:37595660
KEYWORDS ENV, uncultured bacterium
SOURCE uncultured bacterium
ORGANISM Bacteria; environmental samples.
REFERENCE 1 (bases 1 to 388)
AUTHORS Hackl,E., Zechmeister-Boltenstern,S., Bodrossy,L. and Sessitsch,A.
TITLE Comparison of diversities and compositions of bacterial populations
inhabiting natural forest soils
JOURNAL Appl. Environ. Microbiol. 70 (9), 5057-5065 (2004)
PUBMED 15345382
REFERENCE 2 (bases 1 to 388)
AUTHORS Hackl,E. and Sessitsch,A.
TITLE Direct Submission
JOURNAL Submitted (19-SEP-2003) Environmental and Life Sciences, ARC
Seibersdorf research GmbH, Seibersdorf A-2444, Austria
FEATURES
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/organism="uncultured bacterium"
/mol_type="genomic DNA"
/isolation_source="forest soil"
/db_xref="taxon:77133"
/clone="D29ST"
/environmental_sample
<1..388
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 93.6%; Score 23.4; DB 1; Length 388;
Best Local Similarity 96.0%; Pred. No. 5.3e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCCTTCG 25
Db 50 GCAAGTCGACGGAAGGCCCTTCG 74

RESULT 14
LOCUS BSSMKN23 393 bp DNA linear ENV 22-FEB-1995
DEFINITION Bacterium sp. (SMKN23) DNA.
ACCESSION X78659
VERSION X78659.1 GI:509728
KEYWORDS 16S ribosomal RNA.
SOURCE unidentified bacterium
ORGANISM unidentified bacterium
Bacteria; environmental samples.
REFERENCE 1
AUTHORS Schuppler,M., Mertens,F., Schon,G. and Gobel,U.B.

```

TITLE Molecular characterization of nocardioform actinomycetes in activated sludge by 16S rRNA analysis
JOURNAL Microbiology (Reading, Engl.) 141 (Pt 2), 513-521 (1995)
PUBMED 7704280
REFERENCE 2 (bases 1 to 393)
AUTHORS Schuppler,M.
TITLE Direct Submission
JOURNAL Submitted (28-MAR-1994) M. Schuppler, Institut fuer Med. Mikrobiologie & Hygiene, Universitaet Freiburg, Hermann-Herder-St. 11, 79104 Freiburg, FRG

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/mol_type="genomic DNA"
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ORIGIN

Query Match 93.6%; Score 23.4; DB 1; Length 393;
Best Local Similarity 96.0%; Pred. No. 5.3e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GCAAGTCGAACGGAAGGCTTTTCG 25
|||||
Db 7 GCAAGTCGAACGGAAGGCTTTTCG 31

RESULT 15
AY395154

LOCUS Uncultured actinobacterium clone E02ST 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION AY395154
VERSION AY395154.1 GI:37595669
KEYWORDS ENV.
SOURCE uncultured actinobacterium
ORGANISM uncultured actinobacterium
Bacteria; Actinobacteria; environmental samples.

REFERENCE Hackl,E., Zechmeister-Boltenstern,S., Bodrossy,L. and Sessitsch,A.
AUTHORS Comparison of diversities and compositions of bacterial populations inhabiting natural forest soils
TITLE
JOURNAL Appl. Environ. Microbiol. 70 (9), 5057-5065 (2004)
PUBMED 15345382

REFERENCE
AUTHORS Hackl,E. and Sessitsch,A.
TITLE Direct Submission

JOURNAL Submitted (19-SEP-2003) Environmental and Life Sciences, ARC Seibersdorf research GmbH, Seibersdorf A-2444, Austria
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/isolation_source="forest soil"
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/clone="E02ST"
/environmental_sample
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/product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match 93.6%; Score 23.4; DB 1; Length 394;
Best Local Similarity 96.0%; Pred. No. 5.3e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCTTTTCG 25

Db 50 GCAAGTCGAACGGAAGGCTTTTCG 74

RESULT 16

AY043901
LOCUS Uncultured actinobacterium clone SMS9.49WL 16S ribosomal RNA gene, partial sequence.
DEFINITION

ACCESSION AY043901
VERSION AY043901.1 GI:22267274
KEYWORDS ENV.
SOURCE uncultured actinobacterium
ORGANISM uncultured actinobacterium
Bacteria; Actinobacteria; environmental samples.

REFERENCE 1 (bases 1 to 395)
AUTHORS Axelrood,P.E., Chow,M.L., Radomski,C.C., McDermott,J.M. and Davies,J.

TITLE Molecular characterization of bacterial diversity from British Columbia forest soils subjected to disturbance

JOURNAL Can. J. Microbiol. 48 (7), 655-674 (2002)

PUBMED 12224564

REFERENCE 2 (bases 1 to 395)

Axelrood,P.E., Chow,M.L., Radomski,C.C., McDermott,J.M. and Davies,J.

TITLE Direct Submission

JOURNAL Submitted (20-JUN-2001) BC Research Inc., 3650 Westbrook Mall,

Vancouver, BC V6S 2L2, Canada

FEATURES

source

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/organism="uncultured actinobacterium"

/mol_type="genomic DNA"

/db_xref="taxon:152507"

/clone="SMS9.49WL"

/environmental_sample

/note="from forest cut-block mineral soil from the British Columbia Ministry of Forests Long-Term Soil Productivity (LTSP) installation near Williams Lake, BC, Canada"

<1..>395
/product="16S ribosomal RNA"

ORIGIN

Query Match 93.6%; Score 23.4; DB 1; Length 395;
Best Local Similarity 96.0%; Pred. No. 5.3e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCTTTTCG 25

|||||

Db 20 GCAAGTCGAACGGAAGGCTTTTCG 44

RESULT 17

AY395151

LOCUS Uncultured bacterium clone D36ST 16S ribosomal RNA gene, partial sequence.

DEFINITION
ACCESSION AY395151
VERSION AY395151.1 GI:37595666
KEYWORDS ENV.
SOURCE uncultured bacterium
ORGANISM uncultured bacterium
Bacteria; environmental samples.

REFERENCE 1 (bases 1 to 395)

AUTHORS Hackl,E., Zechmeister-Boltenstern,S., Bodrossy,L. and Sessitsch,A.

TITLE Comparison of diversities and compositions of bacterial populations inhabiting natural forest soils

JOURNAL Appl. Environ. Microbiol. 70 (9), 5057-5065 (2004)

PUBMED 15345382

REFERENCE 2 (bases 1 to 395)

AUTHORS Hackl,E. and Sessitsch,A.

TITLE Direct Submission

JOURNAL Submitted (19-SEP-2003) Environmental and Life Sciences, ARC Seibersdorf research GmbH, Seibersdorf A-2444, Austria

FEATURES

source

1..395
/organism="uncultured bacterium"

/mol_type="genomic DNA"

/isolation_source="forest soil"

/product="16S ribosomal RNA"

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/db_xref="taxon:77133"
/clone="D36ST"
/environmental_sample
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/product="16S ribosomal RNA"

ORIGIN
Query Match      93.6%; Score 23.4; DB 1; Length 395;
Best Local Similarity 96.0%; Pred. No. 5.3e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTTCG 25
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Db 50 GCAAGTCGAACGGAAGGCGCTTCG 74

RESULT 18
BSSMKN14
LOCUS      BSSMKN14          396 bp      DNA      linear      ENV 22-FEB-1995
DEFINITION Bacterium sp.(SMKN14) DNA.
ACCESSION  X78655
VERSION     X78655.1 GI:509724
KEYWORDS   16S ribosomal RNA.
SOURCE     unidentified bacterium
ORGANISM   Bacteria; environmental samples.

REFERENCE 1
AUTHORS   Schuppler,M., Mertens,F., Schon,G. and Gobel,U.B.
TITLE     Molecular characterization of nocardiform actinomycetes in
          activated sludge by 16S rRNA analysis
JOURNAL    Microbiology (Reading, Engl.) 141 (Pt 2), 513-521 (1995)
PUBMED     7704280
REFERENCE 2 (bases 1 to 396)
AUTHORS   Schuppler,M.
TITLE     Direct Submission
JOURNAL    Submitted (28-MAR-1994) M. Schuppler, Institut fuer Med.
          Mikrobiologie & Hygiene, Universitaet Freiburg, Hermann-Herder-St.
          11, 79104 Freiburg, FRG

FEATURES   source
            location/Qualifiers
            1..396
            /organism="unidentified bacterium"
            /mol_type="genomic DNA"
            /isolate="SMKN14"
            /db_xref="taxon:2338"
            1..396
            /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.6%; Score 23.4; DB 1; Length 396;
Best Local Similarity 96.0%; Pred. No. 5.3e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTTCG 25
    |||||
Db 7 GCAAGTCGAACGGAAGGCGCTTCG 31

RESULT 19
DQ221681
LOCUS      DQ221681          400 bp      DNA      linear      ENV 12-NOV-2005
DEFINITION Uncultured bacterium clone BPH3088 16S ribosomal RNA gene, partial
          sequence.
ACCESSION  DQ221681
VERSION     DQ221681.1 GI:80978382
KEYWORDS   uncultured bacterium
SOURCE     uncultured bacterium
ORGANISM   Bacteria; environmental samples.

REFERENCE 1 (bases 1 to 400)
AUTHORS   Lambais,M.R., Crowley,D.E., Cury,J.C. and Bull,R.C.
TITLE     Bacterial diversity on leaf surfaces of the Brazilian Atlantic
          Forest
JOURNAL    Unpublished

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2 (bases 1 to 400)
Lambais,M.R., Crowley,D.E., Cury,J.C. and Bull,R.C.
Direct Submission
JOURNAL    Submitted (23-SEP-2005) Solos e Nutricao de Plantas, Universidade
          de Sao Paulo, Av. Padua Dias,11, Piracicaba, SP 13418-900, Brazil
          Location/Qualifiers
FEATURES   source
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            /mol_type="genomic DNA"
            /isolation_source="phylosphere"
            /specific_host="Campomanesia xanthocarpa"
            /db_xref="taxon:77133"
            /clone="BPH3088"
            /environmental_sample
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rRNA

ORIGIN
Query Match      93.6%; Score 23.4; DB 1; Length 400;
Best Local Similarity 96.0%; Pred. No. 5.3e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTTCG 25
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Db 15 GCAAGTCGAACGGAAGGCGCTTCG 39

RESULT 20
AY234665
LOCUS      AY234665          403 bp      DNA      linear      BCT 08-DEC-2003
DEFINITION Bacterium Ellin6013 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY234665
VERSION     AY234665.1 GI:37961822
KEYWORDS   Bacterium Ellin6013
ORGANISM   Bacterium Ellin6013
          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Corynebacterineae; Mycobacteriaceae.

REFERENCE 1 (bases 1 to 403)
AUTHORS   Joseph,S.J., Hugenholtz,P., Sangwan,P., Osborne,C.A. and
          Janssen,P.H.
TITLE     Laboratory Cultivation of Widespread and Previously Uncultured Soil
          Bacteria
JOURNAL    Appl. Environ. Microbiol. 69 (12), 7210-7215 (2003)
PUBMED     14660368
REFERENCE 2 (bases 1 to 403)
AUTHORS   Joseph,S.J., Hugenholtz,P., Rana,P., Osborne,C.A., Sait,M. and
          Janssen,P.H.
TITLE     Direct Submission
JOURNAL    Submitted (12-FEB-2003) Department of Microbiology and Immunology,
          University of Melbourne, Parkville, Victoria 3010, Australia
          Location/Qualifiers
FEATURES   source
            1..403
            /organism="bacterium Ellin6013"
            /mol_type="genomic DNA"
            /isolate="Ellin6013"
            /db_xref="taxon:234120"
            <1..>403
            /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.6%; Score 23.4; DB 15; Length 403;
Best Local Similarity 96.0%; Pred. No. 5.3e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTTCG 25
    |||||
Db 30 GCAAGTCGAACGGAAGGCGCTTCG 54

RESULT 21
AY792017/c
LOCUS      AY792017          407 bp      DNA      linear      BCT 20-NOV-2004

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DEFINITION Mycobacterium sp. 5BR6 16S ribosomal RNA gene, partial sequence.
ACCESSION AY792017
VERSION AY792017.1 GI:55740316
KEYWORDS
SOURCE
ORGANISM
Mycobacterium sp. 5BR6
Mycobacterium sp. 5BR6
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
1 (bases 1 to 407)
AUTHORS Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.
TITLE Bioremediation of radioactive water with metallic materials
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 407)
AUTHORS Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.
TITLE Direct Submission
JOURNAL Submitted (25-OCT-2004) Dep Ingenieria Y Ciencia de los Materiales,
Escuela Tecnica Superior de Ingenieros Industriales, Universidad
Politecnica de Madrid, Jose Gutierrez Abascal, 2, Madrid, Madrid
28006, Spain
FEATURES
Location/Qualifiers
source
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/organism="Mycobacterium sp. 5BR6"
/mol_type="genomic DNA"
/isolate="5BR6"
/isolation_source="radioactive water"
/db_xref="taxon:300866"
<1..>407
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 93.6%; Score 23.4; DB 15; Length 407;
Best Local Similarity 96.0%; Pred. No. 5.3e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
|||||
Db 366 GCAAGTCGAACGGAAGGCGCTTTCG 342

RESULT 22
BSSMKN12
LOCUS Bacterium sp. (SMKN12) DNA. 410 bp DNA linear ENV 22-FEB-1995
DEFINITION
ACCESSION X78654
VERSION X78654.1 GI:509723
KEYWORDS 16S ribosomal RNA.
SOURCE unidentified bacterium
ORGANISM unidentified bacterium
Bacteria; environmental samples.
REFERENCE
1
AUTHORS Schuppler M., Mertens, F., Schon, G. and Gobel, U. B.
TITLE Molecular characterization of nocardiform actinomycetes in
activated sludge by 16S rRNA analysis
JOURNAL Microbiology (Reading, Engl.) 141 (Pt 2), 513-521 (1995)
PUBMED 7704280
REFERENCE
2 (bases 1 to 410)
AUTHORS Schuppler M.
TITLE Direct Submission
JOURNAL Submitted (28-MAR-1994) M. Schuppler, Institut fuer Med.
Mikrobiologie & Hygiene, Universitaet Freiburg, Hermann-Herder-St.
11, 79104 Freiburg, FRG
FEATURES
Location/Qualifiers
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/mol_type="genomic DNA"
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/db_xref="taxon:2338"
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/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 93.6%; Score 23.4; DB 1; Length 410;
Best Local Similarity 96.0%; Pred. No. 5.3e+02;

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Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
|||||
Db 2 GCAAGTCGAACGGAAGGCGCTTTCG 26

RESULT 23
DQ063154
LOCUS actinobacterium BAL218 411 bp DNA linear BCT 27-JUN-2005
DEFINITION actinobacterium BAL218 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ063154
VERSION DQ063154.1 GI:68139192
KEYWORDS
SOURCE
ORGANISM actinobacterium BAL218
actinobacterium BAL218
Bacteria; Actinobacteria.
REFERENCE
1 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE Bacterial community composition in the central Baltic Sea analyzed
by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES
Location/Qualifiers
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/organism="actinobacterium BAL218"
/mol_type="genomic DNA"
/strain="BAL218"
/isolation_source="Baltic Sea, 3m depth, Landsort deep St.
BY31, Zobell/R2A media"
/db_xref="taxon:331796"
/country="Sweden"
/lat_lon="60.42.726N, 05.05.595E"
/collection_date="17 May 2004"
<1..>411
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 93.6%; Score 23.4; DB 15; Length 411;
Best Local Similarity 96.0%; Pred. No. 5.3e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
|||||
Db 10 GCAAGTCGAACGGAAGGCGCTTTCG 34

RESULT 24
DQ063199
LOCUS actinobacterium BAL263 411 bp DNA linear BCT 27-JUN-2005
DEFINITION actinobacterium BAL263 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ063199
VERSION DQ063199.1 GI:68139237
KEYWORDS
SOURCE
ORGANISM actinobacterium BAL263
actinobacterium BAL263
Bacteria; Actinobacteria.
REFERENCE
1 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE Bacterial community composition in the central Baltic Sea analyzed
by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE Direct Submission

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JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
KEYWORDS University of Kalmar, Barlasgatan 11, Kalmar 39231, Sweden
SOURCE Location/Qualifiers
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  /strain="BAL263"
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  BY31, Zobel/RZA media"
  /db_xref="taxon:331810"
  /country="Sweden"
  /lat_lon="60.42.726N, 05.05.595E"
  /collection_date="17 May 2004"
  <1..>411
  /product="16S ribosomal RNA"

rRNA

ORIGIN
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  Best Local Similarity 96.0%; Pred. No. 5.3e+02;
  Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GCAAGTCGACGGAAGGCCCTTCG 25
    |||||
Db 11 GCAAGTCGACGGAAGGCCCTTCG 35

RESULT 25
AY792013 411 bp DNA linear BCT 20-NOV-2004
LOCUS Mycobacterium sp. 4BR14 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION AY792013
VERSION AY792013.1 GI:55740312
KEYWORDS
SOURCE
  ORGANISM
    Mycobacterium sp. 4BR14
    Mycobacterium sp. 4BR14
    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
    Corynebacterineae; Mycobacteriaceae; Mycobacterium.
  1 (bases 1 to 411)
  Sarro.M.I., Garcia.A.M., Moreno.D.A. and Montero.F.
  Direct Submission
  Submitted (25-OCT-2004) Dep Ingenieria y Ciencia de los Materiales,
  Escuela Tecnica Superior de Ingenieros Industriales, Universidad
  Politecnica de Madrid, Jose Gutierrez Abascal, 2, Madrid, Madrid
  28006, Spain
  Location/Qualifiers
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    /isolate="4BR14"
    /isolation_source="radioactive water"
    /db_xref="taxon:300864"
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rRNA

ORIGIN
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  Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GCAAGTCGACGGAAGGCCCTTCG 25
    |||||
Db 51 GCAAGTCGACGGAAGGCCCTTCG 75

RESULT 26
AM085786 416 bp DNA linear ENV 21-SEP-2005
LOCUS Uncultured Mycobacterium sp. partial 16S rRNA gene, clone K11.
DEFINITION
ACCESSION AM085786

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VERSION AM085786.1 GI:75754609
KEYWORDS ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE uncultured Mycobacterium sp.
  ORGANISM
    uncultured Mycobacterium sp.
    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
    Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental
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  1
  Uyttebroek,M., Breugelmans,P., Janssen,M., Wattiau,P., Joffe,B.,
  Karlson,U., Ortega-Calvo,J.J., Bastiaens,L., Ryngaert,A. and
  Springael,D.
  Distribution of the Mycobacterium sp. community and polycyclic
  aromatic hydrocarbons (PAHs) among different size fractions of a
  weathered PAH-contaminated soil
  Unpublished
  2 (bases 1 to 416)
  Uyttebroek,M.
  Direct Submission
  Submitted (13-SEP-2005) Uyttebroek M., Division Soil and Water
  Management, Catholic University of Leuven, Kasteelpark Arenberg 20,
  B-3001 Leuven, BELGIUM
  Location/Qualifiers
    1. 416
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    /isolation_source="PAH-contaminated soil"
    /db_xref="taxon:171292"
    /clone="K11"
    /environmental_sample
    /country="Denmark"
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gene
rRNA

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  Best Local Similarity 96.0%; Pred. No. 5.3e+02;
  Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GCAAGTCGACGGAAGGCCCTTCG 25
    |||||
Db 3 GCAAGTCGACGGAAGGCCCTTCG 27

RESULT 27
AM085788 418 bp DNA linear ENV 21-SEP-2005
LOCUS Uncultured Mycobacterium sp. partial 16S rRNA gene, clone K13.
DEFINITION
ACCESSION AM085788
VERSION AM085788.1 GI:75754611
KEYWORDS ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE uncultured Mycobacterium sp.
  ORGANISM
    uncultured Mycobacterium sp.
    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
    Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental
    samples.
  1
  Uyttebroek,M., Breugelmans,P., Janssen,M., Wattiau,P., Joffe,B.,
  Karlson,U., Ortega-Calvo,J.J., Bastiaens,L., Ryngaert,A. and
  Springael,D.
  Distribution of the Mycobacterium sp. community and polycyclic
  aromatic hydrocarbons (PAHs) among different size fractions of a
  weathered PAH-contaminated soil
  Unpublished
  2 (bases 1 to 418)
  Uyttebroek,M.
  Direct Submission
  Submitted (13-SEP-2005) Uyttebroek M., Division Soil and Water
  Management, Catholic University of Leuven, Kasteelpark Arenberg 20,
  B-3001 Leuven, BELGIUM
  Location/Qualifiers

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/organism="uncultured Mycobacterium sp."
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/clone="K13"
/environmental_sample
/country="Denmark"
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Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
    |||||
Db 3 GCAAGTCGAACGGAAGGCGCTTTCG 27

RESULT 28
AY673261          418 bp DNA linear BCT 20-MAY-2005
DEFINITION
Mycobacteriaceae bacterium Ellin7095 16S ribosomal RNA gene,
partial sequence.
ACCESSION
AY673261
VERSION
AY673261.1 GI:56683118
KEYWORDS
Mycobacteriaceae bacterium Ellin7095
SOURCE
Mycobacteriaceae bacterium Ellin7095
ORGANISM
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
REFERENCE
1 (bases 1 to 418)
Davis,K.E., Joseph,S.J. and Janssen,P.H.
Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
JOURNAL
PUBMED
15691937
REFERENCE
2 (bases 1 to 418)
Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
Direct Submission
TITLE
Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES
source
1. .418
/organism="Mycobacteriaceae bacterium Ellin7095"
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/db_xref="taxon:305281"
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/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          93.6%; Score 23.4; DB 15; Length 418;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
    |||||
Db 30 GCAAGTCGAACGGAAGGCGCTTTCG 54

RESULT 29
AM085770          421 bp DNA linear ENV 21-SEP-2005
LOCUS
AM085770
DEFINITION
Uncultured eubacterium partial 16S rRNA gene, clone T3.
ACCESSION
AM085770

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1. .418
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ORIGIN
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Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
    |||||
Db 3 GCAAGTCGAACGGAAGGCGCTTTCG 27

RESULT 28
AY673261          418 bp DNA linear BCT 20-MAY-2005
DEFINITION
Mycobacteriaceae bacterium Ellin7095 16S ribosomal RNA gene,
partial sequence.
ACCESSION
AY673261
VERSION
AY673261.1 GI:56683118
KEYWORDS
Mycobacteriaceae bacterium Ellin7095
SOURCE
Mycobacteriaceae bacterium Ellin7095
ORGANISM
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
REFERENCE
1 (bases 1 to 418)
Davis,K.E., Joseph,S.J. and Janssen,P.H.
Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
JOURNAL
PUBMED
15691937
REFERENCE
2 (bases 1 to 418)
Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
Direct Submission
TITLE
Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES
source
1. .418
/organism="Mycobacteriaceae bacterium Ellin7095"
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/isolate="Ellin7095"
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<1. .>418
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          93.6%; Score 23.4; DB 15; Length 418;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
    |||||
Db 30 GCAAGTCGAACGGAAGGCGCTTTCG 54

RESULT 29
AM085770          421 bp DNA linear ENV 21-SEP-2005
LOCUS
AM085770
DEFINITION
Uncultured eubacterium partial 16S rRNA gene, clone T3.
ACCESSION
AM085770

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/organism="uncultured Mycobacterium sp."
/mol_type="genomic DNA"
/isolation_source="PAH-contaminated soil"
/db_xref="taxon:171292"
/clone="K13"
/environmental_sample
/country="Denmark"
<1. .>418
/gene="16S rRNA"
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/product="16S ribosomal RNA"

ORIGIN
Query Match          93.6%; Score 23.4; DB 1; Length 421;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
    |||||
Db 9 GCAAGTCGAACGGAAGGCGCTTTCG 33

RESULT 30
AJ786807          422 bp DNA linear BCT 29-OCT-2004
LOCUS
AJ786807
DEFINITION
Mycobacterium sp. R-22838 partial 16S rRNA gene, isolate R-22838.
ACCESSION
AJ786807
VERSION
AJ786807.1 GI:54897545
KEYWORDS
16S ribosomal RNA; 16S rRNA gene.
Mycobacterium sp. R-22838
Mycobacterium sp. R-22838
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
1
Vanparrys,B., Heylen,K., Lebbe,L., Boon,N., Wittebolle,L.,
Verstraete,W. and De Vos,P.
The microbial community composition of a commercial nitrifying
inoculum
Unpublished
2 (bases 1 to 422)
Vanparrys,B.
Direct Submission
TITLE
Submitted (30-JUL-2004) Vanparrys B., Laboratory of Microbiology,
University of Gent, Ledeganckstraat 35, 9000 Gent, BELGIUM
FEATURES
source
1. .422
/organism="Mycobacterium sp. R-22838"
/mol_type="genomic DNA"
/isolate="R-22838"
/isolation_source="commercial nitrifying inoculum"
/db_xref="taxon:288999"
/country="Belgium"
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gene
1. .422

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rRNA      .      /gene="16S rRNA"
           <1..>422
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ORIGIN
Query Match      93.6%; Score 23.4; DB 15; Length 422;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTTCG 25
    |||||
Db 30 GCAAGTCGAACGGAAGGCCTTTTCG 54

RESULT 31
AY673205      423 bp      DNA      linear      BCT 20-MAY-2005
LOCUS      Mycobacteriaceae bacterium Ellin7039 16S ribosomal RNA gene,
DEFINITION      partial sequence.
ACCESSION      AY673205
VERSION      AY673205.1 GI:56683062
KEYWORDS      Mycobacteriaceae bacterium Ellin7039
SOURCE      Mycobacteriaceae bacterium Ellin7039
ORGANISM      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
              Corynebacterineae; Mycobacteriaceae.
REFERENCE      1 (bases 1 to 423)
AUTHORS      Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE      Effects of growth medium, inoculum size, and incubation time on
            culturability and isolation of soil bacteria
JOURNAL      Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED      15691937
AUTHORS      Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE      Effects of growth medium, inoculum size, and incubation time on
            culturability and isolation of soil bacteria
JOURNAL      Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED      15691937

FEATURES
source      1..423
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rRNA

ORIGIN
Query Match      93.6%; Score 23.4; DB 15; Length 423;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTTCG 25
    |||||
Db 30 GCAAGTCGAACGGAAGGCCTTTTCG 54

RESULT 32
AY673206      423 bp      DNA      linear      BCT 20-MAY-2005
LOCUS      Mycobacteriaceae bacterium Ellin7040 16S ribosomal RNA gene,
DEFINITION      partial sequence.
ACCESSION      AY673206
VERSION      AY673206.1 GI:56683063
KEYWORDS      Mycobacteriaceae bacterium Ellin7040
SOURCE      Mycobacteriaceae bacterium Ellin7040
ORGANISM      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
              Corynebacterineae; Mycobacteriaceae.
REFERENCE      1 (bases 1 to 423)
AUTHORS      Davis,K.E., Joseph,S.J. and Janssen,P.H.

```

```

TITLE      Effects of growth medium, inoculum size, and incubation time on
            culturability and isolation of soil bacteria
JOURNAL      Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED      15691937
AUTHORS      Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE      Direct Submission
JOURNAL      Submitted (02-JUL-2004) Department of Microbiology and Immunology,
            University of Melbourne, Grattan Street, Parkville, Victoria 3010,
            Australia
FEATURES
source      1..423
            /organism="Mycobacteriaceae bacterium Ellin7040"
            /mol_type="genomic DNA"
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            /isolation_source="soil"
            /db_xref="taxon:305259"
            <1..>423
            /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.6%; Score 23.4; DB 15; Length 423;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTTCG 25
    |||||
Db 30 GCAAGTCGAACGGAAGGCCTTTTCG 54

RESULT 33
AY673207      423 bp      DNA      linear      BCT 20-MAY-2005
LOCUS      Mycobacteriaceae bacterium Ellin7041 16S ribosomal RNA gene,
DEFINITION      partial sequence.
ACCESSION      AY673207
VERSION      AY673207.1 GI:56683064
KEYWORDS      Mycobacteriaceae bacterium Ellin7041
SOURCE      Mycobacteriaceae bacterium Ellin7041
ORGANISM      Mycobacteriaceae bacterium Ellin7041
              Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
              Corynebacterineae; Mycobacteriaceae.
REFERENCE      1 (bases 1 to 423)
AUTHORS      Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE      Effects of growth medium, inoculum size, and incubation time on
            culturability and isolation of soil bacteria
JOURNAL      Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED      15691937
AUTHORS      Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE      Direct Submission
JOURNAL      Submitted (02-JUL-2004) Department of Microbiology and Immunology,
            University of Melbourne, Grattan Street, Parkville, Victoria 3010,
            Australia
FEATURES
source      1..423
            /organism="Mycobacteriaceae bacterium Ellin7041"
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            /isolation_source="soil"
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            <1..>423
            /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.6%; Score 23.4; DB 15; Length 423;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTTCG 25
    |||||
Db 30 GCAAGTCGAACGGAAGGCCTTTTCG 54

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RESULT 34
DQ063156
LOCUS actinobacterium BAL220 16S ribosomal RNA gene, partial sequence.
DEFINITION actinobacterium BAL220 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ063156
VERSION DQ063156.1 GI:68139194
KEYWORDS
SOURCE actinobacterium BAL220
ORGANISM actinobacterium BAL220
REFERENCE 1 (bases 1 to 424)
AUTHORS Riemann,L., Leitert,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE Bacterial community composition in the central Baltic Sea analyzed by cultivation and molecular-based methods
JOURNAL
REFERENCE 2 (bases 1 to 424)
AUTHORS Riemann,L., Leitert,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences, University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES
source
location/Qualifiers
1..424
/organism="actinobacterium BAL220"
/mol_type="genomic DNA"
/strain="BAL220"
/isolation_source="Baltic Sea, 3m depth, Landsort deep St. BY31, Zobell/RZA media"
/db_xref="taxon:331797"
/country="Sweden"
/lat_lon="60.42.726N, 05.05.5955E"
/collection_date="17 May 2004"
<1..>424
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 93.6%; Score 23.4; DB 15; Length 424;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCTTTTCG 25
|||||
Db 14 GCAAGTCGAACGGAAGGCTTTTCG 38

RESULT 35
AY673287
LOCUS Streptosporangiaceae bacterium Ellin7121 16S ribosomal RNA gene, partial sequence.
DEFINITION Streptosporangiaceae bacterium Ellin7121 16S ribosomal RNA gene, partial sequence.
ACCESSION AY673287
VERSION AY673287.1 GI:56683144
KEYWORDS
SOURCE Streptosporangiaceae bacterium Ellin7121
ORGANISM Streptosporangiaceae bacterium Ellin7121
REFERENCE 1 (bases 1 to 424)
AUTHORS Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE Effects of growth medium, inoculum size, and incubation time on culturability and isolation of soil bacteria
JOURNAL Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED 15691937
REFERENCE 2 (bases 1 to 424)
AUTHORS Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2004) Department of Microbiology and Immunology, University of Melbourne, Grattan Street, Parkville, Victoria 3010, Australia
FEATURES
source
location/Qualifiers
1..424

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/organism="Streptosporangiaceae bacterium Ellin7121"
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/isolation_source="soil"
/db_xref="taxon:305348"
<1..>424
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 93.6%; Score 23.4; DB 15; Length 424;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCTTTTCG 25
|||||
Db 30 GCAAGTCGAGCGGAAGGCTTTTCG 54

RESULT 36
AY394635
LOCUS Uncultured Mycobacterium sp. clone W1-11 16S ribosomal RNA gene, partial sequence.
DEFINITION Uncultured Mycobacterium sp. clone W1-11 16S ribosomal RNA gene, partial sequence.
ACCESSION AY394635
VERSION AY394635.1 GI:37677560
KEYWORDS ENV.
SOURCE uncultured Mycobacterium sp.
ORGANISM uncultured Mycobacterium sp.
REFERENCE 1 (bases 1 to 425)
AUTHORS Benson,D.R., Benson,M.J., Gawronski,J.D. and Eveleigh,D.E.
TITLE Intracellular symbionts and other bacteria associated with deer ticks (Ixodes scapularis) from Nantucket and Wellfleet, Cape Cod, Massachusetts
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 425)
AUTHORS Benson,D.R., Benson,M.J., Gawronski,J.D. and Eveleigh,D.E.
TITLE Direct Submission
JOURNAL Submitted (19-SEP-2003) Molecular & Cell Biology, University of Connecticut, U-3125, North Eagleville Rd., Storrs, CT 06279-3125, USA
FEATURES
source
location/Qualifiers
1..425
/organism="uncultured Mycobacterium sp."
/mol_type="genomic DNA"
/specific_host="Ixodes scapularis"
/db_xref="taxon:171292"
/clones="W1-11"
/environmental_sample
/country="USA; Massachusetts, Cape Cod, Nantucket, Wellfleet"
<1..>425
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 93.6%; Score 23.4; DB 1; Length 425;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCTTTTCG 25
|||||
Db 30 GCAAGTCGAACGGAAGGCTTTTCG 54

RESULT 37
AY673136
LOCUS Mycobacteriaceae bacterium Ellin5409 16S ribosomal RNA gene, partial sequence.
DEFINITION Mycobacteriaceae bacterium Ellin5409 16S ribosomal RNA gene, partial sequence.
ACCESSION AY673136
VERSION AY673136.1 GI:56683290

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[illegible]

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/isolation_source="commercial nitrifying inoculum"
/db_xref="taxon:289008"
/country="Belgium"
1..430
/gene="16S rRNA"
<1..>430
/gene="16S rRNA"
/product="16S ribosomal RNA"

ORIGIN
Query Match          93.6%; Score 23.4; DB 15; Length 430;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTCG 25
    |||||
Db 30 GCAAGTCGAACGGAAGGCGCTTCG 54

RESULT 41
AY673202          430 bp DNA linear BCT 20-MAY-2005
LOCUS
DEFINITION
Mycobacteriaceae bacterium Ellin7036 16S ribosomal RNA gene,
partial sequence.
ACCESSION
AY673202.1 GI:56683059
VERSION
KEYWORDS
ORGANISM
Mycobacteriaceae bacterium Ellin7036
Mycobacteriaceae bacterium Ellin7036
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
REFERENCE
1 (bases 1 to 430)
AUTHORS
Davis, K.E., Joseph, S.J. and Janssen, P.H.
TITLE
Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
JOURNAL
Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED
15691937
AUTHORS
Davis, K.E.R., Joseph, S.J. and Janssen, P.H.
TITLE
Direct Submission
JOURNAL
Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES
Location/Qualifiers
1..430
/organism="Mycobacteriaceae bacterium Ellin7036"
/mol_type="genomic DNA"
/isolate="Ellin7036"
/isolation_source="soil"
/db_xref="taxon:305257"
<1..>430
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          93.6%; Score 23.4; DB 15; Length 430;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTCG 25
    |||||
Db 30 GCAAGTCGAACGGAAGGCGCTTCG 54

RESULT 42
AB106919          431 bp DNA linear BCT 09-SEP-2003
LOCUS
DEFINITION
Gram-positive bacterium 2-1 for 16S ribosomal RNA, partial
sequence.
ACCESSION
AB106919
VERSION
AB106919.1 GI:29421133
KEYWORDS
SOURCE
Gram-positive bacterium 2-1

/isolate="R-23262"
/isolation_source="commercial nitrifying inoculum"
/db_xref="taxon:289008"
/country="Belgium"
1..430
/gene="16S rRNA"
<1..>430
/gene="16S rRNA"
/product="16S ribosomal RNA"

ORIGIN
Query Match          93.6%; Score 23.4; DB 15; Length 430;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTCG 25
    |||||
Db 30 GCAAGTCGAACGGAAGGCGCTTCG 54

RESULT 43
AF078232          432 bp DNA linear ENV 10-MAY-2004
LOCUS
DEFINITION
Grassland soil clone saf2_117 16S ribosomal RNA gene, partial
sequence.
ACCESSION
AF078232
VERSION
AF078232.1 GI:4590103
KEYWORDS
ENV.
SOURCE
grassland soil clone saf2_117
grassland soil clone saf2_117
Bacteria; environmental samples.
REFERENCE
1 (bases 1 to 432)
AUTHORS
McCaig, A.E., Glover, L.A. and Prosser, J.I.
TITLE
Molecular analysis of bacterial community structure and diversity
in unimproved and improved upland grass pastures
JOURNAL
Appl. Environ. Microbiol. 65 (4), 1721-1730 (1999)
PUBMED
10103273
AUTHORS
McCaig, A.E., Prosser, J.I. and Glover, L.A.
TITLE
Direct Submission
JOURNAL
Submitted (16-JUL-1998) Institute of Medical Sciences, Department
of Molecular and Cell Biology, University of Aberdeen,
Foresterhill, Aberdeen AB25 2ZD, Scotland, UK
FEATURES
Location/Qualifiers
1..432
/organism="grassland soil clone saf2_117"
/mol_type="genomic DNA"
/db_xref="taxon:80202"
/clone_lib="unimproved grassland soil SAF2"
/environmental_sample
<1..>432
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          93.6%; Score 23.4; DB 1; Length 432;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTCG 25

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ORGANISM

Gram-positive bacterium 2-1

Bacteria.

REFERENCE

1 Amachi, S., Kasahara, M., Hanada, S., Kamagata, Y., Shinoyama, H.,

Fujii, T. and Muramatsu, Y.

Microbial participation in iodine volatilization from soils

Environ. Sci. Technol. 37, 3885-3890 (2003)

JOURNAL

2 (bases 1 to 431)

AUTHORS

Amachi, S., Kasahara, M., Hanada, S., Kamagata, Y., Shinoyama, H.,

Fujii, T. and Muramatsu, Y.

Direct Submission

JOURNAL

Submitted (27-MAR-2003) Seigo Amachi, Chiba University, Dept. of

Bioreources Chem.; 648 Matsudo, Matsudo-shi, Chiba 271-8510, Japan

(E-mail: amachi@faculty.chiba-u.jp, Tel: 81-47-308-8868,

Fax: 81-47-308-8866)

FEATURES

Location/Qualifiers

1..431

/organism="Gram-positive bacterium 2-1"

/mol_type="genomic DNA"

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/db_xref="taxon:226201"

<1..>431

/product="16S ribosomal RNA"

rRNA

ORIGIN

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Best Local Similarity 96.0%; Pred. No. 5.2e+02;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

1 GCAAGTCGAACGGAAGGCGCTTCG 25

|||||

Db

30 GCAAGTCGAACGGAAGGCGCTTCG 54

RESULT 43

AF078232

LOCUS

DEFINITION

Grassland soil clone saf2_117 16S ribosomal RNA gene, partial

sequence.

ACCESSION

AF078232

VERSION

AF078232.1 GI:4590103

KEYWORDS

SOURCE

grassland soil clone saf2_117

grassland soil clone saf2_117

Bacteria; environmental samples.

REFERENCE

1 (bases 1 to 432)

AUTHORS

McCaig, A.E., Glover, L.A. and Prosser, J.I.

TITLE

Molecular analysis of bacterial community structure and diversity

in unimproved and improved upland grass pastures

JOURNAL

PUBMED

10103273

AUTHORS

McCaig, A.E., Prosser, J.I. and Glover, L.A.

TITLE

Direct Submission

JOURNAL

Submitted (16-JUL-1998) Institute of Medical Sciences, Department

of Molecular and Cell Biology, University of Aberdeen,

Foresterhill, Aberdeen AB25 2ZD, Scotland, UK

FEATURES

Location/Qualifiers

1..432

/organism="grassland soil clone saf2_117"

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/environmental_sample

<1..>432

/product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match 93.6%; Score 23.4; DB 1; Length 432;

Best Local Similarity 96.0%; Pred. No. 5.2e+02;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

1 GCAAGTCGAACGGAAGGCGCTTCG 25

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Db      8  GCAAGTCGAACGGAAGGCCCTTCG 32
|||||
RESULT 44
AY673198      433 bp      DNA      linear      BCT 20-MAY-2005
LOCUS      Mycobacteriaceae bacterium Ellin7032 16S ribosomal RNA gene,
DEFINITION      partial sequence.
ACCESSION      AY673198
VERSION      AY673198.1 GI:56683055
KEYWORDS
SOURCE
ORGANISM      Mycobacteriaceae bacterium Ellin7032
Mycobacteriaceae bacterium Ellin7032
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
REFERENCE
AUTHORS      Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE      Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
JOURNAL      Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED      15691937
REFERENCE
AUTHORS      Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE      Direct Submission
JOURNAL      Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES
source
1. .433
/organism="Mycobacteriaceae bacterium Ellin7032"
/mol_type="genomic DNA"
/isolate="Ellin7032"
/isolation_source="soil"
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<1..>433
/product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match      93.6%; Score 23.4; DB 15; Length 433;
Best Local Similarity      96.0%; Pred. No. 5.2e+02;
Matches      24; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

Qy      1  GCAAGTCGAACGGAAGGCCCTTCG 25
|||||
Db      30  GCAAGTCGAACGGAAGGCCCTTCG 54
|||||

RESULT 45
AY673266      433 bp      DNA      linear      BCT 20-MAY-2005
LOCUS      Mycobacteriaceae bacterium Ellin7100 16S ribosomal RNA gene,
DEFINITION      partial sequence.
ACCESSION      AY673266
VERSION      AY673266.1 GI:56683123
KEYWORDS
SOURCE
ORGANISM      Mycobacteriaceae bacterium Ellin7100
Mycobacteriaceae bacterium Ellin7100
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
REFERENCE
AUTHORS      Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE      Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
JOURNAL      Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED      15691937
REFERENCE
AUTHORS      Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE      Direct Submission
JOURNAL      Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES
Location/Qualifiers

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source
1. .433
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/mol_type="genomic DNA"
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/isolation_source="soil"
/db_xref="taxon:305283"
<1..>433
/product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match      93.6%; Score 23.4; DB 15; Length 433;
Best Local Similarity      96.0%; Pred. No. 5.2e+02;
Matches      24; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

Qy      1  GCAAGTCGAACGGAAGGCCCTTCG 25
|||||
Db      30  GCAAGTCGAACGGAAGGCCCTTCG 54
|||||

RESULT 46
DQ063195      435 bp      DNA      linear      BCT 27-JUN-2005
LOCUS      Actinobacterium BAL259 16S ribosomal RNA gene, partial sequence.
DEFINITION      DQ063195
ACCESSION      DQ063195
VERSION      DQ063195.1 GI:68139233
KEYWORDS      actinobacterium BAL259
SOURCE      actinobacterium BAL259
ORGANISM      Bacteria; Actinobacteria.
REFERENCE      1 (bases 1 to 435)
AUTHORS      Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE      Bacterial community composition in the central Baltic Sea analyzed
by cultivation and molecular-based methods
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 435)
AUTHORS      Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE      Direct Submission
JOURNAL      Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES      Location/Qualifiers
source
1. .435
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BY31, Zobell/R2A media"
/db_xref="taxon:331808"
/country="Sweden"
/lat_lon="60 42.726N, 05.05.595E"
/collection_date="17 May 2004"
<1..>435
/product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match      93.6%; Score 23.4; DB 15; Length 435;
Best Local Similarity      96.0%; Pred. No. 5.2e+02;
Matches      24; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

Qy      1  GCAAGTCGAACGGAAGGCCCTTCG 25
|||||
Db      15  GCAAGTCGAACGGAAGGCCCTTCG 39
|||||

RESULT 47
AY234692      435 bp      DNA      linear      BCT 08-DEC-2003
LOCUS      Bacterium Ellin6040 16S ribosomal RNA gene, partial sequence.
DEFINITION      AY234692
ACCESSION      AY234692
VERSION      AY234692.1 GI:37961849
KEYWORDS      bacterium Ellin6040
SOURCE

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ORGANISM bacterium Ellin6040
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae.
 REFERENCE 1 (bases 1 to 435)
 AUTHORS Joseph,S.J., Hugenholtz,P., Sangwan,P., Osborne,C.A. and Janssen,P.H.
 TITLE Laboratory Cultivation of Widespread and Previously Uncultured Soil Bacteria
 JOURNAL Appl. Environ. Microbiol. 69 (12), 7210-7215 (2003)
 PUBLISHED 14660368
 REFERENCE 2 (bases 1 to 435)
 AUTHORS Joseph,S.J., Hugenholtz,P., Rana,P., Osborne,C.A., Sait,M. and Janssen,P.H.
 TITLE Direct Submission
 JOURNAL Submitted (12-FEB-2003) Department of Microbiology and Immunology, University of Melbourne, Parkville, Victoria 3010, Australia
 FEATURES source
 1..435
 /organism="bacterium Ellin6040"
 /mol_type="genomic DNA"
 /isolate="Ellin6040"
 /db_xref="taxon:234122"
 <1..>435
 /product="16S ribosomal RNA"
 rRNA
 ORIGIN
 Query Match 93.6%; Score 23.4; DB 15; Length 435;
 Best Local Similarity 96.0%; Pred. No. 5.2e+02;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
 |||||
 DB 30 GCAAGTCGAACGGAAGGCGCTTTCG 54
 |||||
 RESULT 48
 AY673233
 LOCUS Mycobacteriaceae bacterium Ellin7067 435 bp DNA linear BCT 20-MAY-2005
 DEFINITION partial sequence.
 ACCESSION AY673233
 VERSION AY673233.1 GI:56683090
 KEYWORDS
 SOURCE
 ORGANISM
 Mycobacteriaceae bacterium Ellin7067
 Mycobacteriaceae bacterium Ellin7067
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae.
 REFERENCE 1 (bases 1 to 435)
 AUTHORS Davis,K.E., Joseph,S.J. and Janssen,P.H.
 TITLE Effects of growth medium, inoculum size, and incubation time on culturability and isolation of soil bacteria
 JOURNAL Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
 PUBLISHED 15691937
 REFERENCE 2 (bases 1 to 435)
 AUTHORS Davis,K.E., Joseph,S.J. and Janssen,P.H.
 TITLE Direct Submission
 JOURNAL Submitted (02-JUL-2004) Department of Microbiology and Immunology, University of Melbourne, Grattan Street, Parkville, Victoria 3010, Australia
 FEATURES source
 1..435
 /organism="Mycobacteriaceae bacterium Ellin7067"
 /mol_type="genomic DNA"
 /isolate="Ellin7067"
 /isolation_source="soil"
 /db_xref="taxon:305274"
 <1..>435
 /product="16S ribosomal RNA"
 rRNA
 ORIGIN
 Query Match 93.6%; Score 23.4; DB 15; Length 435;
 Best Local Similarity 96.0%; Pred. No. 5.2e+02;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
 |||||
 DB 30 GCAAGTCGAACGGAAGGCGCTTTCG 54
 |||||
 RESULT 49
 AY673199
 LOCUS Mycobacteriaceae bacterium Ellin7033 436 bp DNA linear BCT 20-MAY-2005
 DEFINITION partial sequence.
 ACCESSION AY673199
 VERSION AY673199.1 GI:56683056
 KEYWORDS
 SOURCE
 ORGANISM
 Mycobacteriaceae bacterium Ellin7033
 Mycobacteriaceae bacterium Ellin7033
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae.
 REFERENCE 1 (bases 1 to 436)
 AUTHORS Davis,K.E., Joseph,S.J. and Janssen,P.H.
 TITLE Effects of growth medium, inoculum size, and incubation time on culturability and isolation of soil bacteria
 JOURNAL Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
 PUBLISHED 15691937
 REFERENCE 2 (bases 1 to 436)
 AUTHORS Davis,K.E., Joseph,S.J. and Janssen,P.H.
 TITLE Direct Submission

QY 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
 |||||
 DB 30 GCAAGTCGAACGGAAGGCGCTTTCG 54
 |||||
 RESULT 49
 DQ063046
 LOCUS actinobacterium BAL106 436 bp DNA linear BCT 27-JUN-2005
 DEFINITION actinobacterium BAL106 16S ribosomal RNA gene, partial sequence.
 ACCESSION DQ063046
 VERSION DQ063046.1 GI:68139075
 KEYWORDS
 SOURCE
 ORGANISM
 actinobacterium BAL106
 actinobacterium BAL106
 Bacteria; Actinobacteria.
 REFERENCE 1 (bases 1 to 436)
 AUTHORS Riemann,L., Leitert,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
 TITLE Bacterial community composition in the central Baltic Sea analyzed by cultivation and molecular-based methods
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 436)
 AUTHORS Riemann,L., Leitert,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
 TITLE Direct Submission
 JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences, University of Kalmar, Bariasgatan 11, Kalmar 39231, Sweden
 FEATURES source
 1..436
 /organism="actinobacterium BAL106"
 /mol_type="genomic DNA"
 /strain="BAL106"
 /isolation_source="Baltic Sea, 3m depth, Landsort deep St. By31, Zobell/R2A media"
 /db_xref="taxon:331778"
 /country="Sweden"
 /lat_lon="60.42.726N, 05.05.595E"
 /collection_dates="2 July 2003"
 <1..>436
 /product="16S ribosomal RNA"
 rRNA
 ORIGIN
 Query Match 93.6%; Score 23.4; DB 15; Length 436;
 Best Local Similarity 96.0%; Pred. No. 5.2e+02;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
 |||||
 DB 19 GCAAGTCGAACGGAAGGCGCTTTCG 43
 |||||
 RESULT 50
 AY673199
 LOCUS Mycobacteriaceae bacterium Ellin7033 436 bp DNA linear BCT 20-MAY-2005
 DEFINITION partial sequence.
 ACCESSION AY673199
 VERSION AY673199.1 GI:56683056
 KEYWORDS
 SOURCE
 ORGANISM
 Mycobacteriaceae bacterium Ellin7033
 Mycobacteriaceae bacterium Ellin7033
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae.
 REFERENCE 1 (bases 1 to 436)
 AUTHORS Davis,K.E., Joseph,S.J. and Janssen,P.H.
 TITLE Effects of growth medium, inoculum size, and incubation time on culturability and isolation of soil bacteria
 JOURNAL Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
 PUBLISHED 15691937
 REFERENCE 2 (bases 1 to 436)
 AUTHORS Davis,K.E., Joseph,S.J. and Janssen,P.H.
 TITLE Direct Submission

JOURNAL Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia

FEATURES
source Location/Qualifiers
1. .436
/organism="Mycobacteriaceae bacterium Ellin7033"
/mol_type="genomic DNA"
/isolate="Ellin7033"
/isolation_source="soil"
/db_xref="taxon:305286"
<1. .>436
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 93.6%; Score 23.4; DB 15; Length 436;
Best Local Similarity 96.0%; Pred. NO. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCCTTCG 25
Db 30 GCAAGTCGACGGAAGGCCCTTCG 54

RESULT 51
AY673304 436 bp DNA linear BCT 20-MAY-2005
LOCUS Mycobacteriaceae bacterium Ellin7138 16S ribosomal RNA gene,
partial sequence.
DEFINITION
AY673304
VERSION
KEYWORDS
SOURCE
ORGANISM
Mycobacteriaceae bacterium Ellin7138
Mycobacteriaceae bacterium Ellin7138
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
REFERENCE
AUTHORS Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
JOURNAL Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED 15691937
REFERENCE 2 (bases 1 to 436)
AUTHORS Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia

FEATURES
source Location/Qualifiers
1. .436
/organism="Mycobacteriaceae bacterium Ellin7138"
/mol_type="genomic DNA"
/isolate="Ellin7138"
/isolation_source="soil"
/db_xref="taxon:305288"
<1. .>436
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 93.6%; Score 23.4; DB 15; Length 436;
Best Local Similarity 96.0%; Pred. NO. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCCTTCG 25
Db 30 GCAAGTCGACGGAAGGCCCTTCG 54

RESULT 52
AF078419 437 bp DNA linear ENV 10-MAY-2004
LOCUS Grassland soil clone sl3_612 16S ribosomal RNA gene, partial
DEFINITION
AF078419
ACCESSION

AF078419.1 GI:4590290
ENV. Grassland soil clone sl3_612
Grassland soil clone sl3_612
Bacteria; environmental samples.
REFERENCE 1 (bases 1 to 437)
AUTHORS McCaig,A.E., Glover,L.A. and Prosser,J.I.
TITLE Molecular analysis of bacterial community structure and diversity
in unimproved and improved upland grass pastures
JOURNAL Appl. Environ. Microbiol. 65 (4), 1721-1730 (1999)
PUBMED 10103273
REFERENCE 2 (bases 1 to 437)
AUTHORS McCaig,A.E., Prosser,J.I. and Glover,L.A.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-1998) Institute of Medical Sciences, Department
of Molecular and Cell Biology, University of Aberdeen,
Foresterhill, Aberdeen AB25 2ZD, Scotland, UK

FEATURES
source Location/Qualifiers
1. .437
/organism="grassland soil clone sl3_612"
/mol_type="genomic DNA"
/db_xref="taxon:80115"
/clone_lib="improved grassland soil SL3"
/environmental_sample
<1. .>437
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 93.6%; Score 23.4; DB 1; Length 437;
Best Local Similarity 96.0%; Pred. NO. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCCTTCG 25
Db 8 GCAAGTCGACGGAAGGCCCTTCG 32

RESULT 53
AB232370 441 bp DNA linear BCT 25-JAN-2006
LOCUS Mycobacterium kansasii gene for 16S rRNA, partial sequence,
strain:SA-10.
DEFINITION
AB232370
VERSION
AB232370.1 GI:73589607
KEYWORDS
SOURCE Mycobacterium kansasii
ORGANISM Mycobacterium kansasii
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1
AUTHORS Iwamoto,T. and Saito,H.
TITLE Comparative study of two typing methods, hsp65 PRA and ITS
sequencing, revealed a possible evolutionary link between
Mycobacterium kansasii type I and II isolates
JOURNAL FEMS Microbiol. Lett. 254, 129-133 (2006)
REFERENCE 2 (bases 1 to 441)
AUTHORS Iwamoto,T.
TITLE Direct Submission
JOURNAL Submitted (17-AUG-2005) Tomotada Iwamoto, Kobe Institute of Health,
Department of Microbiology; Chuo-ku Minatojima-nakamachi 4-6, Kobe,
Hyogo 6500046, Japan [E-mail:kx2t-iwmt@sasahi-net.or.jp,
URL:http://www.city.kobe.jp/cityoffice/18/menu03/h/kanken/kanken-
top, Tel:81-78-302-6251, Fax:81-78-302-0894]
FEATURES
source Location/Qualifiers
1. .441
/organism="Mycobacterium kansasii"
/mol_type="genomic DNA"
/strain="SA-10"
/db_xref="taxon:1768"
/note="type II"
<1. .>441
/product="16S ribosomal RNA"

rRNA

ORIGIN

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Query Match      93.6%; Score 23.4; DB 15; Length 441;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
   |||||
Db 4 GCAAGTCGAACGGAAGGCGCTTTCG 28

RESULT 54
AY306201
LOCUS      442 bp      DNA      linear      BCT 25-JUN-2003
DEFINITION Mycobacterium sp. 1351 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY306201
VERSION     AY306201.1 GI:32250950
KEYWORDS
SOURCE      Mycobacterium sp. 1351
ORGANISM    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE   1 (bases 1 to 442)
AUTHORS     Pauls,R.J., Turenne,C.Y., Wolfe,J.N. and Kabani,A.
TITLE       A High Proportion of Novel Mycobacteria Species Identified by 16S
            rDNA Analysis Among Slowly Growing AccuProbe Negative Strains in a
            Clinical Setting
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 442)
AUTHORS     Turenne,C.Y.
TITLE       Direct Submission
JOURNAL     Submitted (26-MAY-2003) National Reference Centre for
            Mycobacteriology, National Microbiology Laboratory, Health Canada,
            1015 Arlington Street, Winnipeg, MB R3E 3R2, Canada
FEATURES    source
            1..442
            /organism="Mycobacterium sp. 1351"
            /mol_type="genomic DNA"
            /strain="1351"
            /isolation_source="mouth ulcer"
            /specific_host="Homo sapiens"
            /db_xref="taxon:235254"
            <1..>442
            /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.6%; Score 23.4; DB 15; Length 442;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
   |||||
Db 4 GCAAGTCGAACGGAAGGCGCTTTCG 28

RESULT 55
AY306205
LOCUS      444 bp      DNA      linear      BCT 25-JUN-2003
DEFINITION Mycobacterium sp. HSC507 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY306205
VERSION     AY306205.1 GI:32250954
KEYWORDS
SOURCE      Mycobacterium sp. HSC507
ORGANISM    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE   1 (bases 1 to 444)
AUTHORS     Pauls,R.J., Turenne,C.Y., Wolfe,J.N. and Kabani,A.
TITLE       A High Proportion of Novel Mycobacteria Species Identified by 16S
            rDNA Analysis Among Slowly Growing AccuProbe Negative Strains in a
            Clinical Setting
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 444)
AUTHORS     Turenne,C.Y.

Query Match      93.6%; Score 23.4; DB 15; Length 441;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
   |||||
Db 4 GCAAGTCGAACGGAAGGCGCTTTCG 28

RESULT 56
AB106917
LOCUS      445 bp      DNA      linear      BCT 09-SEP-2003
DEFINITION Gram-positive bacterium 1-3 for 16S ribosomal RNA, partial
            sequence.
ACCESSION  AB106917
VERSION     AB106917.1 GI:29421131
KEYWORDS
SOURCE      Gram-positive bacterium 1-3
ORGANISM    Gram-positive bacterium 1-3
            Bacteria.
REFERENCE   1
AUTHORS     Amachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
            Fujii,T. and Muramatsu,Y.
TITLE       Microbial participation in iodine volatilization from soils
JOURNAL     Environ. Sci. Technol. 37, 3885-3890 (2003)
AUTHORS
REFERENCE   2 (bases 1 to 445)
AUTHORS     Fujii,T. and Muramatsu,Y.
TITLE       Direct Submission
JOURNAL     Submitted (27-MAR-2003) Seigo Amachi, Chiba University, Dept. of
            Bioresources Chem.; 648 Matsudo, Matsudo-shi, Chiba 271-8510, Japan
            (E-mail:amachi@faculty.chiba-u.jp, Tel:81-47-308-8868,
            Fax:81-47-308-8866)
FEATURES    Location/Qualifiers
            source
            1..445
            /organism="Gram-positive bacterium 1-3"
            /mol_type="genomic DNA"
            /strain="1-3"
            /db_xref="taxon:226199"
            <1..>445
            /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.6%; Score 23.4; DB 15; Length 445;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
   |||||
Db 30 GCAAGTCGAACGGAAGGCGCTTTCG 54

RESULT 57
DQ067466
LOCUS      445 bp      DNA      linear      BCT 18-JUL-2005
DEFINITION Mycobacterium sp. F105167 16S ribosomal RNA gene, partial sequence.
ACCESSION  DQ067466
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VERSION      DQ067466.1  GI:67528039
KEYWORDS
SOURCE       Mycobacterium sp. F105167
ORGANISM     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
              Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE    1 (bases 1 to 445)
AUTHORS      Tortoli, E., Mariottini, A. and Mazzarelli, G.
TITLE        Unusual mycobacteria isolated from clinical samples
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 445)
AUTHORS      Tortoli, E., Mariottini, A. and Mazzarelli, G.
TITLE        Direct Submission
JOURNAL      Submitted (17-MAY-2005) Reg. Reference Center for Mycobacteria,
              Careggi Hospital, Piasra dei Servizi, Ospedale Careggi, v.le
              Morgagni 85, Firenze, FI 50134, Italy
FEATURES     Location/Qualifiers
              source
                1..445
                /organism="Mycobacterium sp. F105167"
                /mol_type="genomic DNA"
                /strain="F105167"
                /db_xref="taxon:332013"
                <1..>445
                /product="16S ribosomal RNA"
              rRNA
              1..445
              /product="16S ribosomal RNA"
              ORIGIN
                Query Match      93.6%; Score 23.4; DB 15; Length 445;
                Best Local Similarity 96.0%; Pred. No. 5.1e+02;
                Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTCG 25
Db 8 GCAAGTCGAACGGAAGGCCTTCG 32

RESULT 58
MS91016SR      450 bp      DNA      linear      BCT 01-AUG-1997
LOCUS          Mycobacterium sp.16S rRNA gene, isolate BN910, partial.
DEFINITION
ACCESSION      Y08205
VERSION        Y08205.1  GI:2292948
KEYWORDS       16S ribosomal RNA; 16S rRNA.
SOURCE         Mycobacterium sp.
ORGANISM       Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
              Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE      1
AUTHORS        Hagenau, C., Behringer, K., Naumann, L., Kaiser, R. and
              Schulze-Roebecke, R.
JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 450)
AUTHORS        Hagenau, C.
TITLE          Direct Submission
JOURNAL        Submitted (18-SEP-1996) C. Hagenau, Hygiene-Institute, University
              of Bonn, Sigmund-Freud-Strasse 25, D-53105 Bonn, FRG
COMMENT        Related sequence M95469.
FEATURES       Location/Qualifiers
                source
                  1..450
                  /organism="Mycobacterium sp."
                  /mol_type="genomic DNA"
                  /isolate="BN910"
                  /db_xref="taxon:1785"
                  /map="E.coli position 38-503"
                  1..450
                  /gene="16S rRNA"
                  <1..>450
                  /gene="16S rRNA"
                  /product="16S ribosomal RNA"
                gene
                rRNA

ORIGIN
  Query Match      93.6%; Score 23.4; DB 15; Length 450;
  Best Local Similarity 96.0%; Pred. No. 5.1e+02;
  Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTCG 25
Db 20 GCAAGTCGAACGGAAGGCCTTCG 44

RESULT 60
AY358002      450 bp      DNA      linear      BCT 19-AUG-2005
LOCUS          Actinobacterium iri117 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION      AY358002
VERSION        AY358002.1  GI:34500643
KEYWORDS       actinobacterium iri117
SOURCE         actinobacterium iri117
ORGANISM       Bacteria; Actinobacteria.
REFERENCE      1 (bases 1 to 450)
AUTHORS        Idris, R., Trifonova, R., Puschenreiter, M., Wenzel, W.W. and
              Sessitsch, A.
TITLE          Bacterial Communities Associated with Flowering Plants of the Ni
              Hyperaccumulator Thlaspi goesingense
JOURNAL        Appl. Environ. Microbiol. 70 (5), 2667-2677 (2004)
PUBMED         15128517
REFERENCE      2 (bases 1 to 450)
AUTHORS        Idris, R. and Sessitsch, A.
TITLE          Direct Submission
JOURNAL        Submitted (01-AUG-2003) Environmental and Life Sciences, ARC
              Seibersdorf Research GmbH, Seibersdorf A-2444, Austria
FEATURES       Location/Qualifiers
                source
                  1..450
                  /organism="Mycobacterium sp."
                  /mol_type="genomic DNA"
                  /isolate="BN910"
                  /db_xref="taxon:1785"
                  /map="E.coli position 38-503"
                  1..450
                  /gene="16S rRNA"
                  <1..>450
                  /gene="16S rRNA"
                  /product="16S ribosomal RNA"
                gene
                rRNA

ORIGIN
  Query Match      93.6%; Score 23.4; DB 15; Length 450;
  Best Local Similarity 96.0%; Pred. No. 5.1e+02;
  Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 GCAAGTCGAACGGAAGGCCTTCG 25
Db 20 GCAAGTCGAACGGAAGGCCTTCG 44

RESULT 59
MS916SR      450 bp      DNA      linear      BCT 01-AUG-1997
LOCUS          Mycobacterium sp. 16S rRNA gene.
DEFINITION
ACCESSION      Y07954
VERSION        Y07954.1  GI:2292951
KEYWORDS       16S ribosomal RNA; 16S rRNA gene.
SOURCE         Mycobacterium sp.
ORGANISM       Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
              Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE      1
AUTHORS        Hagenau, C., Behringer, K., Naumann, L., Kaiser, R. and
              Schulze-Roebecke, R.
JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 450)
AUTHORS        Hagenau, C.
TITLE          Direct Submission
JOURNAL        Submitted (12-SEP-1996) C. Hagenau, Hygiene-Institute, University
              of Bonn, Sigmund-Freud-Strasse 25, D-53105 Bonn, FRG
COMMENT        Related sequence: M95469.
FEATURES       Location/Qualifiers
                source
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                  /organism="Mycobacterium sp."
                  /mol_type="genomic DNA"
                  /isolate="BN737"
                  /db_xref="taxon:1785"
                  /map="E.coli 38-503"
                  1..450
                  /gene="16S rRNA"
                  <1..>450
                  /gene="16S rRNA"
                  /product="16S ribosomal RNA"
                gene
                rRNA

ORIGIN
  Query Match      93.6%; Score 23.4; DB 15; Length 450;
  Best Local Similarity 96.0%; Pred. No. 5.1e+02;
  Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTCG 25
Db 20 GCAAGTCGAACGGAAGGCCTTCG 44

RESULT 60
AY358002      450 bp      DNA      linear      BCT 19-AUG-2005
LOCUS          Actinobacterium iri117 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION      AY358002
VERSION        AY358002.1  GI:34500643
KEYWORDS       actinobacterium iri117
SOURCE         actinobacterium iri117
ORGANISM       Bacteria; Actinobacteria.
REFERENCE      1 (bases 1 to 450)
AUTHORS        Idris, R., Trifonova, R., Puschenreiter, M., Wenzel, W.W. and
              Sessitsch, A.
TITLE          Bacterial Communities Associated with Flowering Plants of the Ni
              Hyperaccumulator Thlaspi goesingense
JOURNAL        Appl. Environ. Microbiol. 70 (5), 2667-2677 (2004)
PUBMED         15128517
REFERENCE      2 (bases 1 to 450)
AUTHORS        Idris, R. and Sessitsch, A.
TITLE          Direct Submission
JOURNAL        Submitted (01-AUG-2003) Environmental and Life Sciences, ARC
              Seibersdorf Research GmbH, Seibersdorf A-2444, Austria
FEATURES       Location/Qualifiers
                source
                  1..450
                  /organism="Mycobacterium sp."
                  /mol_type="genomic DNA"
                  /isolate="BN737"
                  /db_xref="taxon:1785"
                  /map="E.coli 38-503"
                  1..450
                  /gene="16S rRNA"
                  <1..>450
                  /gene="16S rRNA"
                  /product="16S ribosomal RNA"
                gene
                rRNA

ORIGIN
  Query Match      93.6%; Score 23.4; DB 15; Length 450;
  Best Local Similarity 96.0%; Pred. No. 5.1e+02;
  Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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SOURCE	actinobacterium irIII6
ORGANISM	actinobacterium irIII6
REFERENCE	Bacteria; Actinobacteria.
AUTHORS	Ildis,R., Trifonova,R., Puschenreiter,M., Wenzel,W.W. and Sessitsch,A.
TITLE	Bacterial Communities Associated with Flowering Plants of the Ni Hyperaccumulator Thlaspi goeingense
JOURNAL	Appl. Environ. Microbiol. 70 (5), 2667-2677 (2004)
PUBLISHED	15128517
REFERENCE	2 (bases 1 to 456)
AUTHORS	Ildis,R. and Sessitsch,A.
TITLE	Direct Submission
JOURNAL	Submitted (01-AUG-2003) Environmental and Life Sciences, ARC Seibersdorf Research GmbH, Seibersdorf A-2444, Austria
FEATURES	Location/Qualifiers 1..456 /organism="actinobacterium irIII6" /mol_type="genomic DNA" /strain="irIII6" /db_xref="taxon:244181" <1..>456 /product="16S ribosomal RNA"
ORIGIN	
Query Match	93.6%; Score 23.4; DB 15; Length 456;
Best Local Similarity	96.0%; Pred.No. 5.1e+02;
Matches	24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 GCAGTCGAACGAAAGGCCTTTCG 25
Db	52 GCAAGTCGAACGAAAGGCCTTTCG 76
RESULT 63	
AJ609008	459 bp DNA linear ENV 20-JAN-2004
LOCUS	Uncultured bacterium partial 16S rRNA gene, clone 24-9.
DEFINITION	AJ609008
ACCESSION	AJ609008.1 GI:41033549
VERSION	ENV; 16S ribosomal RNA; 16S rRNA gene.
KEYWORDS	uncultured bacterium
SOURCE	uncultured bacterium
ORGANISM	Bacteria; environmental samples.
REFERENCE	1 Schneider,B.A., Huetl,R.F. and Schneider,B.U. Evidence for a diverse bacterial consortium specialized to the degradation of aliphatic and aromatic hydrocarbons in lignite matter of a forest reclamation site
AUTHORS	Unpublished
TITLE	2 (bases 1 to 459) Schneider,B.A.
JOURNAL	Direct Submission
REFERENCE	Submitted (20-NOV-2003) Schneider B.A., Soil Protection and Reclamation, Brandenburg Technical University, Theodor-Neubauer-Str. 6, D-03046 Cottbus, GERMANY
AUTHORS	Location/Qualifiers 1..459 /organism="uncultured bacterium" /mol_type="genomic DNA" /isolation_source="lignite matter from the subsurface soil of a 20 year old Black pine forest" /db_xref="taxon:77133" /clone="24-9" /environmental_sample /country="Germany:North-eastern Germany, Lusatian lignite mining area" 1..459 /gene="16S rRNA" <1..>459 /gene="16S rRNA" /product="16S ribosomal RNA"
TITLE	
JOURNAL	
gene	
rRNA	
ORIGIN	


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Query Match      93.6%; Score 23.4; DB 1; Length 459;
Best Local Similarity 96.0%; Pred. No. 5.1e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTTCG 25
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Db 8 GCAAGTCGAACGGTAAGGCGCTTTTCG 32
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RESULT 64
AY754884
LOCUS Mycobacterium vaccae strain FI04098 16S ribosomal RNA gene, partial
DEFINITION sequence.
ACCESSION AY754884
VERSION AY754884.1 GI:54065968
KEYWORDS
SOURCE Mycobacterium vaccae
ORGANISM Mycobacterium vaccae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 459)
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE Unusual mycobacteria isolated from clinical samples
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 459)
AUTHORS Tortoli,E.
DIRECT SUBMISSION
TITLE Submitted (16-SEP-2004) Microbiology, Careggi Hospital, viale
JOURNAL Morgagni 85, Firenze, FI 50134, Italy
LOCATION/Qualifiers
FEATURES
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/db_xref="taxon:1810"
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/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.6%; Score 23.4; DB 15; Length 459;
Best Local Similarity 96.0%; Pred. No. 5.1e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTTCG 25
|||||
Db 24 GCAAGTCGAACGGAAGGCGCTTTTCG 48
|||||

RESULT 65
AY754885
LOCUS Mycobacterium sp. FI02139 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION AY754885
VERSION AY754885.1 GI:54065976
KEYWORDS
SOURCE Mycobacterium sp. FI02139
ORGANISM Mycobacterium sp. FI02139
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 459)
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE Unusual mycobacteria isolated from clinical samples
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 459)
AUTHORS Tortoli,E.
DIRECT SUBMISSION
TITLE Submitted (16-SEP-2004) Microbiology, Careggi Hospital, viale
JOURNAL Morgagni 85, Firenze, FI 50134, Italy
LOCATION/Qualifiers
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/organism="Mycobacterium sp. FI02139"

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/product="16S ribosomal RNA"

rRNA

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Best Local Similarity 96.0%; Pred. No. 5.1e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTTCG 25
|||||
Db 23 GCAAGTCGAACGGAAGGCGCTTTTCG 47
|||||

RESULT 66
AB118817
LOCUS Denitrifying bacterium W67a gene for 16S ribosomal RNA, partial
DEFINITION sequence.
ACCESSION AB118817
VERSION AB118817.1 GI:66841148
KEYWORDS
SOURCE denitrifying bacterium W67a
ORGANISM denitrifying bacterium W67a
Bacteria; Actinobacteria.
REFERENCE 1
AUTHORS Hashimoto,T., Whang,K.S. and Nagaoka,K.
TITLE A Quantitative Evaluation and Phylogenetic Characterization of
Oligotrophic Denitrifying Bacteria Harbored in Subsurface Upland
Soil Using Improved Culturability
JOURNAL Biol. Fertil. Soils (2005) In press
REFERENCE 2 (bases 1 to 464)
AUTHORS Hashimoto,T. and Whang,K.
TITLE Direct Submission
JOURNAL Submitted (29-AUG-2003) Tomoyoshi Hashimoto, National Agricultural
Research Center for Kyushu Okinawa Region, Department of
Agro-Environmental Research; Nishigoushi-cho Suyu 2421,
Kikuchi-gun, Kumamoto, 861-1192, Japan
(E-mail:hashimoto@affrc.go.jp, Tel:0962427765, Fax:0962491002)
LOCATION/Qualifiers
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/organism="denitrifying bacterium W67a"
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rRNA

ORIGIN
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Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTTCG 25
|||||
Db 46 GCAAGTCGAACGGAAGGCGCTTTTCG 70
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RESULT 67
DQ142669
LOCUS Mycobacterium sp. FI03023 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION DQ142669
VERSION DQ142669.1 GI:71912648
KEYWORDS
SOURCE Mycobacterium sp. FI03023
ORGANISM Mycobacterium sp. FI03023
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 464)

```

AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE Unusual mycobacteria isolated from clinical specimens
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 464)
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE Direct Submission
JOURNAL Submitted (18-JUL-2005) Microbiology, Careggi Hospital, Viale Morgagni 85, Firenze, FI 50134, Italy
FEATURES
source
1. .464
/organism="Mycobacterium sp. FI03023"
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/db_xref="taxon:339672"
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Query Match 93.6%; Score 23.4; DB 15; Length 464;
Best Local Similarity 96.0%; Pred. No. 5.1e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
|||||
Db 23 GCAAGTCGAACGGAAGGCGCTTTCG 47
RESULT 68
DQ142672
LOCUS DQ142672 464 bp DNA linear BCT 13-AUG-2005
DEFINITION Mycobacterium sp. FI05244 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ142672
VERSION DQ142672.1 GI:71912651
KEYWORDS
SOURCE Mycobacterium sp. FI05244
ORGANISM Mycobacterium sp. FI05244
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE Unusual mycobacteria isolated from clinical specimens
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 464)
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE Direct Submission
JOURNAL Submitted (25-JUL-2005) Microbiology, Careggi Hospital, Viale Morgagni 85, Firenze, FI 50134, Italy
FEATURES
source
1. .464
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/strain="FI05244"
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/product="16S ribosomal RNA"
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Query Match 93.6%; Score 23.4; DB 15; Length 464;
Best Local Similarity 96.0%; Pred. No. 5.1e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
|||||
Db 23 GCAAGTCGAACGGAAGGCGCTTTCG 47
RESULT 69
DQ067465
LOCUS DQ067465 466 bp DNA linear BCT 05-JAN-2006
DEFINITION Mycobacterium sp. FI05038 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ067465
VERSION DQ067465.1 GI:67528030
KEYWORDS

SOURCE Mycobacterium sp. FI05038
ORGANISM Mycobacterium sp. FI05038
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS Tortoli,E., Mantella,A., Mariottini,A., Mazzarelli,G., Pecile,P., Rogasi,P.G., Sterrantino,G., Fantoni,E. and Leoncini,F.
TITLE Successfully treated spondylodiscitis due to a previously unreported mycobacterium
JOURNAL J. Med. Microbiol. 55 (PT 1), 119-121 (2006)
PUBMED 16388040
REFERENCE 2 (bases 1 to 466)
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE Direct Submission
JOURNAL Submitted (18-MAY-2005) Reg. Reference Center for Mycobacteria, Careggi Hospital, Piastra dei Servizi, Ospedale Careggi, v.le Morgagni 85, Firenze, FI 50134, Italy
FEATURES
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/organism="Mycobacterium sp. FI05038"
/mol_type="genomic DNA"
/strain="FI05038"
/db_xref="taxon:332012"
<1. .>466
/product="16S ribosomal RNA"
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Query Match 93.6%; Score 23.4; DB 15; Length 466;
Best Local Similarity 96.0%; Pred. No. 5.1e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
|||||
Db 27 GCAAGTCGAACGGAAGGCGCTTTCG 51
RESULT 70
AY524839
LOCUS AY524839 466 bp DNA linear BCT 03-FEB-2004
DEFINITION Mycobacterium sp. FI02027 16S ribosomal RNA gene, partial sequence.
ACCESSION AY524839
VERSION AY524839.1 GI:41387175
KEYWORDS
SOURCE Mycobacterium sp. FI02027
ORGANISM Mycobacterium sp. FI02027
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE Unusual mycobacteria isolated from clinical samples
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 466)
AUTHORS Tortoli,E.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-2004) Microbiology, Careggi Hospital, viale Morgagni 85, Firenze, FI 50134, Italy
FEATURES
source
1. .466
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ORIGIN
Query Match 93.6%; Score 23.4; DB 15; Length 466;
Best Local Similarity 96.0%; Pred. No. 5.1e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
|||||
Db 27 GCAAGTCGAACGGAAGGCGCTTTCG 51

[illegible]

partial sequence.	
ACCESSION	AY251205
VERSION	AY251205.1
KEYWORDS	GI:30027023
SOURCE	ENV.
ORGANISM	uncultured actinobacterium
REFERENCE	Bacteria: Actinobacteria; environmental samples.
AUTHORS	1 (bases 1 to 478)
TITLE	Vanbroekhoven,K.; Bastiaens,L., De mot,R. and Springael,D.
JOURNAL	Microbial community changes during different bioremediation strategies in diesel fuel-contaminated laboratory microcosms
REFERENCE	Unpublished
AUTHORS	2 (bases 1 to 478)
TITLE	Vanbroekhoven,K.; Bastiaens,L., De mot,R. and Springael,D.
JOURNAL	Direct Submission
FEATURES	Submitted (07-MAR-2003) Environmental Technology, Flemish Institut for Technological Research, Boeretang 200, Mol 2400, Belgium
source	Location/Qualifiers
	1..478
	/organism="uncultured actinobacterium"
	/mol_type="genomic DNA"
	/isolation_source="unfertilized soil"
	/db_xref="taxon:152507"
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	/environmental_sample
rRNA	<1..>478
	/product="16S ribosomal RNA"
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Query Match	93.6%; Score 23.4; DB 1; Length 478;
Best Local Similarity	96.0%; Pred. No. 5.1e+02;
Matches	24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy	1 GCAAGTCGAGCGGAAGGCGCTTCG 25
Dd	15 GCAAGTCGAGCGGAAGGCGCTTCG 39
RESULT 77	
MSP413603/c	
LOCUS	MSP413603 481 bp DNA linear BCT 06-JUN-2000
DEFINITION	Mycobacterium sp. dtb94 partial 16S rRNA gene, strain dtb94.
ACCESSION	AJ413603
VERSION	AJ413603.1
KEYWORDS	GI:16151371
SOURCE	16S ribosomal RNA; 16S rRNA gene.
ORGANISM	Mycobacterium sp. dtb94
REFERENCE	Mycobacterium sp. dtb94
AUTHORS	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
TITLE	Corynebacterineae; Mycobacteriaceae; Mycobacterium.
JOURNAL	1
REFERENCE	Oravec,O.
AUTHORS	Identification of cultured bacteria from the gut of the millipede
TITLE	Cylindrojulus boleti (Diplopoda)
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 481)
AUTHORS	Oravec,O.
TITLE	Direct Submission
JOURNAL	Submitted (26-SEP-2001) Oravec O., Dept. of Microbiology, Eotvos Lorand University, Pazmany Peter setany 1/C, H-1117, HUNGARY
FEATURES	Location/Qualifiers
source	1..481
	/organism="Mycobacterium sp. dtb94"
	/mol_type="genomic DNA"
	/strain="dtb94"
	/db_xref="taxon:172993"
	/country="Hungary"
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	/gene="16S rRNA"
rRNA	<1..481
	/gene="16S rRNA"
	/product="16S ribosomal RNA"

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Query Match      93.6%; Score 23.4; DB 15; Length 481;
Best Local Similarity 96.0%; Pred. No. 5, 1e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCCTTCG 25
    |||||
Db 432 GCAAGTCGAACGGAAGGCCCTTCG 408

RESULT 78
AY943206
LOCUS      495 bp DNA linear BCT 20-MAR-2005
DEFINITION Mycobacterium brisbanense strain CIP 107830 16S ribosomal RNA gene,
            partial sequence.
ACCESSION  AY943206
VERSION     AY943206.1 GI:61200493
KEYWORDS   .
SOURCE     Mycobacterium brisbanense
ORGANISM   Mycobacterium brisbanense
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE  1 (bases 1 to 495)
AUTHORS    Pichat,C. and Flandrois,J.P.
TITLE      Direct Submission
JOURNAL    Submitted (24-FEB-2005) Dynamique Des Populations Bacteriennes,
            Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
            Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
            Location/Qualifiers
FEATURES   source
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            /db_xref="taxon:146020"
            /note="type strain of Mycobacterium brisbanense"
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            /product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match      93.6%; Score 23.4; DB 15; Length 495;
Best Local Similarity 96.0%; Pred. No. 5e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCCTTCG 25
    |||||
Db 11 GCAAGTCGAACGGAAGGCCCTTCG 35

RESULT 79
DQ154344
LOCUS      496 bp DNA linear ENV 27-AUG-2005
DEFINITION Uncultured soil bacterium clone RFS-C14 16S ribosomal RNA gene,
            partial sequence.
ACCESSION  DQ154344
VERSION     DQ154344.1 GI:73672134
KEYWORDS   ENV.
SOURCE     uncultured soil bacterium
            uncultured soil bacterium
            Bacteria; environmental samples.
REFERENCE  1 (bases 1 to 496)
AUTHORS    Becker,J.M., Nakatsu,C.H., Turco,R.F. and Konopka,A.
TITLE      Low nutrient fluxes result in high cultivation efficiencies of soil
            bacteria
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 496)
AUTHORS    Becker,J.M., Nakatsu,C.H., Turco,R.F. and Konopka,A.
TITLE      Direct Submission
JOURNAL    Submitted (04-AUG-2005) Biological Sciences, Purdue University, 915
            West State Street, West Lafayette, IN 47907-2054, USA
            Location/Qualifiers
FEATURES   source
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            /isolation_source="Ross Forest soil"

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rRNA
/db_xref="taxon:164851"
/clone="RFS-C14"
/environmental_sample
<1..>496
/product="16S ribosomal RNA"

ORIGIN

Query Match      93.6%; Score 23.4; DB 1; Length 496;
Best Local Similarity 96.0%; Pred. No. 5e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCCTTCG 25
    |||||
Db 50 GCAAGTCGAACGGAAGGCCCTTCG 74

RESULT 80
AY215287
LOCUS      498 bp DNA linear BCT 08-APR-2003
DEFINITION Mycobacterium mucogenicum isolate N241 16S ribosomal RNA gene,
            partial sequence.
ACCESSION  AY215287
VERSION     AY215287.1 GI:28274541
KEYWORDS   .
SOURCE     Mycobacterium mucogenicum
ORGANISM   Mycobacterium mucogenicum
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE  1 (bases 1 to 498)
AUTHORS    Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
TITLE      Evaluation of the MicroSeq System for Identification of
            Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
            into a Routine Clinical Mycobacteriology Laboratory
            J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
            12682128
REFERENCE  2 (bases 1 to 498)
AUTHORS    Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.
TITLE      Direct Submission
JOURNAL    Submitted (08-JAN-2003) Department of Laboratory Medicine and
            Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
            Location/Qualifiers
FEATURES   source
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            /organism="Mycobacterium mucogenicum"
            /mol_type="genomic DNA"
            /isolate="N241"
            /db_xref="taxon:56689"
            <1..>498
            /product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match      93.6%; Score 23.4; DB 15; Length 498;
Best Local Similarity 96.0%; Pred. No. 5e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCCTTCG 25
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Db 53 GCAAGTCGAACGGAAGGCCCTTCG 77

RESULT 81
AY215324
LOCUS      498 bp DNA linear BCT 08-APR-2003
DEFINITION Mycobacterium sp. N141 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY215324
VERSION     AY215324.1 GI:28274578
KEYWORDS   .
SOURCE     Mycobacterium sp. N141
ORGANISM   Mycobacterium sp. N141
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE  1 (bases 1 to 498)
AUTHORS    Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
TITLE      Evaluation of the MicroSeq System for Identification of

```

Mycobacteria by 16S Ribosomal DNA Sequencing and its Integration into a Routine Clinical Mycobacteriology Laboratory
J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
12682128
2 (bases 1 to 498)
Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.
Direct Submission
Submitted (08-JAN-2003) Department of Laboratory Medicine and Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
Location/Qualifiers

FEATURES

source
1..498
/organism="Mycobacterium sp. N141"
/mol_type="genomic DNA"
/isolate="N141"
/db_xref="taxon:220003"
<1..>498
/product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match 93.6%; Score 23.4; DB 15; Length 498;
Best Local Similarity 96.0%; Pred. No. 5e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GCAAGTCGAACGGAAGGCGCTTCG 25

Db 53 GCAAGTCGAACGGAAGGCGCTTCG 77

RESULT 82

AY215336

LOCUS
Mycobacterium sp. N1772T 498 bp DNA linear BCT 08-APR-2003
Mycobacterium sp. N1772T 16S ribosomal RNA gene, partial sequence.

ACCESSION

AY215336

VERSION

AY215336.1 GI:28274590

KEYWORDS

SOURCE

ORGANISM

Mycobacterium sp. N1772T

Mycobacterium sp. N1772T

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

Corynebacterineae; Mycobacteriaceae; Mycobacterium.

1 (bases 1 to 498)

Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.

Evaluation of the MicroSeq System for Identification of

Mycobacteria by 16S Ribosomal DNA Sequencing and its Integration

into a Routine Clinical Mycobacteriology Laboratory

J. Clin. Microbiol. 41 (4), 1447-1453 (2003)

12682128

2 (bases 1 to 498)

Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.

Direct Submission

Submitted (08-JAN-2003) Department of Laboratory Medicine and

Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA

Location/Qualifiers

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/organism="Mycobacterium sp. N1772T"

/mol_type="genomic DNA"

/isolate="N1772T"

/db_xref="taxon:220014"

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/product="16S ribosomal RNA"

source

Query Match 93.6%; Score 23.4; DB 15; Length 498;

Best Local Similarity 96.0%; Pred. No. 5e+02;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GCAAGTCGAACGGAAGGCGCTTCG 25

Db 53 GCAAGTCGAACGGAAGGCGCTTCG 77

RESULT 83

DQ154566

LOCUS

Mycobacterium sp. N1772T 499 bp DNA linear ENV 27-AUG-2005

Uncultured soil bacterium clone RFS-C252 16S ribosomal RNA gene, partial sequence.

ACCESSION DQ154566

VERSION DQ154566.1 GI:73672356

KEYWORDS ENV.

SOURCE uncultured soil bacterium

ORGANISM uncultured soil bacterium

REFERENCE 1 (bases 1 to 499)

Bacteria; environmental samples.

AUTHORS Becker,J.M., Nakatsu,C.H., Turco,R.F. and Konopka,A.

TITLE Low nutrient fluxes result in high cultivation efficiencies of soil

journal bacterium

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 499)

Becker,J.M., Nakatsu,C.H., Turco,R.F. and Konopka,A.

AUTHORS Direct Submission

TITLE Submitted (04-AUG-2005) Biological Sciences, Purdue University, 915

JOURNAL West State Street, West Lafayette, IN 47907-2054, USA

Location/Qualifiers

1..499

/organism="uncultured soil bacterium"

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/isolation_source="Ross Forest soil"

/db_xref="taxon:164851"

/clone="RFS-C252"

/environmental_sample

<1..>499

/product="16S ribosomal RNA"

source

Query Match 93.6%; Score 23.4; DB 1; Length 499;

Best Local Similarity 96.0%; Pred. No. 5e+02;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GCAAGTCGAACGGAAGGCGCTTCG 25

Db 50 GCAAGTCGAACGGAAGGCGCTTCG 74

RESULT 84

DQ154328

LOCUS

Soil bacterium RFS-I117 499 bp DNA linear BCT 27-AUG-2005

Soil bacterium RFS-I117 16S ribosomal RNA gene, partial sequence.

ACCESSION DQ154328

VERSION DQ154328.1 GI:73672118

KEYWORDS

soil bacterium RFS-I117

soil bacterium RFS-I117

Bacteria.

REFERENCE 1 (bases 1 to 499)

Becker,J.M., Nakatsu,C.H., Turco,R.F. and Konopka,A.

Low nutrient fluxes result in high cultivation efficiencies of soil

bacteria

unpublished

JOURNAL 2 (bases 1 to 499)

Becker,J.M., Nakatsu,C.H., Turco,R.F. and Konopka,A.

AUTHORS Direct Submission

TITLE Submitted (03-AUG-2005) Biological Sciences, Purdue University, 915

JOURNAL West State Street, West Lafayette, IN 47907-2054, USA

Location/Qualifiers

1..499

/organism="soil bacterium RFS-I117"

/mol_type="genomic DNA"

/isolate="RFS-I117"

/isolation_source="Ross Forest soil"

/db_xref="taxon:341511"

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/product="16S ribosomal RNA"

source

Query Match 93.6%; Score 23.4; DB 15; Length 499;

Best Local Similarity 96.0%; Pred. No. 5e+02;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 GCAAGTCGAACGGAAGGCCTTTCG 25
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/mol_type="genomic DNA"
/db_xref="taxon:83097"
/clone="WR169"
/note="RT-PCR amplification of 16S ribosomal RNA from soil"
1. .500
/product="16S ribosomal RNA"

RESULT 85
AY215236 499 bp DNA linear BCT 08-APR-2003
LOCUS Mycobacterium abscessus isolate N418 16S ribosomal RNA gene, partial sequence.
ACCESSION AY215236
VERSION AY215236.1 GI:28274490
SOURCE Mycobacterium abscessus
ORGANISM Mycobacterium abscessus
REFERENCE 1 (bases 1 to 499)
AUTHORS Hall, L., Doerr, K.A., Wohlfiel, S.L. and Roberts, G.D.
TITLE Evaluation of the MicroSeq System for identification of Mycobacteria by 16S Ribosomal DNA Sequencing and its Integration into a Routine Clinical Mycobacteriology Laboratory
J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
JOURNAL 12682128
PUBMED 12682128
REFERENCE 2 (bases 1 to 499)
AUTHORS Roberts, G.D., Hall, L., Doerr, K.A. and Wohlfiel, S.L.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-2003) Department of Laboratory Medicine and Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
FEATURES Location/Qualifiers
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/organism="Mycobacterium abscessus"
/mol_type="genomic DNA"
/isolate="N418"
/db_xref="taxon:36809"
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/product="16S ribosomal RNA"

rRNA

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Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTCG 25
Db 53 GCAAGTCGAACGGAAGGCCTTTCG 77

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/clone="WR169"
/note="RT-PCR amplification of 16S ribosomal RNA from soil"
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/product="16S ribosomal RNA"

RESULT 87
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LOCUS Mycobacterium rhodesiae strain K1 16S ribosomal RNA gene, partial sequence.
ACCESSION AF498660
VERSION AF498660.1 GI:21686167
KEYWORDS Mycobacterium rhodesiae
SOURCE Mycobacterium rhodesiae
ORGANISM Mycobacterium rhodesiae
REFERENCE 1 (bases 1 to 500)
AUTHORS Coleman, N.V., Mattes, T.E., Gossett, J.M. and Spain, J.C.
TITLE Phylogenetic and kinetic diversity of aerobic vinyl chloride-assimilating bacteria from contaminated sites
Appl. Environ. Microbiol. 68 (12), 6162-6171 (2002)
JOURNAL 13450841
PUBMED 13450841
REFERENCE 2 (bases 1 to 500)
AUTHORS Coleman, N.V.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2002) Air Force Research Laboratory - MLOI, Building 1117, 139 Barnes Dr., Tyndall AFB, FL 32403, USA
FEATURES Location/Qualifiers
source 1. .500
/organism="Mycobacterium rhodesiae"
/mol_type="genomic DNA"
/strain="K1"
/db_xref="taxon:36814"
/note="biodegrades the groundwater pollutant vinyl chloride"
<1. .>500
/product="16S ribosomal RNA"

rRNA

ORIGIN
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Qy 1 GCAAGTCGAACGGAAGGCCTTTCG 25
Db 53 GCAAGTCGAACGGAAGGCCTTTCG 77

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/db_xref="taxon:36814"
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/product="16S ribosomal RNA"

RESULT 88
AF498661 500 bp DNA linear BCT 02-DEC-2002
LOCUS Mycobacterium rhodesiae strain TM1 16S ribosomal RNA gene, partial sequence.
ACCESSION AF498661
VERSION AF498661.1 GI:21686168
KEYWORDS Mycobacterium rhodesiae
SOURCE Mycobacterium rhodesiae
ORGANISM Mycobacterium rhodesiae
FEATURES Location/Qualifiers
source 1. .500

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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 500)
AUTHORS Coleman,N.V., Mattes,T.E., Gossett,J.M. and Spain,J.C.
TITLE Phylogenetic and kinetic diversity of aerobic vinyl
chloride-assimilating bacteria from contaminated sites
JOURNAL Appl. Environ. Microbiol. 68 (12), 6162-6171 (2002)
PUBMED 12450841
REFERENCE 2 (bases 1 to 500)
AUTHORS Coleman,N.V.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2002) Air Force Research Laboratory - MLQL,
Building 1117, 139 Barnes Dr., Tyndall AFB, FL 32403, USA
FEATURES
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                /note="Biodegrades the groundwater pollutant vinyl
                chloride"
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Qy 1 GCAAGTCGACGGAAGGCCCTTCG 25
    |||||
Db 53 GCAAGTCGACGGAAGGCCCTTCG 77

RESULT 89
AY162027
LOCUS Mycobacterium rhodesiae 500 bp DNA linear BCT 01-OCT-2003
DEFINITION Mycobacterium rhodesiae 16S ribosomal RNA gene, partial sequence.
ACCESSION AY162027
VERSION AY162027.1 GI:24850312
KEYWORDS
SOURCE
ORGANISM
    Mycobacterium rhodesiae
    Bacteria; Actinobacteridae; Actinobacteriaceae; Actinomycetales;
    Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 500)
AUTHORS Coleman,N.V. and Spain,J.C.
TITLE Distribution of the Coenzyme M Pathway of Epoxide Metabolism among
Ethene- and Vinyl Chloride-Degrading Mycobacterium Strains
JOURNAL Appl. Environ. Microbiol. 69 (10), 6041-6046 (2003)
AUTHORS Coleman,N.V. and Henley,C.M.
TITLE Direct Submission
JOURNAL Submitted (10-OCT-2002) Air Force Research Laboratory - MLQL,
Building 1117, 139 Barnes Dr., Tyndall AFB, FL 32403, USA
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    Best Local Similarity 96.0%; Pred. No. 5e+02;
    Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCCTTCG 25
    |||||
Db 53 GCAAGTCGACGGAAGGCCCTTCG 77

RESULT 91
AY215218
LOCUS Mycobacterium sp. N661 500 bp DNA linear BCT 08-APR-2003
DEFINITION Mycobacterium sp. N661 16S ribosomal RNA gene, partial sequence.
ACCESSION AY215218
VERSION AY215218.1 GI:28274472
KEYWORDS
SOURCE
ORGANISM
    Mycobacterium sp. N661
    Bacteria; Actinobacteridae; Actinobacteriaceae; Actinomycetales;
    Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
    avium complex (MAC).
REFERENCE 1 (bases 1 to 500)
AUTHORS Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
TITLE Evaluation of the MicroSeq System for Identification of
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
into a Routine Clinical Mycobacteriology Laboratory
JOURNAL J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
PUBMED 12682128
REFERENCE 2 (bases 1 to 500)
AUTHORS Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-2003) Department of Laboratory Medicine and
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
FEATURES
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    rRNA

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RESULT 90
AY162030
LOCUS Mycobacterium mageritense 500 bp DNA linear BCT 01-OCT-2003
DEFINITION Mycobacterium mageritense 16S ribosomal RNA gene, partial sequence.
ACCESSION AY162030
VERSION AY162030.1 GI:24850315
KEYWORDS
SOURCE
ORGANISM
    Mycobacterium mageritense
    Bacteria; Actinobacteridae; Actinobacteriaceae; Actinomycetales;
    Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 500)
AUTHORS Coleman,N.V. and Spain,J.C.
TITLE Distribution of the Coenzyme M Pathway of Epoxide Metabolism among
Ethene- and Vinyl Chloride-Degrading Mycobacterium Strains
JOURNAL Appl. Environ. Microbiol. 69 (10), 6041-6046 (2003)
AUTHORS Coleman,N.V. and Henley,C.M.
TITLE Direct Submission
JOURNAL Submitted (10-OCT-2002) Air Force Research Laboratory - MLQL,
Building 1117, 139 Barnes Dr., Tyndall AFB, FL 32403, USA
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                <1..>500
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    Best Local Similarity 96.0%; Pred. No. 5e+02;
    Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCCTTCG 25
    |||||
Db 53 GCAAGTCGACGGAAGGCCCTTCG 77

RESULT 91
AY215218
LOCUS Mycobacterium sp. N661 500 bp DNA linear BCT 08-APR-2003
DEFINITION Mycobacterium sp. N661 16S ribosomal RNA gene, partial sequence.
ACCESSION AY215218
VERSION AY215218.1 GI:28274472
KEYWORDS
SOURCE
ORGANISM
    Mycobacterium sp. N661
    Bacteria; Actinobacteridae; Actinobacteriaceae; Actinomycetales;
    Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
    avium complex (MAC).
REFERENCE 1 (bases 1 to 500)
AUTHORS Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
TITLE Evaluation of the MicroSeq System for Identification of
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
into a Routine Clinical Mycobacteriology Laboratory
JOURNAL J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
PUBMED 12682128
REFERENCE 2 (bases 1 to 500)
AUTHORS Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-2003) Department of Laboratory Medicine and
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
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ORIGIN
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Best Local Similarity 96.0%; Pred. No. 5e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
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Db 53 GCAAGTCGAACGGAAGGCGCTTTCG 77

RESULT 92
AV215228      500 bp      DNA      linear      BCT 08-APR-2003
LOCUS      Mycobacterium sp. N110 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION      AY215228
VERSION      AY215228.1 GI:28274482
KEYWORDS
SOURCE      Mycobacterium sp. N110
ORGANISM      Mycobacterium sp. N110
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS      Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
TITLE      Evaluation of the MicroSeq System for Identification of
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
into a Routine Clinical Mycobacteriology Laboratory
J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
JOURNAL
PUBMED      12682128
REFERENCE
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/product="16S ribosomal RNA"

rRNA

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Query Match      93.6%; Score 23.4; DB 15; Length 500;
Best Local Similarity 96.0%; Pred. No. 5e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
    |||
Db 53 GCAAGTCGAACGGAAGGCGCTTTCG 77

RESULT 93
AV215234      500 bp      DNA      linear      BCT 08-APR-2003
LOCUS      Mycobacterium abscessus isolate N019 16S ribosomal RNA gene,
partial sequence.
DEFINITION
ACCESSION      AY215234
VERSION      AY215234.1 GI:28274488
KEYWORDS
SOURCE      Mycobacterium abscessus
ORGANISM      Mycobacterium abscessus
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
1 (bases 1 to 500)
Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
AUTHORS
TITLE      Evaluation of the MicroSeq System for Identification of
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
into a Routine Clinical Mycobacteriology Laboratory
J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
JOURNAL
PUBMED      12682128

ORIGIN
Query Match      93.6%; Score 23.4; DB 15; Length 500;
Best Local Similarity 96.0%; Pred. No. 5e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
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Db 53 GCAAGTCGAACGGAAGGCGCTTTCG 77

RESULT 94
AV215235      500 bp      DNA      linear      BCT 08-APR-2003
LOCUS      Mycobacterium abscessus isolate N416 16S ribosomal RNA gene,
partial sequence.
DEFINITION
ACCESSION      AY215235
VERSION      AY215235.1 GI:28274489
KEYWORDS
SOURCE      Mycobacterium abscessus
ORGANISM      Mycobacterium abscessus
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
1 (bases 1 to 500)
Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
AUTHORS
TITLE      Evaluation of the MicroSeq System for Identification of
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
into a Routine Clinical Mycobacteriology Laboratory
J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
JOURNAL
PUBMED      12682128
REFERENCE
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/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.6%; Score 23.4; DB 15; Length 500;
Best Local Similarity 96.0%; Pred. No. 5e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
    |||
Db 53 GCAAGTCGAACGGAAGGCGCTTTCG 77

RESULT 95
AV215237      500 bp      DNA      linear      BCT 08-APR-2003
LOCUS      Mycobacterium sp. N570 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION      AY215237
VERSION      AY215237.1 GI:28274491
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KEYWORDS
SOURCE Mycobacterium sp. N570
ORGANISM Mycobacterium sp. N570
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS Hall, L., Doerr, K.A., Wohlfiel, S.L. and Roberts, G.D.
TITLE Evaluation of the MicroSeq System for Identification of
 Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
 into a Routine Clinical Mycobacteriology Laboratory
JOURNAL J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
PUBMED 12682128
REFERENCE 2 (bases 1 to 500)
AUTHORS Roberts, G.D., Hall, L., Doerr, K.A. and Wohlfiel, S.L.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-2003) Department of Laboratory Medicine and
 Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
FEATURES
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 /note="Mycobacterium cf. chelonae"
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 /product="16S ribosomal RNA"
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 Qy 1 GCAAGTCGACGAAAGGCGCTTCG 25
 Db 54 GCAAGTCGACGAAAGGCGCTTCG 78
 RESULT 96
 AY215245 500 bp DNA linear BCT 08-APR-2003
LOCUS Mycobacterium fortuitum isolate 6841A 16S ribosomal RNA gene,
 partial sequence.
DEFINITION
ACCESSION AY215245
VERSION AY215245.1 GI:28274499
KEYWORDS
SOURCE Mycobacterium fortuitum
ORGANISM Mycobacterium fortuitum
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS Hall, L., Doerr, K.A., Wohlfiel, S.L. and Roberts, G.D.
TITLE Evaluation of the MicroSeq System for Identification of
 Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
 into a Routine Clinical Mycobacteriology Laboratory
JOURNAL J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
PUBMED 12682128
REFERENCE 2 (bases 1 to 500)
AUTHORS Roberts, G.D., Hall, L., Doerr, K.A. and Wohlfiel, S.L.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-2003) Department of Laboratory Medicine and
 Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
FEATURES
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rRNA
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 Best Local Similarity 96.0%; Pred. No. 5e+02;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GCAAGTCGACGAAAGGCGCTTCG 25
 Db 54 GCAAGTCGACGAAAGGCGCTTCG 78

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GCAAGTCGACGAAAGGCGCTTCG 25
 Db 53 GCAAGTCGACGAAAGGCGCTTCG 77
 RESULT 97
 AY215247 500 bp DNA linear BCT 08-APR-2003
LOCUS Mycobacterium fortuitum isolate N419 16S ribosomal RNA gene,
 partial sequence.
DEFINITION
ACCESSION AY215247
VERSION AY215247.1 GI:28274501
KEYWORDS
SOURCE Mycobacterium fortuitum
ORGANISM Mycobacterium fortuitum
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS Hall, L., Doerr, K.A., Wohlfiel, S.L. and Roberts, G.D.
TITLE Evaluation of the MicroSeq System for Identification of
 Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
 into a Routine Clinical Mycobacteriology Laboratory
JOURNAL J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
PUBMED 12682128
REFERENCE 2 (bases 1 to 500)
AUTHORS Roberts, G.D., Hall, L., Doerr, K.A. and Wohlfiel, S.L.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-2003) Department of Laboratory Medicine and
 Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
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rRNA
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 Query Match 93.6%; Score 23.4; DB 15; Length 500;
 Best Local Similarity 96.0%; Pred. No. 5e+02;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GCAAGTCGACGAAAGGCGCTTCG 25
 Db 53 GCAAGTCGACGAAAGGCGCTTCG 77
 RESULT 98
 AY215251 500 bp DNA linear BCT 08-APR-2003
LOCUS Mycobacterium sp. N665
DEFINITION Mycobacterium sp. N665
ACCESSION AY215251
VERSION AY215251.1 GI:28274505
KEYWORDS
SOURCE Mycobacterium sp. N665
ORGANISM Mycobacterium sp. N665
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS Hall, L., Doerr, K.A., Wohlfiel, S.L. and Roberts, G.D.
TITLE Evaluation of the MicroSeq System for Identification of
 Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
 into a Routine Clinical Mycobacteriology Laboratory
JOURNAL J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
PUBMED 12682128
REFERENCE 2 (bases 1 to 500)
AUTHORS Roberts, G.D., Hall, L., Doerr, K.A. and Wohlfiel, S.L.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-2003) Department of Laboratory Medicine and
 Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA

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FEATURES             Location/Qualifiers
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                             peregrinum"
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                             /product="16S ribosomal RNA"

ORIGIN
Query Match               93.6%;   Score 23.4;   DB 15;   Length 500;
Best Local Similarity     96.0%;   Pred. No. 5e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy  1  GCAAGTCGACGGAAGGCCCTTTCG 25
      |||||
Db    53  GCAAGTCGACGGAAGGCCCTTCG 77

RESULT 99
AY215252
LOCUS               500 bp      DNA      linear      BCT 08-APR-2003
DEFINITION          Mycobacterium sp. N667 16S ribosomal RNA gene, partial sequence.
ACCESSION            AY215252
VERSION              AY215252.1  GI:28274506
KEYWORDS
SOURCE
ORGANISM             Mycobacterium sp. N667
                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                     Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS              Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
                     Evaluation of the MicroSeq System for Identification of
                     Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
                     into a Routine Clinical Mycobacteriology Laboratory
                     J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
JOURNAL              12682128
PUBMED
REFERENCE
AUTHORS              Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.
                     Direct Submission
                     Submitted (08-JAN-2003) Department of Laboratory Medicine and
                     Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
JOURNAL              Location/Qualifiers
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                     /product="16S ribosomal RNA"

     rRNA
ORIGIN
Query Match               93.6%;   Score 23.4;   DB 15;   Length 500;
Best Local Similarity     96.0%;   Pred. No. 5e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy  1  GCAAGTCGACGGAAGGCCCTTTCG 25
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Db    53  GCAAGTCGACGGAAGGCCCTTCG 77

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ORIGIN
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Best Local Similarity     96.0%;   Pred. No. 5e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy  1  GCAAGTCGACGGAAGGCCCTTTCG 25
      |||||
Db    53  GCAAGTCGACGGAAGGCCCTTCG 77

RESULT 100
AY215266
LOCUS               500 bp      DNA      linear      BCT 08-APR-2003
DEFINITION          Mycobacterium immunogenum 16S ribosomal RNA gene, partial sequence.
ACCESSION            AY215266
VERSION              AY215266.1  GI:28274520
KEYWORDS
SOURCE
ORGANISM             Mycobacterium immunogenum

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ORGANISM               Mycobacterium immunogenum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS              Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
                     Evaluation of the MicroSeq System for Identification of
                     Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
                     into a Routine Clinical Mycobacteriology Laboratory
                     J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
JOURNAL              12682128
PUBMED
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AUTHORS              Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.
                     Direct Submission
                     Submitted (08-JAN-2003) Department of Laboratory Medicine and
                     Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
JOURNAL              Location/Qualifiers
FEATURES             source
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                     /product="16S ribosomal RNA"

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Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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      |||||
Db    53  GCAAGTCGACGGAAGGCCCTTCG 77

Search completed: May 19, 2006, 04:00:15
Job time : 880.946 secs

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 02:23:06 ; Search time 838.988 Seconds
(without alignments)
1829.273 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

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15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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271 22.4 93.3 1428 15 MG16RRNA
272 22.4 93.3 1428 15 MSBB116SR
273 22.4 93.3 1429 15 AB010912 Mycobacte
274 22.4 93.3 1430 15 AF408984 Mycobacte
275 22.4 93.3 1432 15 DQ372735 Mycobacte
276 22.4 93.3 1433 15 DQ370009 Mycobacte
277 22.4 93.3 1433 15 AY255478 Mycobacte
278 22.4 93.3 1435 15 AF480585 Mycobacte
279 22.4 93.3 1438 15 DQ372733 Mycobacte
280 22.4 93.3 1439 15 AF480591 Mycobacte
281 22.4 93.3 1440 15 DQ372728 Mycobacte
282 22.4 93.3 1440 15 AF130308 Mycobacte
283 22.4 93.3 1440 15 AY012579 Mycobacte
284 22.4 93.3 1440 15 AY436799 Mycobacte
285 22.4 93.3 1441 15 AF480592 Mycobacte
286 22.4 93.3 1441 15 AF480594 Mycobacte
287 22.4 93.3 1441 15 AY337605 Mycobacte
288 22.4 93.3 1442 15 MSP245702 Mycobacte
289 22.4 93.3 1442 15 MSP245704 Mycobacte
290 22.4 93.3 1444 15 MSU90876 Mycobacteri
291 22.4 93.3 1446 15 RS16SRNA2
292 22.4 93.3 1446 15 AF480587 Mycobacte
293 22.4 93.3 1447 15 MSU90877 Mycobacteri
294 22.4 93.3 1448 15 DQ372731 Mycobacte
295 22.4 93.3 1448 15 DQ372732 Mycobacte
296 22.4 93.3 1448 15 MCH16SRN
297 22.4 93.3 1449 15 AF480582 Mycobacte
298 22.4 93.3 1449 15 MFO16SRN
299 22.4 93.3 1450 15 MSY15709 Mycobacteri
300 22.4 93.3 1450 15

ALIGNMENTS

RESULT 1
AR438654
LOCUS AR438654 linear PAT 20-FEB-2004
DEFINITION Sequence 22 from patent US 6664081.
ACCESSION AR438654

VERSION AR438654.1 GI:42663578
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 24)
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
Rodrigue,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: US 6664081-A 22 16-DEC-2003;
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA
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location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
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Db 1 CAAGTCGAACGGAAGGCGCTTTCG 24
RESULT 2
AX166856 24 bp DNA linear PAT 04-JUL-2001
LOCUS AX166856
DEFINITION Sequence 22 from Patent WO0144510.
ACCESSION AX166856
VERSION AX166856.1 GI:14596459
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
Rodrigue,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: WO 0144510-A 22 21-JUN-2001;
Gen-Probe Incorporated (US); Biomerieux S.A. (FR)
FEATURES
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location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer oligonucleotide"
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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
|||||
Db 1 CAAGTCGAACGGAAGGCGCTTTCG 24
RESULT 3
AR438653 25 bp DNA linear PAT 20-FEB-2004
LOCUS AR438653
DEFINITION Sequence 21 from patent US 6664081.
ACCESSION AR438653
VERSION AR438653.1 GI:42663577
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
Rodrigue,M.
TITLE Nucleic acid amplification and detection of mycobacterium species

JOURNAL Patent: US 6664081-A 21 16-DEC-2003;
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA

FEATURES
source
Location/Qualifiers
1. .25
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 24; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTTCG 24
|||||
Db 2 CAAGTCGAACGGAAGGCGCTTTTCG 25
|||||

RESULT 4
AX166855
LOCUS AX166855 25 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 21 from Patent WO0144510.
ACCESSION AX166855
VERSION AX166855.1 GI:14596458
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and Rodrigue,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: WO 0144510-A 21 21-JUN-2001;
Gen-Probe Incorporated (US); Biomerieux S.A. (FR)

FEATURES
source
Location/Qualifiers
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer oligonucleotide"

ORIGIN
Query Match 100.0%; Score 24; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTTCG 24
|||||
Db 2 CAAGTCGAACGGAAGGCGCTTTTCG 25
|||||

RESULT 5
AF547926
LOCUS AF547926 541 bp DNA linear BCT 24-JAN-2006
DEFINITION Mycobacterium gadium strain CIP 105388 16S ribosomal RNA gene, partial sequence.
ACCESSION AF547926
VERSION AF547926.1 GI:27733750
KEYWORDS
SOURCE
ORGANISM
Mycobacterium gadium
Mycobacterium gadium
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 541)
Devulder,G., de Montclos,M.P. and Flandrois,J.P.
A multigenic approach to phylogenetic analysis using the genus Mycobacterium as a model
Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
15653890
PUBMED
REFERENCE 2 (bases 1 to 541)
AUTHORS Devulder,G., Pichat,C. and Flandrois,J.P.
TITLE Direct Submission
JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes, Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,

JOURNAL Patent: US 6664081-A 21 16-DEC-2003;
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA

FEATURES
source
Location/Qualifiers
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/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 24; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTTCG 24
|||||
Db 2 CAAGTCGAACGGAAGGCGCTTTTCG 25
|||||

RESULT 4
AX166855
LOCUS AX166855 25 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 21 from Patent WO0144510.
ACCESSION AX166855
VERSION AX166855.1 GI:14596458
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and Rodrigue,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: WO 0144510-A 21 21-JUN-2001;
Gen-Probe Incorporated (US); Biomerieux S.A. (FR)

FEATURES
source
Location/Qualifiers
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer oligonucleotide"

ORIGIN
Query Match 100.0%; Score 24; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTTCG 24
|||||
Db 2 CAAGTCGAACGGAAGGCGCTTTTCG 25
|||||

RESULT 5
AF547926
LOCUS AF547926 541 bp DNA linear BCT 24-JAN-2006
DEFINITION Mycobacterium gadium strain CIP 105388 16S ribosomal RNA gene, partial sequence.
ACCESSION AF547926
VERSION AF547926.1 GI:27733750
KEYWORDS
SOURCE
ORGANISM
Mycobacterium gadium
Mycobacterium gadium
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 541)
Devulder,G., de Montclos,M.P. and Flandrois,J.P.
A multigenic approach to phylogenetic analysis using the genus Mycobacterium as a model
Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
15653890
PUBMED
REFERENCE 2 (bases 1 to 541)
AUTHORS Devulder,G., Pichat,C. and Flandrois,J.P.
TITLE Direct Submission
JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes, Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,

Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

FEATURES
source
Location/Qualifiers
1. .541
/organism="Mycobacterium gadium"
/mol_type="genomic DNA"
/strain="CIP 105388"
/db_xref="taxon:1794"
/note="type strain of Mycobacterium gadium"
<1. .541
/product="16S ribosomal RNA"

ORIGIN
Query Match 100.0%; Score 24; DB 15; Length 541;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTTCG 24
|||||
Db 15 CAAGTCGAACGGAAGGCGCTTTTCG 38
|||||

RESULT 6
MGAD16S
LOCUS MGAD16S 1456 bp DNA linear BCT 06-JUN-2003
DEFINITION M.gadium 16S ribosomal RNA, part.
ACCESSION X55594
VERSION X55594.1 GI:44291
KEYWORDS
SOURCE
ORGANISM
Mycobacterium gadium
Mycobacterium gadium
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 1456)
Pitulle,C., Dorsch,M., Kazda,J., Wolters,J. and Stackebrandt,E.
Phylogeny of rapidly growing members of the genus Mycobacterium
Int. J. Syst. Bacteriol. 42 (3), 337-343 (1992)
1380284
PUBMED
REFERENCE 2 (bases 1 to 1456)
AUTHORS Wolters,J.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-1990) Wolters J., Institut fuer Allgemeine Mikrobiologie der Universitaet, Biologiezentrum, Am Botanischen Garten 1-9, 2300 Kiel 1

FEATURES
source
Location/Qualifiers
1. .1456
/organism="Mycobacterium gadium"
/mol_type="genomic DNA"
/strain="ATCC 27726"
/db_xref="taxon:1794"
1. _>1456
/product="16S ribosomal RNA"

ORIGIN
Query Match 100.0%; Score 24; DB 15; Length 1456;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTTCG 24
|||||
Db 59 CAAGTCGAACGGAAGGCGCTTTTCG 82
|||||

RESULT 7
MCO16S
LOCUS MCO16S 1459 bp DNA linear BCT 11-JUN-2003
DEFINITION Mycobacterium cookii partial 16S rRNA.
ACCESSION X53896
VERSION X53896.1 GI:44201
KEYWORDS
SOURCE
ORGANISM
Mycobacterium cookii
Mycobacterium cookii
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

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REFERENCE 1 (bases 1 to 1225)
AUTHORS Kazda,J., Stackebrandt,E., Smida,J., Minnikin,D.E., Daffe,M.,
          Parlett,J.H. and Piuille,C.
TITLE    Mycobacterium cookii sp. nov
JOURNAL  Int.J. Syst. Bacteriol. 40 (3), 217-223 (1990)
PUBMED   1697763
REFERENCE 2 (bases 1 to 1459)
AUTHORS Stackebrandt,E.
TITLE    Direct Submission
JOURNAL  Submitted (01-AUG-1990) Stackebrandt E
FEATURES
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            1..1459
                /organism="Mycobacterium cookii"
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                /db_xref="taxon:1775"
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            /product="16S ribosomal RNA"

ORIGIN
Query Match      100.0%; Score 24; DB 15; Length 1459;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTTCG 24
Db 59 CAACTCGAACGGAAGGCGCTTTTCG 82

RESULT 8
MSGRGDSA
LOCUS    Mycobacterium celatum 1460 bp DNA linear BCT 21-SEP-1993
ACCESSION L08169
VERSION   L08169.1 GI:293249
KEYWORDS  16S ribosomal RNA
SOURCE    Mycobacterium celatum
ORGANISM  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1 (bases 1 to 1460)
AUTHORS Butler,W.R., O'Connor,S.P., Yakrus,M.A., Smithwick,R.W.,
          Plikaytis,B.B., Moss,C.W., Floyd,M.M., Woodley,C.L., Kilburn,J.O.,
          Vadney,F.S. and Gross,W.M.
TITLE    Mycobacterium celatum sp. nov
JOURNAL  Int. J. Syst. Bacteriol. 43 (3), 539-548 (1993)
PUBMED   8102246
COMMENT   Original source text: Mycobacterium celatum (library: ATCC 51131)
          DNA.
FEATURES
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        Location/Qualifiers
            1..1460
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                /mol_type="genomic DNA"
                /db_xref="taxon:28045"
                /tissue_lib="ATCC 51131"
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                /product="16S ribosomal RNA"
                /note="putative"
    rRNA

ORIGIN
Query Match      95.8%; Score 23; DB 15; Length 1460;
Best Local Similarity 95.8%; Pred. No. 1.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTTCG 24
Db 9 CAACTCGAACGGAAGGCGCTTTTCG 32

RESULT 9
MSGRGDSB
LOCUS    Mycobacterium celatum 1479 bp DNA linear BCT 21-SEP-1993
DEFINITION

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L08170
ACCESSION L08170.1 GI:293250
VERSION   16S ribosomal RNA.
KEYWORDS  Mycobacterium celatum
SOURCE    Mycobacterium celatum
ORGANISM  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1 (bases 1 to 1479)
AUTHORS Butler,W.R., O'Connor,S.P., Yakrus,M.A., Smithwick,R.W.,
          Plikaytis,B.B., Moss,C.W., Floyd,M.M., Woodley,C.L., Kilburn,J.O.,
          Vadney,F.S. and Gross,W.M.
TITLE    Mycobacterium celatum sp. nov
JOURNAL  Int. J. Syst. Bacteriol. 43 (3), 539-548 (1993)
PUBMED   8102246
COMMENT   Original source text: Mycobacterium celatum (library: ATCC 51130)
          DNA.
FEATURES
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            1..1479
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                /mol_type="genomic DNA"
                /db_xref="taxon:28045"
                /tissue_lib="ATCC 51130"
            <1..>1479
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                /note="putative"
    rRNA

ORIGIN
Query Match      95.8%; Score 23; DB 15; Length 1479;
Best Local Similarity 95.8%; Pred. No. 1.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTTCG 24
Db 30 CAACTCGAACGGAAGGCGCTTTTCG 53

RESULT 10
MSGRR16S
LOCUS    Mycobacterium kansasii 268 bp rRNA linear BCT 27-APR-1993
DEFINITION
ACCESSION M95469
VERSION   M95469.1 GI:175317
KEYWORDS  16S ribosomal RNA.
SOURCE    Mycobacterium kansasii
ORGANISM  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1 (bases 1 to 268)
AUTHORS Ross,B.C., Jackson,K., Yang,M., Sievers,A. and Dwyer,B.
TITLE    Identification of a genetically distinct sub-species of
          Mycobacterium kansasii
JOURNAL  Unpublished (1992)
COMMENT   Original source text: Mycobacterium kansasii rRNA.
          DNA.
FEATURES
    source
        Location/Qualifiers
            1..268
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                /mol_type="rRNA"
                /db_xref="taxon:1768"
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                /gene="16S rRNA"
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                /gene="16S rRNA"
                /product="16S ribosomal RNA"
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    rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 268;
Best Local Similarity 95.8%; Pred. No. 4.1e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTTCG 24
Db 39 CAACTCGAACGGAAGGCGCTTTTCG 62

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RESULT 11
MSP404591          293 bp   DNA       linear   ENV 06-JUN-2003
LOCUS              Uncultured Mycobacterium MB1 partial 16S rRNA gene.
DEFINITION
ACCESSION          AJ404591
VERSION            AJ404591.1  GI:8926769
KEYWORDS           16S ribosomal RNA; 16S rRNA gene.
SOURCE             uncultured Mycobacterium MB1
ORGANISM           uncultured Mycobacterium MB1
                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                   Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental
                   samples.
REFERENCE
AUTHORS            Kempell,K.E., Cox,C.J., Hurie,M., Wong,A., Wilkie,S.,
                   Zanders,E.D., Gaston,J. and Crowe,J.
TITLE              Reverse Transcriptase-Polymerase Chain Reaction of Bacterial rRNA
                   for Detection and Characterisation of Bacterial Species in
                   Arthritis Synovial Tissue
JOURNAL            Unpublished
REFERENCE          2 (bases 1 to 293)
AUTHORS            Cox,C.J.
TITLE              Direct Submission
JOURNAL            Submitted (05-JUN-2000) Cox C.J., Cancer Research, Sanger Centre,
                   Wellcome Trust Genome Campus, Hinxton Hall, Hinxton,
                   Cambridgeshire, CB10 1SA, UNITED KINGDOM
FEATURES
source            1..293
                   /organism="uncultured Mycobacterium MB1"
                   /mol_type="genomic DNA"
                   /db_xref="taxon:129682"
                   /clone="MB1"
                   /tissue type="Synovium"
gene              1..293
                   /gene="16S rRNA"
rRNA              <1..293
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ORIGIN
Query Match       93.3%;   Score 22.4;   DB 1;   Length 293;
Best Local Similarity 95.8%;   Pred. No. 4e+02;
Matches 23;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy  1  CAAGTCGAACGGAAGGCGCTTTCG  24
    |||||
Db   21 CAAGTCGAACGGAAGGCGCTTTCG  44

RESULT 12
MF168RRN
LOCUS              MF168RRN          316 bp   DNA       linear   BCT 14-NOV-1996
DEFINITION         M.fortuitum 16S rRNA gene, partial.
ACCESSION          Y09325
VERSION            Y09325.1  GI:1669698
KEYWORDS           16S ribosomal RNA; rrn gene.
SOURCE             Mycobacterium fortuitum
ORGANISM           Mycobacterium fortuitum
                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                   Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS            De Smet,K., Kampmann,B., Marshall,B., Kroll,S. and Levin,M.
JOURNAL            Unpublished
REFERENCE          2 (bases 1 to 316)
AUTHORS            De Smet,K.A.L.
TITLE              Direct Submission
JOURNAL            Submitted (08-NOV-1996) K.A.L. De Smet, Imperial College Medical
                   School at St Marys, Medical Microbiology, Norfolk Place, London, W2
                   1PG, UK
FEATURES
source            1..316
                   /organism="Mycobacterium fortuitum"
                   /mol_type="genomic DNA"

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TITLE Molecular characterization of nocardioform actinomycetes in activated sludge by 16S rRNA analysis
JOURNAL Microbiology (Reading, Engl.) 141 (Pt 2), 513-521 (1995)
PUBMED 7704280
REFERENCE 2 (bases 1 to 393)
AUTHORS Schuppler,M.
TITLE Direct Submission
JOURNAL Submitted (28-MAR-1994) M. Schuppler, Institut fuer Med. Mikrobiologie & Hygiene, Universitaet Freiburg, Hermann-Herder-St. 11, 79104 Freiburg, FRG

FEATURES

source

1..393
 Location/Qualifiers
 /organism="unidentified bacterium"
 /mol_type="genomic DNA"
 /isolate="SMKN23"
 /db_xref="taxon:2338"
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 /product="16S ribosomal RNA"

ORIGIN

Query Match 93.3%; Score 22.4; DB 1; Length 393;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
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Db 8 CAAGTCGAACGGAAGGCGCTTTCG 31

RESULT 15

AY395154

LOCUS

DEFINITION Uncultured actinobacterium clone E02ST 16S ribosomal RNA gene, partial sequence.
 394 bp DNA linear ENV 07-SEP-2004

ACCESSION AY395154

VERSION AY395154.1

GI:37595669

ENV.

SOURCE uncultured actinobacterium

ORGANISM uncultured actinobacterium

REFERENCE Bacteria; Actinobacteria; environmental samples.

AUTHORS Hackl,E., Zechmeister-Boltenstern,S., Bodrossy,L. and Sessitsch,A.
TITLE Comparison of diversities and compositions of bacterial populations inhabiting natural forest soils

JOURNAL

PUBMED

15345382

REFERENCE 2 (bases 1 to 394)

Hackl,E. and Sessitsch,A.

Direct Submission

TITLE Submitted (19-SEP-2003) Environmental and Life Sciences, ARC

JOURNAL Seibersdorf research GmbH, Seibersdorf A-2444, Austria

FEATURES

source

1..394
 Location/Qualifiers
 /organism="uncultured actinobacterium"
 /mol_type="genomic DNA"
 /isolation_source="forest soil"
 /db_xref="taxon:152507"
 /clone="E02ST"
 /environmental_sample
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 /product="16S ribosomal RNA"

ORIGIN

Query Match 93.3%; Score 22.4; DB 1; Length 394;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24

|||||

Db 51 CAAGTCGAACGGAAGGCGCTTTCG 74

RESULT 16

AY043901

LOCUS

DEFINITION

Uncultured actinobacterium clone SMS9.49WL 16S ribosomal RNA gene, partial sequence.
 395 bp DNA linear ENV 05-MAY-2004

ACCESSION AY043901

VERSION AY043901.1

GI:22267274

ENV.

KEYWORDS uncultured actinobacterium

SOURCE uncultured actinobacterium

ORGANISM uncultured actinobacterium

REFERENCE Bacteria; Actinobacteria; environmental samples.

AUTHORS Axelrood,P.E., Chow,M.L., Radomski,C.C., McDermott,J.M. and Davies,J.

TITLE Molecular characterization of bacterial diversity from British Columbia forest soils subjected to disturbance

JOURNAL Can. J. Microbiol. 48 (7), 655-674 (2002)

PUBMED 12224564

REFERENCE 2 (bases 1 to 395)

Axelrood,P.E., Chow,M.L., Radomski,C.C., McDermott,J.M. and Davies,J.

Direct Submission

TITLE Submitted (20-JUN-2001) BC Research Inc., 3650 Westbrook Mall,

JOURNAL Vancouver, BC V6S 2L2, Canada

FEATURES Location/Qualifiers

source

1..395

/organism="uncultured actinobacterium"

/mol_type="genomic DNA"

/db_xref="taxon:152507"

/clone="SMS9.49WL"

/environmental_sample

/note="from forest cut-block mineral soil from the British Columbia Ministry of Forests Long-Term Soil Productivity (LTSP) installation near Williams Lake, BC, Canada"

<1..>395

/product="16S ribosomal RNA"

ORIGIN

Query Match 93.3%; Score 22.4; DB 1; Length 395;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24

|||||

Db 21 CAAGTCGAACGGAAGGCGCTTTCG 44

RESULT 17

AY395151

LOCUS

DEFINITION

Uncultured bacterium clone D36ST 16S ribosomal RNA gene, partial sequence.
 395 bp DNA linear ENV 07-SEP-2004

ACCESSION AY395151

VERSION AY395151.1

GI:37595666

ENV.

KEYWORDS uncultured bacterium

SOURCE uncultured bacterium

ORGANISM uncultured bacterium

REFERENCE Bacteria; environmental samples.

AUTHORS Hackl,E., Zechmeister-Boltenstern,S., Bodrossy,L. and Sessitsch,A.

TITLE Comparison of diversities and compositions of bacterial populations inhabiting natural forest soils

JOURNAL Appl. Environ. Microbiol. 70 (9), 5057-5065 (2004)

PUBMED 15345382

REFERENCE 2 (bases 1 to 395)

Hackl,E. and Sessitsch,A.

Direct Submission

TITLE Submitted (19-SEP-2003) Environmental and Life Sciences, ARC

JOURNAL Seibersdorf research GmbH, Seibersdorf A-2444, Austria

FEATURES Location/Qualifiers

source

1..395

/organism="uncultured bacterium"

/mol_type="genomic DNA"

/isolation_source="forest soil"

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/db xref="taxon:77133"
/clone="D36ST"
/environmental_sample
<1..>395
/product="16S ribosomal RNA"

ORIGIN
Query Match      93.3%; Score 22.4; DB 1; Length 395;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTCG 24
|||||
Db 51 CAACTCGAACGGAAGGCGCTTTCG 74

RESULT 18
BSSMKN14
LOCUS      BSSMKN14          396 bp      DNA      linear      ENV 22-FEB-1995
DEFINITION Bacterium sp.(SMKN14) DNA.
ACCESSION  X78655
VERSION     X78655.1 GI:509724
KEYWORDS   16S ribosomal RNA.
SOURCE     unidentified bacterium
ORGANISM   Bacteria; environmental samples.

REFERENCE
1 Schuppler,M., Mertens,F., Schon,G. and Gobel,U.B.
Molecular characterization of nocardioform actinomycetes in
activated sludge by 16S rRNA analysis
Microbiology (Reading, Engl.) 141 (Pt 2), 513-521 (1995)
7704280
2 (bases 1 to 396)
Schuppler,M.
Direct Submission
Submitted (28-MAR-1994) M. Schuppler, Institut fuer Med.
Mikrobiologie & Hygiene, Universitaet Freiburg, Hermann-Herder-St.
11, 79104 Freiburg, FRG

FEATURES
source
1..396
/organism="unidentified bacterium"
/mol_type="genomic DNA"
/isolate="SMKN14"
/db_xref="taxon:2338"
1..396
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 1; Length 396;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTCG 24
|||||
Db 8 CAACTCGAACGGAAGGCGCTTTCG 31

RESULT 19
DQ221681
LOCUS      DQ221681          400 bp      DNA      linear      ENV 12-NOV-2005
DEFINITION Uncultured bacterium clone BPH3088 16S ribosomal RNA gene, partial
sequence.
ACCESSION  DQ221681
VERSION     DQ221681.1 GI:80978382
KEYWORDS   uncultured bacterium
SOURCE     uncultured bacterium
ORGANISM   Bacteria; environmental samples.

REFERENCE
1 (bases 1 to 400)
Lambais,M.R., Crowley,D.E., Cury,J.C. and Bull,R.C.
Bacterial diversity on leaf surfaces of the Brazilian Atlantic
Forest
Unpublished

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 401;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTCG 24
|||||
Db 1 CAACTCGAACGGAAGGCGCTTTCG 24

REFERENCE
2 (bases 1 to 400)
Lambais,M.R., Crowley,D.E., Cury,J.C. and Bull,R.C.
Direct Submission
Submitted (23-SEP-2005) Solos e Nutricao de Plantas, Universidade
de Sao Paulo, Av. Padua Dias,11, Piracicaba, SP 13418-900, Brazil
Location/Qualifiers
1..400
/organism="uncultured bacterium"
/mol_type="genomic DNA"
/isolation_source="phyllosphere"
/specific_host="Campomanesia xanthocarpa"
/db_xref="taxon:77133"
/clone="BPH3088"
/environmental_sample
<1..>400
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 1; Length 400;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTCG 24
|||||
Db 16 CAACTCGAACGGAAGGCGCTTTCG 39

RESULT 20
DQ063065
LOCUS      DQ063065          401 bp      DNA      linear      BCT 27-JUN-2005
DEFINITION Actinobacterium BAL125 16S ribosomal RNA gene, partial sequence.
ACCESSION  DQ063065
VERSION     DQ063065.1 GI:68139094
KEYWORDS   actinobacterium BAL125
SOURCE     actinobacterium BAL125
ORGANISM   Bacteria; Actinobacteria.

REFERENCE
1 (bases 1 to 401)
Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
Bacterial community composition in the central Baltic Sea analyzed
by cultivation and molecular-based methods
Unpublished
2 (bases 1 to 401)
Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
Direct Submission
Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
Location/Qualifiers
1..401
/organism="actinobacterium BAL125"
/mol_type="genomic DNA"
/strain="BAL125"
/isolation_source="Baltic Sea, 3m depth, Landsort deep St.
BV31, Zobel/R2A media"
/db_xref="taxon:331783"
/country="Sweden"
/lat_lon="60.42.726N, 05.05.595E"
/collection_date="2 July 2003"
<1..>401
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 401;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTCG 24
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Db 1 CAACTCGAACGGAAGGCGCTTTCG 24

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RESULT 21
AY234665
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Bacterium Ellin6013 403 bp DNA linear BCT 08-DEC-2003
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
REFERENCE
AUTHORS
Joseph,S.J., Hugenholtz,P., Sangwan,P., Osborne,C.A., Sait,M. and
Janssen,P.H.
TITLE
Laboratory Cultivation of Widespread and Previously Uncultured Soil
Bacteria
JOURNAL
APPL. ENVIRON. MICROBIOL. 69 (12), 7210-7215 (2003)
PUBMED
14860368
REFERENCE
2 (bases 1 to 403)
AUTHORS
Joseph,S.J., Hugenholtz,P., Rana,P., Osborne,C.A., Sait,M. and
Janssen,P.H.
TITLE
Direct Submission
JOURNAL
Submitted (12-FEB-2003) Department of Microbiology and Immunology,
University of Melbourne, Parkville, Victoria 3010, Australia
LOCATION/Qualifiers
1. .403
/organism="Bacterium Ellin6013"
/mol_type="genomic DNA"
/isolate="Ellin6013"
/db_xref="taxon:234120"
<1. .>403
/product="16S ribosomal RNA"
rRNA
ORIGIN
Query Match 93.3%; Score 22.4; DB 15; Length 403;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAAGTCGAACGGAAGGCGCTTTCG 24
|||||
31 CAAGTCGAACGGAAGGCGCTTTCG 54
Db
ORIGIN
Query Match 93.3%; Score 22.4; DB 15; Length 403;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
AY792017 407 bp DNA linear BCT 20-NOV-2004
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mycobacterium sp. 5BR6 16S ribosomal RNA gene, partial sequence.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS
Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.
TITLE
Bioremediation of radioactive water with metallic materials
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 407)
AUTHORS
Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.
TITLE
Direct Submission
JOURNAL
Submitted (25-OCT-2004) Dep Ingenieria y Ciencia de los Materiales,
Escuela Tecnica Superior de Ingenieros Industriales, Universidad
Politcnica de Madrid, Jose Gutierrez Abascal, 2, Madrid, Madrid
28006, Spain
LOCATION/Qualifiers
1. .407
/organism="Mycobacterium sp. 5BR6"
/mol_type="genomic DNA"
/isolate="5BR6"
/isolation_source="radioactive water"
/db_xref="taxon:300866"
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rRNA
ORIGIN
FEATURES
source
Location/Qualifiers
1. .407
/organism="Mycobacterium sp. 5BR6"
/mol_type="genomic DNA"
/isolate="5BR6"
/isolation_source="radioactive water"
/db_xref="taxon:300866"
<1. .>407
rRNA
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ORIGIN
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Query Match 93.3%; Score 22.4; DB 15; Length 407;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAAGTCGAACGGAAGGCGCTTTCG 24
|||||
365 CAAGTCGAACGGAAGGCGCTTTCG 342
Db
ORIGIN
BSSMKN12 410 bp DNA linear ENV 22-FEB-1995
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Bacterium sp. (SMKN12) DNA.
X78654
X78654.1 GI:509723
16S ribosomal RNA.
unidentified bacterium
unidentified bacterium
Bacteria; environmental samples.
REFERENCE
1
AUTHORS
Schuppler,M., Mertens,F., Schon,G. and Gobel,U.B.
TITLE
Molecular characterization of nocardioform actinomycetes in
activated sludge by 16S rRNA analysis
JOURNAL
Microbiology (Reading, Engl.) 141 (Pt 2), 513-521 (1995)
PUBMED
7704280
REFERENCE
2 (bases 1 to 410)
AUTHORS
Schuppler,M.
TITLE
Direct Submission
JOURNAL
Submitted (28-MAR-1994) M. Schuppler, Institut fuer Med.
Mikrobiologie & Hygiene, Universitaet Freiburg, Hermann-Herder-St.
11, 79104 Freiburg, FRG
LOCATION/Qualifiers
1. .410
/organism="unidentified bacterium"
/mol_type="genomic DNA"
/isolate="SMKN12"
/db_xref="taxon:2338"
1. .410
/product="16S ribosomal RNA"
rRNA
ORIGIN
Query Match 93.3%; Score 22.4; DB 1; Length 410;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAAGTCGAACGGAAGGCGCTTTCG 24
|||||
3 CAAGTCGAACGGAAGGCGCTTTCG 26
Db
ORIGIN
DQ063154 411 bp DNA linear BCT 27-JUN-2005
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
actinobacterium BAL218
actinobacterium BAL218
Bacteria; Actinobacteria.
1 (bases 1 to 411)
AUTHORS
Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE
Bacterial community composition in the central Baltic Sea analyzed
by cultivation and molecular-based methods
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 411)
AUTHORS
Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE
Direct Submission
```

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JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
FEATURES University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
source Location/Qualifiers
1..411
/organism="actinobacterium BAL218"
/mol_type="genomic DNA"
/strain="BAL218"
/isolation_source="Baltic Sea, 3m depth, Landsort deep St.
BY31, Zobel/R2A media"
/db_xref="taxon:3311796"
/country="Sweden"
/lat_lon="60.42.726N, 05.05.595E"
/collection_dates="17 May 2004"
<1..>411
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 93.3%; Score 22.4; DB 15; Length 411;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCGCTTTCG 24
Db 11 CAAGTCGAACGGAAGGCGCTTTCG 34

RESULT 25
DQ063199 411 bp DNA linear BCT 27-JUN-2005
LOCUS Actinobacterium BAL263 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION DQ063199
VERSION DQ063199.1 GI:68139237
KEYWORDS actinobacterium BAL263
SOURCE actinobacterium BAL263
ORGANISM Bacteria; Actinobacteri-
REFERENCE 1 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE Bacterial community composition in the central Baltic Sea analyzed by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
FEATURES University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
source Location/Qualifiers
1..411
/organism="actinobacterium BAL263"
/mol_type="genomic DNA"
/strain="BAL263"
/isolation_source="Baltic Sea, 3m depth, Landsort deep St.
BY31, Zobel/R2A media"
/db_xref="taxon:3311810"
/country="Sweden"
/lat_lon="60.42.726N, 05.05.595E"
/collection_dates="17 May 2004"
<1..>411
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 93.3%; Score 22.4; DB 15; Length 411;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCGCTTTCG 24
Db 12 CAAGTCGAACGGAAGGCGCTTTCG 35

RESULT 26

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AV792013 411 bp DNA linear BCT 20-NOV-2004
LOCUS Mycobacterium sp. 4BR14 16S ribosomal RNA gene, partial sequence.
FEATURES
ACCESSION AV792013
VERSION AV792013.1 GI:55740312
KEYWORDS
SOURCE
ORGANISM Mycobacterium sp. 4BR14
Mycobacterium sp. 4BR14
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 411)
AUTHORS Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.
TITLE Biorremediation of radioactive water with metallic materials
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 411)
AUTHORS Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.
TITLE Direct Submission
JOURNAL Submitted (25-OCT-2004) Dep Ingenieria y Ciencia de los Materiales,
Escuela Tecnica Superior de Ingenieros Industriales, Universidad
Politecnica de Madrid, Jose Gutierrez Abascal, 2, Madrid, Madrid
28006, Spain
FEATURES Location/Qualifiers
1..411
/organism="Mycobacterium sp. 4BR14"
/mol_type="genomic DNA"
/strain="4BR14"
/isolation_source="radioactive water"
/db_xref="taxon:300864"
<1..>411
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 93.3%; Score 22.4; DB 15; Length 411;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCGCTTTCG 24
Db 52 CAAGTCGAACGGAAGGCGCTTTCG 75

RESULT 27
AM085773 414 bp DNA linear ENV 21-SEP-2005
LOCUS Uncultured Mycobacterium sp. partial 16S rRNA gene, clone T6.
DEFINITION
ACCESSION AM085773
VERSION AM085773.1 GI:75754596
KEYWORDS ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE uncultured Mycobacterium sp.
ORGANISM uncultured Mycobacterium sp.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental
samples.
REFERENCE 1
AUTHORS Uytendaele,M., Vermeir,S., Wattiau,P., Ryngaert,A. and Springael,D.
TITLE Enrichment and characterization of a bacterial culture utilizing pyrene at pH 2 and dominated by a slow-growing Mycobacterium sp. from acidic polycyclic aromatic hydrocarbon contaminated soil
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 414)
AUTHORS Uytendaele,M.
TITLE Direct Submission
JOURNAL Submitted (13-SEP-2005) Uytendaele M., Division Soil and Water
Management, Catholic University of Leuven, Kasteelpark Arenberg 20,
B-3001 Leuven, BELGIUM
FEATURES Location/Qualifiers
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/organism="uncultured Mycobacterium sp."
/mol_type="genomic DNA"
/isolation_source="PAH-contaminated soil"
/db_xref="taxon:171292"
/clone="T6"
/environmental_sample

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gene          /country="Belgium"
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rRNA          /gene="16S rRNA"
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              /product="16S ribosomal RNA"

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Query Match   93.3%; Score 22.4; DB 1; Length 414;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAGGCGCTTTCG 24
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Db 1 CAAAGTCGAACGGAAGGCGCTTTCG 24

RESULT 28
DQ063108      415 bp DNA linear BCT 27-JUN-2005
LOCUS        Actinobacterium BAL168 16S ribosomal RNA gene, partial sequence.
DEFINITION   DQ063108
ACCESSION    DQ063108
VERSION      DQ063108.1 GI:68139141
KEYWORDS     actinobacterium BAL168
SOURCE       actinobacterium BAL168
ORGANISM     Bacteria; Actinobacteria.
REFERENCE    1 (bases 1 to 415)
AUTHORS      Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
              Hagstrom,A.
TITLE        Bacterial community composition in the central Baltic Sea analyzed
              by cultivation and molecular-based methods
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 415)
AUTHORS      Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
              Hagstrom,A.
TITLE        Direct Submission
JOURNAL      Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
              University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES     Location/Qualifiers
              1..415
              /organism="actinobacterium BAL168"
              /mol_type="genomic DNA"
              /strain="BAL168"
              /isolation_source="Baltic Sea, 3m depth, Landsort deep St.
              By31, Zobel1/R2A media"
              /db_xref="taxon:331762"
              /country="Sweden"
              /lat_lon="60.42.726N, 05.05.595E"
              /collection_date="8 October 2003"
              <1..>415
              /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match   93.3%; Score 22.4; DB 15; Length 415;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 1 CAAAGTCGAACGGAAGGCGCTTTCG 24

RESULT 29
AM085786      416 bp DNA linear ENV 21-SEP-2005
LOCUS        Uncultured Mycobacterium sp. partial 16S rRNA gene, clone K11.
DEFINITION   AM085786
ACCESSION    AM085786
VERSION      AM085786.1 GI:75754609
KEYWORDS     ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE       uncultured Mycobacterium sp.
ORGANISM     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

gene          /country="Belgium"
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rRNA          /gene="16S rRNA"
              <1..>414
              /gene="16S rRNA"
              /product="16S ribosomal RNA"

ORIGIN
Query Match   93.3%; Score 22.4; DB 1; Length 414;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 1 CAAAGTCGAACGGAAGGCGCTTTCG 24

RESULT 30
AM085788      418 bp DNA linear ENV 21-SEP-2005
LOCUS        Uncultured Mycobacterium sp. partial 16S rRNA gene, clone K13.
DEFINITION   AM085788
ACCESSION    AM085788
VERSION      AM085788.1 GI:75754611
KEYWORDS     ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE       uncultured Mycobacterium sp.
ORGANISM     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
              Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental
              samples.

REFERENCE    1
AUTHORS      Uytendaele,M., Breugelmans,P., Janssen,M., Wattiau,P., Joffe,B.,
              Karlson,U., Ortega-Calvo,J.J., Bastiaens,L., Ryngaert,A. and
              Springael,D.
TITLE        Distribution of the Mycobacterium sp. community and polycyclic
              aromatic hydrocarbons (PAHs) among different size fractions of a
              weathered PAH-contaminated soil
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 418)
AUTHORS      Uytendaele,M.
TITLE        Direct Submission
JOURNAL      Submitted (13-SEP-2005) Uytendaele M., Division Soil and Water
              Management, Catholic University of Leuven, Kasteelpark Arenberg 20,
              B-3001 Leuven, BELGIUM
FEATURES     Location/Qualifiers
              1..418
              /organism="uncultured Mycobacterium sp."
              /mol_type="genomic DNA"
              /isolation_source="PAH-contaminated soil"
              /db_xref="taxon:171292"

gene          /country="Denmark"
              <1..>416
rRNA          /gene="16S rRNA"
              <1..>416
              /gene="16S rRNA"
              /product="16S ribosomal RNA"

ORIGIN
Query Match   93.3%; Score 22.4; DB 1; Length 416;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 1 CAAAGTCGAACGGAAGGCGCTTTCG 24

RESULT 31
AM085788      418 bp DNA linear ENV 21-SEP-2005
LOCUS        Uncultured Mycobacterium sp. partial 16S rRNA gene, clone K13.
DEFINITION   AM085788
ACCESSION    AM085788
VERSION      AM085788.1 GI:75754611
KEYWORDS     ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE       uncultured Mycobacterium sp.
ORGANISM     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
              Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental
              samples.

REFERENCE    1
AUTHORS      Uytendaele,M., Breugelmans,P., Janssen,M., Wattiau,P., Joffe,B.,
              Karlson,U., Ortega-Calvo,J.J., Bastiaens,L., Ryngaert,A. and
              Springael,D.
TITLE        Distribution of the Mycobacterium sp. community and polycyclic
              aromatic hydrocarbons (PAHs) among different size fractions of a
              weathered PAH-contaminated soil
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 418)
AUTHORS      Uytendaele,M.
TITLE        Direct Submission
JOURNAL      Submitted (13-SEP-2005) Uytendaele M., Division Soil and Water
              Management, Catholic University of Leuven, Kasteelpark Arenberg 20,
              B-3001 Leuven, BELGIUM
FEATURES     Location/Qualifiers
              1..418
              /organism="uncultured Mycobacterium sp."
              /mol_type="genomic DNA"
              /isolation_source="PAH-contaminated soil"
              /db_xref="taxon:171292"

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/clone="K13"
/environmental_sample
/country="Denmark"
<1..>418
/gene="16S rRNA"
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/product="16S ribosomal RNA"

ORIGIN
Query Match      93.3%; Score 22.4; DB 1; Length 418;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCCTTCG 24
    |||||
Db 4 CAAGTCGAACGGAAGGCCCTTCG 27

RESULT 31
AY673261      418 bp      DNA      linear      BCT 20-MAY-2005
DEFINITION   Mycobacteriaceae bacterium Ellin7095 16S ribosomal RNA gene,
partial sequence.
ACCESSION    AY673261
VERSION      AY673261.1 GI:56683118
KEYWORDS     Mycobacteriaceae bacterium Ellin7095
SOURCE       Mycobacteriaceae bacterium Ellin7095
ORGANISM     Mycobacteriaceae bacterium Ellin7095
              Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
              Corynebacterineae; Mycobacteriaceae.
REFERENCE    1 (bases 1 to 418)
AUTHORS      Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE        Effects of growth medium, inoculum size, and incubation time on
              culturability and isolation of soil bacteria
JOURNAL      Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED       15691937
REFERENCE    2 (bases 1 to 418)
AUTHORS      Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE        Direct Submission
JOURNAL      Submitted (02-JUL-2004) Department of Microbiology and Immunology,
              University of Melbourne, Grattan Street, Parkville, Victoria 3010,
              Australia
FEATURES     Location/Qualifiers
              source      1..418
                        /organism="Mycobacteriaceae bacterium Ellin7095"
                        /mol_type="genomic DNA"
                        /isolate="Ellin7095"
                        /isolation_source="soil"
                        /db_xref="taxon:305281"
                        <1..>418
                        /product="16S ribosomal RNA"
              rRNA
ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 418;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCCTTCG 24
    |||||
Db 31 CAAGTCGAACGGAAGGCCCTTCG 54

RESULT 32
AM085770
LOCUS        AM085770      421 bp      DNA      linear      ENV 21-SEP-2005
DEFINITION   Uncultured eubacterium partial 16S rRNA gene, clone T3.
ACCESSION    AM085770
VERSION      AM085770.1 GI:75754591
KEYWORDS     ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE       uncultured bacterium
ORGANISM     Bacteria; environmental samples.

REFERENCE    1
AUTHORS      Uyttebroeck,M., Vermeir,S., Wattiau,P., Ryngaert,A. and Springael,D.
TITLE        Enrichment and characterization of a bacterial culture utilizing
              pyrene at pH 2 and dominated by a slow-growing Mycobacterium sp.
              from acidic polycyclic aromatic hydrocarbon contaminated soil
              Unpublished
JOURNAL      2 (bases 1 to 421)
AUTHORS      Uyttebroeck,M.
TITLE        Direct Submission
JOURNAL      Submitted (13-SEP-2005) Uyttebroeck M., Division Soil and Water
              Management, Catholic University of Leuven, Kasteelpark Arenberg 20,
              B-3001 Leuven, BELGIUM
FEATURES     Location/Qualifiers
              source      1..421
                        /organism="uncultured bacterium"
                        /mol_type="genomic DNA"
                        /isolation_source="PAH-contaminated soil"
                        /db_xref="taxon:77133"
                        /clone="T3"
                        /environmental_sample
                        /country="Belgium"
                        <1..>421
                        /gene="16S rRNA"
                        <1..>421
                        /gene="16S rRNA"
                        /product="16S ribosomal RNA"
              gene
              rRNA
ORIGIN
Query Match      93.3%; Score 22.4; DB 1; Length 421;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCCTTCG 24
    |||||
Db 10 CAAGTCGAACGGAAGGCCCTTCG 33

RESULT 33
AJ786807
LOCUS        AJ786807      422 bp      DNA      linear      BCT 29-OCT-2004
DEFINITION   Mycobacterium sp. R-22838 partial 16S rRNA gene, isolate R-22838.
ACCESSION    AJ786807
VERSION      AJ786807.1 GI:54887545
KEYWORDS     16S ribosomal RNA; 16S rRNA gene.
SOURCE       Mycobacterium sp. R-22838
ORGANISM     Mycobacterium sp. R-22838
              Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
              Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE    1
AUTHORS      Vanparys,B., Heylen,K., Lebbe,L., Boon,N., Wittebolle,L.,
              Verstraete,W. and De Vos,P.
TITLE        The microbial community composition of a commercial nitrifying
              inoculum
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 422)
AUTHORS      Vanparys,B.
TITLE        Direct Submission
JOURNAL      Submitted (30-JUL-2004) Vanparys B., Laboratory of Microbiology,
              University of Gent, Ledeganckstraat 35, 9000 Gent, BELGIUM
FEATURES     Location/Qualifiers
              source      1..422
                        /organism="Mycobacterium sp. R-22838"
                        /mol_type="genomic DNA"
                        /isolate="R-22838"
                        /isolation_source="commercial nitrifying inoculum"
                        /db_xref="taxon:288999"
                        /country="Belgium"
                        <1..>422
                        /gene="16S rRNA"
                        <1..>422
                        /gene="16S rRNA"
                        /product="16S ribosomal RNA"
              gene
              rRNA
ORIGIN

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Davis, K.E.R., Joseph, S.J. and Janssen, P.H.
 Direct Submission
 Submitted (02-JUL-2004) Department of Microbiology and Immunology,
 University of Melbourne, Grattan Street, Parkville, Victoria 3010,
 Australia

AUTHORS
TITLE
JOURNAL
FEATURES
 source
 Location/Qualifiers
 1. .423
 /organism="Mycobacteriaceae bacterium Ellin7039"
 /mol_type="genomic DNA"
 /isolate="Ellin7039"
 /isolation_source="soil"
 /db_xref="taxon:305258"
 <1..>423
 /product="16S ribosomal RNA"

rRNA
 <1..>423
 /product="16S ribosomal RNA"

ORIGIN
 Query Match 93.3%; Score 22.4; DB 15; Length 423;
 Best Local Similarity 95.8%; Pred. No. 3.6e+02;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGCCCTTCG 24
 |||||
 Db 31 CAAGTCGAACGGAAGCCCTTCG 54

RESULT 36
 AY673206
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mycobacteriaceae bacterium Ellin7040
 Mycobacteriaceae bacterium Ellin7040
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae.
 1 (bases 1 to 423)
 Davis, K.E., Joseph, S.J. and Janssen, P.H.
 Effects of growth medium, inoculum size, and incubation time on
 culturability and isolation of soil bacteria
 Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
 15691937

REFERENCE
 PUBLISHED
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 PUBLISHED
 REFERENCE
 TITLE
 JOURNAL
 Submitted (02-JUL-2004) Department of Microbiology and Immunology,
 University of Melbourne, Grattan Street, Parkville, Victoria 3010,
 Australia

FEATURES
 source
 Location/Qualifiers
 1. .423
 /organism="Mycobacteriaceae bacterium Ellin7040"
 /mol_type="genomic DNA"
 /isolate="Ellin7040"
 /isolation_source="soil"
 /db_xref="taxon:305259"
 <1..>423
 /product="16S ribosomal RNA"

rRNA
 <1..>423
 /product="16S ribosomal RNA"

ORIGIN
 Query Match 93.3%; Score 22.4; DB 15; Length 423;
 Best Local Similarity 95.8%; Pred. No. 3.6e+02;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGCCCTTCG 24
 |||||
 Db 31 CAAGTCGAACGGAAGCCCTTCG 54

RESULT 37
 AY673207
 LOCUS
 DEFINITION
 Mycobacteriaceae bacterium Ellin7041 16S ribosomal RNA gene.
 1 (bases 1 to 423)
 Davis, K.E., Joseph, S.J. and Janssen, P.H.
 Effects of growth medium, inoculum size, and incubation time on
 culturability and isolation of soil bacteria
 Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
 15691937


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partial sequence.
ACCESSION      AY673207
VERSION        AY673207.1  GI:56683064
KEYWORDS
SOURCE
ORGANISM       .
Mycobacteriaceae bacterium Ellin7041
Mycobacteriaceae bacterium Ellin7041
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
REFERENCE
1 (bases 1 to 423)
Davis,K.E., Joseph,S.J. and Janssen,P.H.
Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
JOURNAL
PUBMED
15691937
REFERENCE
2 (bases 1 to 423)
Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
Direct Submission
Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES
Location/Qualifiers
1..423
/organism="Mycobacteriaceae bacterium Ellin7041"
/mol_type="genomic DNA"
/isolate="Ellin7041"
/isolation_source="soil"
/db_xref="taxon:305260"
<1..>423
/product="16S ribosomal RNA"

rRNA
Query Match      93.3%; Score 22.4; DB 15; Length 423;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
|||||
Db 31 CAAGTCGAACGGAAGGCGCTTTCG 54

RESULT 38
DQ063156
LOCUS      actinobacterium BAL220
DEFINITION actinobacterium BAL220
Bacteria; Actinobacteria.
ACCESSION  DQ063156
VERSION    DQ063156.1  GI:68139194
KEYWORDS
SOURCE      actinobacterium BAL220
actinobacterium BAL220
Bacteria; Actinobacteria.
REFERENCE
1 (bases 1 to 424)
Riemann,L., Leitert,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
Bacterial community composition in the central Baltic Sea analyzed
by cultivation and molecular-based methods
Unpublished
2 (bases 1 to 424)
Riemann,L., Leitert,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
Direct Submission
Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES
Location/Qualifiers
1..424
/organism="actinobacterium BAL220"
/mol_type="genomic DNA"
/strain="BAL220"
/isolation_source="Baltic Sea, 3m depth, Landsort deep St.
BY31, Zobe[1/R2A media"
/db_xref="taxon:331797"
/country="Sweden"
/lat_lon="60.42.726N, 05.05.595E"
/collection_date="17 May 2004"

rRNA
<1..>424
/product="16S ribosomal RNA"

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 423;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
|||||
Db 31 CAAGTCGAACGGAAGGCGCTTTCG 54

RESULT 38
DQ063156
LOCUS      actinobacterium BAL220
DEFINITION actinobacterium BAL220
Bacteria; Actinobacteria.
ACCESSION  DQ063156
VERSION    DQ063156.1  GI:68139194
KEYWORDS
SOURCE      actinobacterium BAL220
actinobacterium BAL220
Bacteria; Actinobacteria.
REFERENCE
1 (bases 1 to 424)
Riemann,L., Leitert,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
Bacterial community composition in the central Baltic Sea analyzed
by cultivation and molecular-based methods
Unpublished
2 (bases 1 to 424)
Riemann,L., Leitert,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
Direct Submission
Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES
Location/Qualifiers
1..424
/organism="Streptosporangiaceae bacterium Ellin7121"
/mol_type="genomic DNA"
/isolate="Ellin7121"
/isolation_source="soil"
/db_xref="taxon:305348"
<1..>424
/product="16S ribosomal RNA"

rRNA
<1..>424
/product="16S ribosomal RNA"

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 424;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
|||||
Db 31 CAAGTCGAGCGGAAGGCGCTTTCG 54

RESULT 40
AY756031
LOCUS      Unidentified bacterium TMB805
DEFINITION Unidentified bacterium TMB805
Unidentified bacterium TMB805
Bacteria.
REFERENCE
1 (bases 1 to 424)
Chapon,V., Benzerara,K., Barakat,M., Achouak,W., Barras,F.,
Christen,R., Chevenet,F. and Heulin,T.
Diversity of Bacteria and Archaea in the arid desert of Tataouine
Unpublished
JOURNAL

```

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REFERENCE
AUTHORS      2 (bases 1 to 424)
              Chapon,V., Benzerara,K., Barakat,M., Achouak,W., Barras,F.,
              Christen,R., Chevenet,F. and Heulin,T.
TITLE        Direct Submission
JOURNAL      Submitted (21-SEP-2004) LEMIR-DEVW-DSV, CEA, Cadarache, Saint Paul
              Lez Durance 13108, France
FEATURES
source      Location/Qualifiers
            1..424
              /organism="Unidentified bacterium TMB805"
              /mol_type="genomic DNA"
              /strain="TMB805"
              /isolation_source="arid soil"
              /db_xref="taxon:297191"
              <1..>424
              /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 424;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 1 CAAGTCGAACGGAAGGCGCTTTCG 24

RESULT 41
LOCUS      AY394635          425 bp DNA linear ENV 20-OCT-2003
DEFINITION Uncultured Mycobacterium sp. Clone W1-11 16S ribosomal RNA gene,
            partial sequence.
ACCESSION  AY394635
VERSION     AY394635.1 GI:37677560
KEYWORDS   ENV.
SOURCE     uncultured Mycobacterium sp.
ORGANISM   uncultured Mycobacterium sp.
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental
            samples.
REFERENCE  1 (bases 1 to 425)
            Benson,D.R., Benson,M.J., Gawronski,J.D. and Eveleigh,D.E.
            Intracellular symbionts and other bacteria associated with deer
            ticks (Ixodes scapularis) from Nantucket and Wellfleet, Cape Cod,
            Massachusetts
            Unpublished
JOURNAL
REFERENCE  2 (bases 1 to 425)
            Benson,D.R., Benson,M.J., Gawronski,J.D. and Eveleigh,D.E.
            Direct Submission
AUTHORS    Submitted (19-SEP-2003) Molecular & Cell Biology, University of
            Connecticut, U-3125, North Eagleville Rd., Storrs, CT 06279-3125,
            USA
FEATURES
source      Location/Qualifiers
            1..425
              /organism="uncultured Mycobacterium sp."
              /mol_type="genomic DNA"
              /specific_host="Ixodes scapularis"
              /db_xref="taxon:171292"
              /clone="W1-11"
              /environmental_sample
              /country="USA: Massachusetts, Cape Cod, Nantucket,
              Wellfleet"
              <1..>425
              /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 1; Length 425;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 31 CAAGTCGAACGGAAGGCGCTTTCG 54

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RESULT 42
LOCUS      AY673136          426 bp DNA linear BCT 22-DEC-2004
DEFINITION Mycobacteriaceae bacterium Ellin5409 16S ribosomal RNA gene,
            partial sequence.
ACCESSION  AY673136
VERSION     AY673136
KEYWORDS
SOURCE     Mycobacteriaceae bacterium Ellin5409
ORGANISM   Mycobacteriaceae bacterium Ellin5409
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae.
REFERENCE  1 (bases 1 to 426)
            Osborne,C.A. and Janssen,P.H.
            Direct Submission
AUTHORS    Submitted (30-JUN-2004) Department of Microbiology and Immunology,
            University of Melbourne, Grattan Street, Parkville, Victoria 3010,
            Australia
FEATURES
source      Location/Qualifiers
            1..426
              /organism="Mycobacteriaceae bacterium Ellin5409"
              /mol_type="genomic DNA"
              /isolate="Ellin5409"
              /isolation_source="soil"
              /db_xref="taxon:305244"
              <1..>426
              /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 426;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 31 CAAGTCGAACGGAAGGCGCTTTCG 54

RESULT 43
LOCUS      AB106918          428 bp DNA linear BCT 09-SEP-2003
DEFINITION Gram-positive bacterium 1-6 for 16S ribosomal RNA, partial
            sequence.
ACCESSION  AB106918
VERSION     AB106918.1 GI:29421132
KEYWORDS
SOURCE     Gram-positive bacterium 1-6
            Gram-positive bacterium 1-6
            Bacteria.
REFERENCE  1
            Anachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
            Fujii,T. and Muramatsu,Y.
            Microbial participation in iodine volatilization from soils
            Environ. Sci. Technol. 37, 3885-3890 (2003)
JOURNAL
REFERENCE  2 (bases 1 to 428)
            Anachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
            Fujii,T. and Muramatsu,Y.
            Direct Submission
AUTHORS    Submitted (27-MAR-2003) Seigo Anachi, Chiba University, Dept. of
            Bioresources Chem.; 648 Matsudo, Matsudo-shi, Chiba 271-8510, Japan
            (E-mail:amachi@faculty.chiba-u.jp, Tel:81-47-308-8868,
            Fax:81-47-308-8866)
FEATURES
source      Location/Qualifiers
            1..428
              /organism="Gram-positive bacterium 1-6"
              /mol_type="genomic DNA"
              /strain="1-6"
              /db_xref="taxon:226200"
              <1..>428
              /product="16S ribosomal RNA"

rRNA

ORIGIN

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Query Match      93.3%; Score 22.4; DB 15; Length 428;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 31 CAAGTCGAACGGAAGGCGCTTTCG 54

RESULT 44
DQ063058
LOCUS      DQ063058      428 bp      DNA      linear      BCT 27-JUN-2005
DEFINITION Actinobacterium BAL118 16S ribosomal RNA gene, partial sequence.
ACCESSION  DQ063058
VERSION     DQ063058.1 GI:58139087
KEYWORDS
SOURCE      actinobacterium BAL118
ORGANISM    actinobacterium BAL118
REFERENCE   1 (bases 1 to 428)
AUTHORS     Riemann,L., Leitet,C., Pomnier,T., Simu,K., Holmfeldt,K. and
            Hegstrom,A.
TITLE       Bacterial community composition in the central Baltic Sea analyzed
            by cultivation and molecular-based methods
JOURNAL
REFERENCE   2 (bases 1 to 428)
AUTHORS     Riemann,L., Leitet,C., Pomnier,T., Simu,K., Holmfeldt,K. and
            Hegstrom,A.
TITLE       Direct Submission
JOURNAL     Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
            University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES
    source   1..428
             /organism="actinobacterium BAL118"
             /mol_type="genomic DNA"
             /strain="BAL118"
             /isolation_source="Baltic Sea, 3m depth, Landsort deep St.
             BY31, Zobeil/R2A media"
             /db_xref="taxon:331781"
             /country="Sweden"
             /lat_lon="60.42.726N, 05.05.595E"
             /collection_dates="2 July 2003"
             <1..>428
             /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 428;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 9 CAAGTCGAACGGAAGGCGCTTTCG 32

RESULT 45
AJ786822
LOCUS      AJ786822      430 bp      DNA      linear      BCT 29-OCT-2004
DEFINITION Mycobacterium sp. R-23262 partial 16S rRNA gene, isolate R-23262.
ACCESSION  AJ786822
VERSION     AJ786822.1 GI:54887560
KEYWORDS    16S ribosomal RNA; 16S rRNA gene.
SOURCE      Mycobacterium sp. R-23262
ORGANISM    Mycobacterium sp. R-23262
REFERENCE   1
AUTHORS     Vanparys,B., Heylen,K., Lebbe,L., Boon,N., Wittebolle,L.,
            Verstraete,W. and De Vos,P.
TITLE       The microbial community composition of a commercial nitrifying
            inoculum
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 430)

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AUTHORS      Vanparys,B.
TITLE         Direct Submission
JOURNAL       Submitted (30-JUL-2004) Vanparys B., Laboratory of Microbiology,
            University of Gent, Ledeganckstraat 35, 9000 Gent, BELGIUM
FEATURES
    source    1..430
             /organism="Mycobacterium sp. R-23262"
             /mol_type="genomic DNA"
             /isolate="R-23262"
             /isolation_source="commercial nitrifying inoculum"
             /db_xref="taxon:289008"
             /country="Belgium"
             1..430
             /gene="16S rRNA"
             <1..>430
             /gene="16S rRNA"
             /product="16S ribosomal RNA"

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 430;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 31 CAAGTCGAACGGAAGGCGCTTTCG 54

RESULT 46
AY673202
LOCUS      AY673202      430 bp      DNA      linear      BCT 20-MAY-2005
DEFINITION Mycobacteriaceae bacterium Ellin7036 16S ribosomal RNA gene,
            partial sequence.
ACCESSION  AY673202
VERSION     AY673202.1 GI:56683059
KEYWORDS
SOURCE      Mycobacteriaceae bacterium Ellin7036
ORGANISM    Mycobacteriaceae bacterium Ellin7036
REFERENCE   1
AUTHORS     Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE       Effects of growth medium, inoculum size, and incubation time on
            culturability and isolation of soil bacteria
JOURNAL     Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED      15691937
REFERENCE   2 (bases 1 to 430)
AUTHORS     Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE       Direct Submission
JOURNAL     Submitted (02-JUL-2004) Department of Microbiology and Immunology,
            University of Melbourne, Grattan Street, Parkville, Victoria 3010,
            Australia
FEATURES
    source    1..430
             /organism="Mycobacteriaceae bacterium Ellin7036"
             /mol_type="genomic DNA"
             /isolate="Ellin7036"
             /isolation_source="soil"
             /db_xref="taxon:305257"
             <1..>430
             /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 430;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 31 CAAGTCGAACGGAAGGCGCTTTCG 54

RESULT 47

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AB106919
LOCUS      AB106919             431 bp    DNA          linear      BCT 09-SEP-2003
DEFINITION Gram-positive bacterium 2-1 for 16S ribosomal RNA, partial
sequence.
ACCESSION  AB106919
VERSION     AB106919.1  GI:29421133
KEYWORDS
SOURCE      Gram-positive bacterium 2-1
ORGANISM    Gram-positive bacterium 2-1
            Bacteria.
REFERENCE   1
AUTHORS     Amachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
            Fujii,T. and Muramatsu,Y.
TITLE       Microbial participation in iodine volatilization from soils
JOURNAL     Environ. Sci. Technol. 37, 3885-3890 (2003)
REFERENCE   2  (bases 1 to 431)
AUTHORS     Amachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
            Fujii,T. and Muramatsu,Y.
TITLE       Direct Submission
JOURNAL     Submitted (27-MAR-2003) Seigo Amachi, Chiba University, Dept. of
            Bioresources Chem.; 648 Matsudo, Matsudo-shi, Chiba 271-8510, Japan
            (E-mail:amachi@faculty.chiba-u.jp, Tel:81-47-308-8868,
            Fax:81-47-308-8866)
FEATURES   Location/Qualifiers
            source
            1..431
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                /mol_type="genomic DNA"
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rRNA

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Query Match      93.3%; Score 22.4; DB 15; Length 431;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTTCG 24
    |||||
Db 31 CAACTCGAACGGAAGGCGCTTTTCG 54

RESULT 48
AF078232
LOCUS      AF078232             432 bp    DNA          linear      ENV 10-MAY-2004
DEFINITION Grassland soil clone saf2_117 16S ribosomal RNA gene, partial
sequence.
ACCESSION  AF078232
VERSION     AF078232.1  GI:4590103
KEYWORDS    ENV.
SOURCE      grassland soil clone saf2_117
            grassland soil clone saf2_117
            Bacteria; environmental samples.
REFERENCE   1  (bases 1 to 432)
AUTHORS     McCaig,A.E., Glover,L.A. and Prosser,J.I.
TITLE       Molecular analysis of bacterial community structure and diversity
            in unimproved and improved upland grass pastures
JOURNAL     Appl. Environ. Microbiol. 65 (4), 1721-1730 (1999)
PUBMED     10103273
REFERENCE   2  (bases 1 to 432)
AUTHORS     McCaig,A.E., Prosser,J.I. and Glover,L.A.
TITLE       Direct Submission
JOURNAL     Submitted (16-JUL-1998) Institute of Medical Sciences, Department
            of Molecular and Cell Biology, University of Aberdeen,
            Foresterhill, Aberdeen AB25 2ZD, Scotland, UK
FEATURES   Location/Qualifiers
            source
            1..432
                /organism="grassland soil clone saf2_117"
                /mol_type="genomic DNA"
                /db_xref="taxon:80202"
                /clone_lib="unimproved grassland soil SAF2"
                /environmental_sample
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rRNA

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ORIGIN
Query Match      93.3%; Score 22.4; DB 1; Length 432;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTTCG 24
    |||||
Db 9 CAACTCGAACGGAAGGCGCTTTTCG 32

RESULT 49
AY673198
LOCUS      AY673198             433 bp    DNA          linear      BCT 20-MAY-2005
DEFINITION Mycobacteriaceae bacterium Ellin7032 16S ribosomal RNA gene,
partial sequence.
ACCESSION  AY673198
VERSION     AY673198.1  GI:56683055
KEYWORDS
SOURCE      Mycobacteriaceae bacterium Ellin7032
ORGANISM    Mycobacteriaceae bacterium Ellin7032
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae.
REFERENCE   1  (bases 1 to 433)
AUTHORS     Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE       Effects of growth medium, inoculum size, and incubation time on
            culturability and isolation of soil bacteria
JOURNAL     Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED     15691937
REFERENCE   2  (bases 1 to 433)
AUTHORS     Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE       Direct Submission
JOURNAL     Submitted (02-JUL-2004) Department of Microbiology and Immunology,
            University of Melbourne, Grattan Street, Parkville, Victoria 3010,
            Australia
FEATURES   Location/Qualifiers
            source
            1..433
                /organism="Mycobacteriaceae bacterium Ellin7032"
                /mol_type="genomic DNA"
                /isolate="Ellin7032"
                /isolation_source="soil"
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                <1..>433
                /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 433;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTTCG 24
    |||||
Db 31 CAACTCGAACGGAAGGCGCTTTTCG 54

RESULT 50
AY673266
LOCUS      AY673266             433 bp    DNA          linear      BCT 20-MAY-2005
DEFINITION Mycobacteriaceae bacterium Ellin7100 16S ribosomal RNA gene,
partial sequence.
ACCESSION  AY673266
VERSION     AY673266.1  GI:56683123
KEYWORDS
SOURCE      Mycobacteriaceae bacterium Ellin7100
ORGANISM    Mycobacteriaceae bacterium Ellin7100
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae.
REFERENCE   1  (bases 1 to 433)
AUTHORS     Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE       Effects of growth medium, inoculum size, and incubation time on
            culturability and isolation of soil bacteria
JOURNAL     Appl. Environ. Microbiol. 71 (2), 826-834 (2005)

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PUBMED 15691937
REFERENCE 2 (bases 1 to 433)
AUTHORS Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES
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                /organism="Mycobacteriaceae bacterium Ellin7100"
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                /db_xref="taxon:305283"
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                /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 433;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 31 CAACTCGAACGGAAGGCGCTTTCG 54

RESULT 51
DQ0631195
LOCUS actinobacterium BAL259 435 bp DNA linear BCT 27-JUN-2005
DEFINITION actinobacterium BAL259 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ0631195
VERSION DQ0631195.1 GI:68139233
KEYWORDS
SOURCE actinobacterium BAL259
ORGANISM actinobacterium BAL259
REFERENCE 1 (bases 1 to 435)
AUTHORS Riemann,L., Leitert,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE Bacterial community composition in the central Baltic Sea analyzed
by cultivation and molecular-based methods
JOURNAL Unpublished
AUTHORS Riemann,L., Leitert,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES
    source      Location/Qualifiers
                1..435
                /organism="actinobacterium BAL259"
                /mol_type="genomic DNA"
                /strain="BAL259"
                /isolation_source="Baltic Sea, 3m depth, Landsort deep St.
                BY31, Zobe1/R2A media"
                /db_xref="taxon:331808"
                /country="Sweden"
                /lat_lon="60.42.726N, 05.05.595E"
                /collection_dates="17 May 2004"
                <1..>435
                /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 435;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 16 CAACTCGAACGGAAGGCGCTTTCG 39

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RESULT 52
AY234692
LOCUS Bacterium Ellin6040 16S ribosomal RNA gene, partial sequence.
DEFINITION Bacterium Ellin6040 16S ribosomal RNA gene, partial sequence.
ACCESSION AY234692
VERSION AY234692.1 GI:37961849
KEYWORDS
SOURCE Bacterium Ellin6040
ORGANISM Bacterium Ellin6040
REFERENCE 1 (bases 1 to 435)
AUTHORS Corynebacterineae; Actinobacteridae; Actinomycetales;
Joseph,S.J., Hugenholtz,P., Sangwan,P., Osborne,C.A. and
Janssen,P.H.
TITLE Laboratory Cultivation of Widespread and Previously Uncultured Soil
Bacteria
JOURNAL Appl. Environ. Microbiol. 69 (12), 7210-7215 (2003)
PUBMED 14660368
REFERENCE 2 (bases 1 to 435)
AUTHORS Joseph,S.J., Hugenholtz,P., Rana,P., Osborne,C.A., Sait,M. and
Janssen,P.H.
TITLE Direct Submission
JOURNAL Submitted (12-FEB-2003) Department of Microbiology and Immunology,
University of Melbourne, Parkville, Victoria 3010, Australia
FEATURES
    source      Location/Qualifiers
                1..435
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                /mol_type="genomic DNA"
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                /db_xref="taxon:234122"
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                /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 435;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 31 CAACTCGAACGGAAGGCGCTTTCG 54

RESULT 53
AY673233
LOCUS Mycobacteriaceae bacterium Ellin7067 16S ribosomal RNA gene,
DEFINITION Mycobacteriaceae bacterium Ellin7067 16S ribosomal RNA gene,
partial sequence.
ACCESSION AY673233
VERSION AY673233.1 GI:56683090
KEYWORDS
SOURCE Mycobacteriaceae bacterium Ellin7067
ORGANISM Mycobacteriaceae bacterium Ellin7067
REFERENCE 1 (bases 1 to 435)
AUTHORS Bacteria; Actinobacteriae; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
Joseph,K.E., Joseph,S.J. and Janssen,P.H.
TITLE Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
JOURNAL Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED 15691937
REFERENCE 2 (bases 1 to 435)
AUTHORS Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES
    source      Location/Qualifiers
                1..435
                /organism="Mycobacteriaceae bacterium Ellin7067"
                /mol_type="genomic DNA"
                /isolate="Ellin7067"
                /isolation_source="soil"

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AUTHORS	Davis, K.E., Joseph, S.J. and Janssen, P.H.
TITLE	Effects of growth medium, inoculum size, and incubation time on culturability and isolation of soil bacteria
JOURNAL	Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBLISHED	15691937
REFERENCE	2 (bases 1 to 436)
AUTHORS	Davis, K.E.R., Joseph, S.J. and Janssen, P.H.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUL-2004) Department of Microbiology and Immunology, University of Melbourne, Grattan Street, Parkville, Victoria 3010, Australia
FEATURES	Location/Qualifiers
source	1..436
	/organism="Mycobacteriaceae bacterium Ellin7033"
	/mol_type="genomic DNA"
	/isolate="Ellin7033"
	/isolation_source="soil"
	/db_xref="taxon:305256"
	<1..>436
	/product="16S ribosomal RNA"
rRNA	
ORIGIN	
Query Match	93.3%; Score 22.4; DB 15; Length 436;
Best Local Similarity	95.8%; Pred. No. 3.6e+02;
Matches	23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 CAAGTCGAACGGAAGGCGCTTTTCG 24
Db	31 CAAGTCGAACGGAAGGCGCTTTTCG 54
RESULT 56	
LOCUS	AY673304
DEFINITION	Mycobacteriaceae bacterium Ellin7138 16S ribosomal RNA gene, partial sequence.
ACCESSION	AY673304
VERSION	AY673304.1
KEYWORDS	GI:56683161
SOURCE	
ORGANISM	
REFERENCE	1 (bases 1 to 436)
AUTHORS	Davis, K.E., Joseph, S.J. and Janssen, P.H.
TITLE	Effects of growth medium, inoculum size, and incubation time on culturability and isolation of soil bacteria
JOURNAL	Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBLISHED	15691937
REFERENCE	2 (bases 1 to 436)
AUTHORS	Davis, K.E.R., Joseph, S.J. and Janssen, P.H.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUL-2004) Department of Microbiology and Immunology, University of Melbourne, Grattan Street, Parkville, Victoria 3010, Australia
FEATURES	Location/Qualifiers
source	1..436
	/organism="Mycobacteriaceae bacterium Ellin7138"
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	/isolate="Ellin7138"
	/isolation_source="soil"
	/db_xref="taxon:305288"
	<1..>436
	/product="16S ribosomal RNA"
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ORIGIN	
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Best Local Similarity	95.8%; Pred. No. 3.6e+02;
Matches	23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 CAAGTCGAACGGAAGGCGCTTTTCG 24
Db	31 CAAGTCGAACGGAAGGCGCTTTTCG 54
RESULT 55	
LOCUS	AY673199
DEFINITION	Mycobacteriaceae bacterium Ellin7033 16S ribosomal RNA gene, partial sequence.
ACCESSION	AY673199
VERSION	AY673199.1
KEYWORDS	GI:56683056
SOURCE	
ORGANISM	
REFERENCE	1 (bases 1 to 436)
AUTHORS	Davis, K.E., Joseph, S.J. and Janssen, P.H.
TITLE	Effects of growth medium, inoculum size, and incubation time on culturability and isolation of soil bacteria
JOURNAL	Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBLISHED	15691937
REFERENCE	2 (bases 1 to 436)
AUTHORS	Davis, K.E.R., Joseph, S.J. and Janssen, P.H.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUL-2004) Department of Microbiology and Immunology, University of Melbourne, Grattan Street, Parkville, Victoria 3010, Australia
FEATURES	Location/Qualifiers
source	1..436
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	/mol_type="genomic DNA"
	/strain="BAL106"
	/isolation_source="Baltic Sea, 3m depth, Landsort deep St. BY31, Zobell/RZA media"
	/db_xref="taxon:331778"
	/country="Sweden"
	/lat_lon="60.42.726N, 05.05.595E"
	/collection_date="2 July 2003"
	<1..>436
	/product="16S ribosomal RNA"
rRNA	
ORIGIN	
Query Match	93.3%; Score 22.4; DB 15; Length 436;
Best Local Similarity	95.8%; Pred. No. 3.6e+02;
Matches	23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 CAAGTCGAACGGAAGGCGCTTTTCG 24
Db	20 CAAGTCGAACGGAAGGCGCTTTTCG 43
RESULT 54	
LOCUS	AY673199
DEFINITION	Mycobacteriaceae bacterium Ellin7033 16S ribosomal RNA gene, partial sequence.
ACCESSION	AY673199
VERSION	AY673199.1
KEYWORDS	GI:56683056
SOURCE	
ORGANISM	
REFERENCE	1 (bases 1 to 436)
AUTHORS	Davis, K.E., Joseph, S.J. and Janssen, P.H.
TITLE	Effects of growth medium, inoculum size, and incubation time on culturability and isolation of soil bacteria
JOURNAL	Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBLISHED	15691937
REFERENCE	2 (bases 1 to 436)
AUTHORS	Davis, K.E.R., Joseph, S.J. and Janssen, P.H.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUL-2004) Department of Microbiology and Immunology, University of Melbourne, Grattan Street, Parkville, Victoria 3010, Australia
FEATURES	Location/Qualifiers
source	1..436
	/organism="actinobacterium BAL106"
	/mol_type="genomic DNA"
	/strain="BAL106"
	/isolation_source="Baltic Sea, 3m depth, Landsort deep St. BY31, Zobell/RZA media"
	/db_xref="taxon:331778"
	/country="Sweden"
	/lat_lon="60.42.726N, 05.05.595E"
	/collection_date="2 July 2003"
	<1..>436
	/product="16S ribosomal RNA"
rRNA	
ORIGIN	
Query Match	93.3%; Score 22.4; DB 15; Length 436;
Best Local Similarity	95.8%; Pred. No. 3.6e+02;
Matches	23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 CAAGTCGAACGGAAGGCGCTTTTCG 24
Db	20 CAAGTCGAACGGAAGGCGCTTTTCG 43
RESULT 54	
LOCUS	AY673199
DEFINITION	Mycobacteriaceae bacterium Ellin7033 16S ribosomal RNA gene, partial sequence.
ACCESSION	AY673199
VERSION	AY673199.1
KEYWORDS	GI:56683056
SOURCE	
ORGANISM	
REFERENCE	1 (bases 1 to 436)
AUTHORS	Davis, K.E., Joseph, S.J. and Janssen, P.H.
TITLE	Effects of growth medium, inoculum size, and incubation time on culturability and isolation of soil bacteria
JOURNAL	Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBLISHED	15691937
REFERENCE	2 (bases 1 to 436)
AUTHORS	Davis, K.E.R., Joseph, S.J. and Janssen, P.H.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUL-2004) Department of Microbiology and Immunology, University of Melbourne, Grattan Street, Parkville, Victoria 3010,

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RESULT 57
AF078419
LOCUS      437 bp      DNA      linear      ENV 10-MAY-2004
DEFINITION  Grassland soil clone sl3_612 16S ribosomal RNA gene, partial
sequence.
ACCESSION  AF078419
VERSION    AF078419.1 GI:4590290
KEYWORDS   ENV.
SOURCE     Grassland soil clone sl3_612
ORGANISM   Grassland soil clone sl3_612
           Bacteria; environmental samples.
REFERENCE  1 (bases 1 to 437)
AUTHORS    McCaig,A.E., Glover,L.A. and Prosser,J.I.
TITLE      Molecular analysis of bacterial community structure and diversity
           in unimproved and improved upland grass pastures
JOURNAL    Appl. Environ. Microbiol. 65 (4), 1721-1730 (1999)
PUBMED     10103273
REFERENCE  2 (bases 1 to 437)
AUTHORS    McCaig,A.E., Prosser,J.I. and Glover,L.A.
TITLE      Direct Submission
JOURNAL    Submitted (16-JUL-1998) Institute of Medical Sciences, Department
           of Molecular and Cell Biology, University of Aberdeen,
           Foresterhill, Aberdeen AB25 2ZD, Scotland, UK
FEATURES   Location/Qualifiers
            source
              1..437
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              /mol_type="genomic DNA"
              /db_xref="taxon:80115"
              /clone_lib="Improved grassland soil SL3"
              /environmental_sample
              <1..>437
              /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 1; Length 437;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 9 CAAGTCGACGGAAGGCGCTTTCG 32

RESULT 58
AB232370
LOCUS      441 bp      DNA      linear      BCT 25-JAN-2006
DEFINITION  Mycobacterium kansasii gene for 16S rRNA, partial sequence,
strain:SA-10.
ACCESSION  AB232370
VERSION    AB232370.1 GI:73589607
KEYWORDS   Mycobacterium kansasii
SOURCE     Mycobacterium kansasii
ORGANISM   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
           Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE  1
AUTHORS    Iwamoto,T. and Saito,H.
TITLE      Comparative study of two typing methods, hsp65 PRA and ITS
           sequencing, revealed a possible evolutionary link between
           Mycobacterium kansasii type I and II isolates
JOURNAL    FEMS Microbiol. Lett. 254, 129-133 (2006)
PUBMED     16103273
REFERENCE  2 (bases 1 to 441)
AUTHORS    Iwamoto,T.
TITLE      Direct Submission
JOURNAL    Submitted (17-AUG-2005) Tomotada Iwamoto, Kobe Institute of Health,
           Department of Microbiology; Chuo-ku Minatojima-nakamachi 4-6, Kobe,
           Hyogo 6500046, Japan (E-mail: kx2t-iwmt@asahi-net.or.jp,
           URL: http://www.city.kobe.jp/cityoffice/18/menu03/h/kanken/kanken-
           top, Tel:81-78-302-6251, Fax:81-78-302-0894)
           Location/Qualifiers
            source
              1..441

/organism="Mycobacterium kansasii"
/mol_type="genomic DNA"
/db_xref="taxon:1768"
/notes="type II"
<1..>441
/product="16S ribosomal RNA"

Query Match      93.3%; Score 22.4; DB 15; Length 441;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 5 CAAGTCGAACGGAAGGCGCTTTCG 28

RESULT 60
AY306205
LOCUS      444 bp      DNA      linear      BCT 25-JUN-2003
DEFINITION  Mycobacterium sp. HSC507 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY306205
VERSION    AY306205.1 GI:32250954
KEYWORDS   Mycobacterium sp. HSC507
SOURCE     Mycobacterium sp. HSC507
           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
           Corynebacterineae; Mycobacteriaceae; Mycobacterium.

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REFERENCE 1 (bases 1 to 444)
AUTHORS Pauls,R.J., Turenne,C.Y., Wolfe,J.N. and Kabani,A.
TITLE A High Proportion of Novel Mycobacteria Species Identified by 16S
rDNA Analysis Among Slowly Growing AccuProbe Negative Strains in a
Clinical Setting
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 444)
AUTHORS Turenne,C.Y.
TITLE Direct Submission
JOURNAL Submitted (26-MAY-2003) National Reference Centre for
Mycobacteriology, National Microbiology Laboratory, Health Canada,
1015 Arlington Street, Winnipeg, MB R3E 3R2, Canada
FEATURES
source
1..444
/organism="Mycobacterium sp. HSC507"
/mol_type="genomic DNA"
/strain="HSC507"
/isolation_source="sputum"
/specific_host="Homo sapiens"
/db_xref="taxon:235258"
<1..>444
/product="16S ribosomal RNA"
rRNA
ORIGIN
Query Match 93.3%; Score 22.4; DB 15; Length 444;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAAGTCGAACGGAAGGCCCTTCG 24
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Db 5 CAAGTCGAACGGAAGGCCCTTCG 28
|||||

RESULT 61
LOCUS AB106917 445 bp DNA linear BCT 09-SEP-2003
DEFINITION Gram-positive bacterium 1-3 for 16S ribosomal RNA, partial
sequence.
ACCESSION AB106917
VERSION AB106917.1 GI:29421131
KEYWORDS
SOURCE Gram-positive bacterium 1-3
ORGANISM Gram-positive bacterium 1-3
Bacteria.
REFERENCE 1
AUTHORS Amachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
Fujii,T. and Muramatsu,Y.
TITLE Microbial participation in iodine volatilization from soils
JOURNAL Environ. Sci. Technol. 37, 3885-3890 (2003)
REFERENCE 2 (bases 1 to 445)
AUTHORS Amachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
Fujii,T. and Muramatsu,Y.
TITLE Direct Submission
JOURNAL Submitted (27-MAR-2003) Seigo Amachi, Chiba University, Dept. of
Bioresources Chem.; 648 Matsudo, Matsudo-shi, Chiba 271-8510, Japan
(E-mail:amachi@faculty.chiba-u.jp, Tel:81-47-308-8868,
Fax:81-47-308-8866)
FEATURES
source
1..445
/organism="Gram-positive bacterium 1-3"
/mol_type="genomic DNA"
/strain="1-3"
/db_xref="taxon:226199"
<1..>445
/product="16S ribosomal RNA"
rRNA
ORIGIN
Query Match 93.3%; Score 22.4; DB 15; Length 445;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAAGTCGAACGGAAGGCCCTTCG 24
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Db 31 CAAGTCGAACGGAAGGCCCTTCG 54
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RESULT 62
LOCUS DQ067466 445 bp DNA linear BCT 18-JUL-2005
DEFINITION Mycobacterium sp. FI05167 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ067466
VERSION DQ067466.1 GI:67528039
KEYWORDS
SOURCE Mycobacterium sp. FI05167
ORGANISM Mycobacterium sp. FI05167
Bacteria; Actinobacteriia; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 445)
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE Unusual mycobacteria isolated from clinical samples
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 445)
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-2005) Reg. Reference Center for Mycobacteria,
Careggi Hospital, Piastra dei Servizi, Ospedale Careggi, v.le
Morgagni 85, Firenze, FI 50134, Italy
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QY 1 CAAGTCGAACGGAAGGCCCTTCG 24
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Db 9 CAAGTCGAACGGAAGGCCCTTCG 32
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RESULT 63
LOCUS MS91016SR 450 bp DNA linear BCT 01-AUG-1997
DEFINITION Mycobacterium sp.16S rRNA gene, isolate BN910, partial.
ACCESSION Y08205
VERSION Y08205.1 GI:2292948
KEYWORDS 16S ribosomal RNA; 16S rRNA.
SOURCE Mycobacterium sp.
ORGANISM Mycobacterium sp.
Bacteria; Actinobacteriia; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1
AUTHORS Hagenau,C., Behringer,K., Naumann,L., Kaiser,R. and
Schulze-Roebebecke,R.
TITLE Unpublished
JOURNAL 2 (bases 1 to 450)
REFERENCE Hagenau,C.
AUTHORS Direct Submission
TITLE Submitted (18-SEP-1996) C. Hagenau, Hygiene-Institute, University
of Bonn, Sigmund-Freud-Strasse 25, D-53105 Bonn, FRG
JOURNAL Related sequence M95469.
COMMENT Location/Qualifiers
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Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCCTTTCG 24
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Db 21 CAAGTCGAACGGAAGGCCCTTTCG 44

RESULT 64
MSPI6SR
LOCUS      MSP16SR
DEFINITION Mycobacterium sp. 16S rRNA gene.
ACCESSION Y07954
VERSION Y07954.1 GI:2292951
KEYWORDS 16S ribosomal RNA; 16S rRNA gene.
SOURCE Mycobacterium sp.
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 Hagenau,C., Behringer,K., Naumann,L., Kaiser,R. and
          Schulze-Roebecke,R.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 450)
AUTHORS Hagenau,C.
TITLE Direct Submission
JOURNAL Submitted (12-SEP-1996) C. Hagenau, Hygiene-Institute, University
of Bonn, Sigmund-Freud-Strasse 25, D-53105 Bonn, FRG
COMMENT Related sequence: M95469.
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              /mol_type="genomic DNA"
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            /gene="16S rRNA"
            /product="16S ribosomal RNA"

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 450;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCCTTTCG 24
    |||||
Db 21 CAAGTCGAACGGAAGGCCCTTTCG 44

RESULT 65
AY358002
LOCUS      AY358002
DEFINITION Actinobacterium iri117 16S ribosomal RNA gene, partial sequence.
ACCESSION AY358002
VERSION AY358002.1 GI:34500643
KEYWORDS actinobacterium iri117
SOURCE actinobacterium iri117
ORGANISM Bacteria; Actinobacteria.
REFERENCE 1 (bases 1 to 450)
AUTHORS Idris,R., Trifonova,R., Puschenreiter,M., Wenzel,W.W. and
          Sessitsch,A.
TITLE Bacterial Communities Associated with Flowering Plants of the Ni
          Hyperaccumulator Thlaspi goesingense

JOURNAL Appl. Environ. Microbiol. 70 (5), 2667-2677 (2004)
PUBMED 15128517
REFERENCE 2 (bases 1 to 450)
AUTHORS Idris,R. and Sessitsch,A.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Environmental and Life Sciences, ARC
          Seibersdorf Research GmbH, Seibersdorf A-2444, Austria
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              /db_xref="taxon:244182"
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              /product="16S ribosomal RNA"

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Query Match      93.3%; Score 22.4; DB 15; Length 450;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCCTTTCG 24
    |||||
Db 53 CAAGTCGAACGGAAGGCCCTTTCG 76

RESULT 66
AJ746062
LOCUS      AJ746062
DEFINITION Mycobacterium sp. MG5 partial 16S rRNA gene, isolate MGS.
ACCESSION AJ746062
VERSION AJ746062.1 GI:161097518
KEYWORDS 16S ribosomal RNA; 16S rRNA gene.
SOURCE Mycobacterium sp. MG5
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 Gomila,M., Gasco,J., Busquets,A., Gil,J., Bernabeu,R., Buades,J.M.
          and Lalucat,J.
TITLE Identification of culturable bacteria present in haemodialysis
          water and fluid
JOURNAL FEMS Microbiol. Ecol. 52 (1), 101-114 (2005)
REFERENCE 2 (bases 1 to 454)
AUTHORS Gomila,M.
TITLE Direct Submission
JOURNAL Submitted (07-JUN-2004) Gomila M., Biologia-IMEDEA. Microbiologia,
          Universitat de les Illes Balears, Ctra. Valldemossa, km. 7.5, 07122
          Palma de Mallorca, SPAIN
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              /mol_type="genomic DNA"
              /isolate="MGS"
              /isolation_source="haemodialysis water distribution
              system"
              /db_xref="taxon:280864"
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Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCCTTTCG 24
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Db 24 CAAGTCGAACGGAAGGCCCTTTCG 47

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RESULT 67
AY358001
LOCUS      AY358001          456 bp      DNA      linear      BCT 19-AUG-2005
DEFINITION Actinobacterium irIII6 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY358001
VERSION     AY358001.1  GI:34500642
KEYWORDS
SOURCE      actinobacterium irIII6
ORGANISM    actinobacterium irIII6
REFERENCE   1 (bases 1 to 456)
AUTHORS     Idris,R., Trifonova,R., Puschenreiter,M., Wenzel,W.W. and
            Sessitsch,A.
TITLE       Bacterial Communities Associated with Flowering Plants of the Ni
            Hyperaccumulator Thlaspi goesingense
JOURNAL     Appl. Environ. Microbiol. 70 (5), 2667-2677 (2004)
PUBMED      15128517
REFERENCE   2 (bases 1 to 456)
AUTHORS     Idris,R. and Sessitsch,A.
TITLE       Direct Submission
JOURNAL     Submitted (01-AUG-2003) Environmental and Life Sciences, ARC
            Seibersdorf Research GmbH, Seibersdorf A-2444, Austria
FEATURES   .
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            /db_xref="taxon:244181"
            <1..>456
            /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%;   Score 22.4;   DB 15;   Length 456;
Best Local Similarity 95.8%;   Pred. No. 3.6e+02;   Indels 0;   Gaps 0;
Matches 23;   Conservative 0;   Mismatches 1;

Qy 1 CAACTCGAACGGAAGGCGCTTTTCG 24
|||||
Db 53 CAACTCGAACGGAAGGCGCTTTTCG 76

RESULT 68
AJ609008
LOCUS      AJ609008          459 bp      DNA      linear      ENV 20-JAN-2004
DEFINITION Uncultured bacterium partial 16S rRNA gene, clone 24-9.
ACCESSION  AJ609008
VERSION     AJ609008.1  GI:41033549
KEYWORDS    ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE      uncultured bacterium
ORGANISM    Bacteria; environmental samples.
REFERENCE   1
AUTHORS     Schneider,B.A., Huettl,R.F. and Schneider,B.U.
TITLE       Evidence for a diverse bacterial consortium specialized to the
            degradation of aliphatic and aromatic hydrocarbons in lignite
            matter of a forest reclamation site
JOURNAL     Unpublished
AUTHORS     2 (bases 1 to 459)
            Schneider,B.A.
TITLE       Direct Submission
JOURNAL     Submitted (20-NOV-2003) Schneider B.A., Soil Protection and
            Reclamation, Brandenburg Technical University,
            Theodor-Neubauer-Str. 6, D-03046 Cottbus, GERMANY
FEATURES   .
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            /isolation_source="lignite matter from the subsurface soil
            of a 20 year old Black pine forest"
            /db_xref="taxon:77133"
            /clone="24-9"
            /environmental_sample

ACTINOMYCETALES

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/country="Germany:North-eastern Germany, Lusatian lignite
mining area"
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/product="16S ribosomal RNA"

ORIGIN
Query Match      93.3%;   Score 22.4;   DB 1;   Length 459;
Best Local Similarity 95.8%;   Pred. No. 3.6e+02;   Indels 0;   Gaps 0;
Matches 23;   Conservative 0;   Mismatches 1;

Qy 1 CAACTCGAACGGAAGGCGCTTTTCG 24
|||||
Db 9 CAACTCGAACGGAAGGCGCTTTTCG 32

RESULT 69
AY754884
LOCUS      AY754884          459 bp      DNA      linear      BCT 17-OCT-2004
DEFINITION Mycobacterium vaccae strain FI04098 16S ribosomal RNA gene, partial
            sequence.
ACCESSION  AY754884
VERSION     AY754884.1  GI:54065968
KEYWORDS
SOURCE      Mycobacterium vaccae
ORGANISM    Mycobacterium vaccae
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE   1 (bases 1 to 459)
AUTHORS     Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE       Unusual mycobacteria isolated from clinical samples
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 459)
AUTHORS     Tortoli,E.
TITLE       Direct Submission
JOURNAL     Submitted (16-SEP-2004) Microbiology, Careggi Hospital, viale
            Morgagni 85, Firenze, FI 50134, Italy
FEATURES   .
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rRNA

ORIGIN
Query Match      93.3%;   Score 22.4;   DB 15;   Length 459;
Best Local Similarity 95.8%;   Pred. No. 3.6e+02;   Indels 0;   Gaps 0;
Matches 23;   Conservative 0;   Mismatches 1;

Qy 1 CAACTCGAACGGAAGGCGCTTTTCG 24
|||||
Db 25 CAACTCGAACGGAAGGCGCTTTTCG 48

RESULT 70
AY754885
LOCUS      AY754885          459 bp      DNA      linear      BCT 17-OCT-2004
DEFINITION Mycobacterium sp. FI02139 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY754885
VERSION     AY754885.1  GI:54065976
KEYWORDS
SOURCE      Mycobacterium sp. FI02139
ORGANISM    Mycobacterium sp. FI02139
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE   1 (bases 1 to 459)
AUTHORS     Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE       Unusual mycobacteria isolated from clinical samples
JOURNAL     Unpublished

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REFERENCE 2 (bases 1 to 459)
AUTHORS Tortoli,E.
TITLE Direct Submission
JOURNAL Submitted (16-SEP-2004) Microbiology, Careggi Hospital, viale
Morgagni 85, Firenze, FI 50134, Italy
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/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 93.3%; Score 22.4; DB 15; Length 459;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
|||||
Db 24 CAAGTCGAACGGAAGGCGCTTTCG 47

RESULT 71
AB118817 464 bp DNA linear BCT 01-JUN-2005
LOCUS Denitrifying bacterium W67a gene for 16S ribosomal RNA, partial
DEFINITION sequence.
AB118817
ACCESSION AB118817.1 GI:56841148
VERSION
KEYWORDS denitrifying bacterium W67a
SOURCE denitrifying bacterium W67a
ORGANISM Bacteria; Actinobacteria.

REFERENCE 1
AUTHORS Hashimoto,T., Whang,K.S. and Nagaoka,K.
TITLE A Quantitative Evaluation and Phylogenetic Characterization of
Oligotrophic Denitrifying Bacteria Harbored in Subsurface Upland
Soil Using Improved Culturability
JOURNAL Biol. Fertil. Soils (2005) In press
REFERENCE 2 (bases 1 to 464)
AUTHORS Hashimoto,T. and Whang,K.
TITLE Direct Submission
JOURNAL Submitted (29-AUG-2003) Tomoyoshi Hashimoto, National Agricultural
Research Center for Kyushu Okinawa Region, Department of
Agro-Environmental Research; Nishigoushi-cho Suyu 2421,
Kikuchi-gun, Kumamoto, 861-1192, Japan
(E-mail:hashimoto@affrc.go.jp, Tel:0962427765, Fax:0962491002)
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rRNA

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Query Match 93.3%; Score 22.4; DB 15; Length 464;
Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
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Db 47 CAAGTCGAACGGAAGGCGCTTTCG 70

RESULT 72
DQ142669 464 bp DNA linear BCT 13-AUG-2005
LOCUS Mycobacterium sp. FI03023 16S ribosomal RNA gene, partial sequence.
DEFINITION

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ACCESSION DQ142669
VERSION DQ142669.1 GI:71912648
KEYWORDS
SOURCE
ORGANISM Mycobacterium sp. FI03023
Mycobacterium sp. FI03023
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 464)
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE Unusual mycobacteria isolated from clinical specimens
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 464)
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE Direct Submission
JOURNAL Submitted (18-JUL-2005) Microbiology, Careggi Hospital, Viale
Morgagni 85, Firenze, FI 50134, Italy
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rRNA

ORIGIN
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Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
|||||
Db 24 CAAGTCGAACGGAAGGCGCTTTCG 47

RESULT 73
DQ142672 464 bp DNA linear BCT 13-AUG-2005
LOCUS Mycobacterium sp. FI05244 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION DQ142672
VERSION DQ142672.1 GI:71912651
KEYWORDS
SOURCE Mycobacterium sp. FI05244
Mycobacterium sp. FI05244
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 464)
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE Unusual mycobacteria isolated from clinical specimens
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 464)
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE Direct Submission
JOURNAL Submitted (25-JUL-2005) Microbiology, Careggi Hospital, Viale
Morgagni 85, Firenze, FI 50134, Italy
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rRNA

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Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
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Db 24 CAAGTCGAACGGAAGGCGCTTTCG 47

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RESULT 74
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mycobacterium sp. FI05038
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 466)
Tortoli,E., Mantella,A., Mariottini,A., Mazzarelli,G., Pecile,P.,
Rogasi,P.G., Sterratino,G., Pantoni,E. and Leoncini,F.
Successfully treated spondylodiscitis due to a previously
unreported mycobacterium
J. Med. Microbiol. 55 (PT 1), 119-121 (2006)
16388040
Mycobacterium sp. FI05038
Mycobacterium sp. FI05038
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 466)
Tortoli,E., Mariottini,A. and Mazzarelli,G.
Direct Submission
Submitted (18-MAY-2005) Reg. Reference Center for Mycobacteria,
Careggi Hospital, Piasra dei Servi, Ospedale Careggi, v.le
Morgagni 85, Firenze, FI 50134, Italy
Morgagni
Location/Qualifiers
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Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
Db 28 CAAGTCGAACGGAAGGCGCTTTCG 51
RESULT 75
AY524839
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mycobacterium sp. FI02027
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 466)
Tortoli,E., Mariottini,A. and Mazzarelli,G.
Unusual mycobacteria isolated from clinical samples
Unpublished
2 (bases 1 to 466)
Tortoli,E.
Direct Submission
Submitted (08-JAN-2004) Microbiology, Careggi Hospital, viale
Morgagni 85, Firenze, FI 50134, Italy
Morgagni
Location/Qualifiers
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rRNA
ORIGIN

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Query Match 93.3%; Score 22.4; DB 15; Length 466;
Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
Db 28 CAAGTCGAACGGAAGGCGCTTTCG 51
RESULT 76
DQ154332
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mycobacterium sp. FI05038
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 466)
Tortoli,E., Mariottini,A., Mazzarelli,G., Pecile,P.,
Rogasi,P.G., Sterratino,G., Pantoni,E. and Leoncini,F.
Successfully treated spondylodiscitis due to a previously
unreported mycobacterium
J. Med. Microbiol. 55 (PT 1), 119-121 (2006)
16388040
Mycobacterium sp. FI05038
Mycobacterium sp. FI05038
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 466)
Tortoli,E., Mariottini,A. and Mazzarelli,G.
Direct Submission
Submitted (18-MAY-2005) Reg. Reference Center for Mycobacteria,
Careggi Hospital, Piasra dei Servi, Ospedale Careggi, v.le
Morgagni 85, Firenze, FI 50134, Italy
Morgagni
Location/Qualifiers
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/product="16S ribosomal RNA"
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Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
Db 20 CAAGTCGAACGGAAGGCGCTTTCG 43
RESULT 77
AY043719
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mycobacterium sp. FI02027
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 466)
Tortoli,E., Mariottini,A. and Mazzarelli,G.
Unusual mycobacteria isolated from clinical samples
Unpublished
2 (bases 1 to 466)
Tortoli,E.
Direct Submission
Submitted (08-JAN-2004) Microbiology, Careggi Hospital, viale
Morgagni 85, Firenze, FI 50134, Italy
Morgagni
Location/Qualifiers
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Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
Db 20 CAAGTCGAACGGAAGGCGCTTTCG 43
RESULT 78
AY043719
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
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ORGANISM
Mycobacterium sp. FI02027
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 466)
Tortoli,E., Mariottini,A. and Mazzarelli,G.
Unusual mycobacteria isolated from clinical samples
Unpublished
2 (bases 1 to 466)
Tortoli,E.
Direct Submission
Submitted (08-JAN-2004) Microbiology, Careggi Hospital, viale
Morgagni 85, Firenze, FI 50134, Italy
Morgagni
Location/Qualifiers
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rRNA
ORIGIN

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FEATURES
source Vancouver, BC V6S 2L2, Canada
Location/Qualifiers
1..473
/organism="uncultured actinobacterium"
/mol_type="genomic DNA"
/db_xref="taxon:152507"
/clone="NOW2.35WL"
/environmental_sample
/note="from forest cut-block surface organic matter from the British Columbia Ministry of Forests Long-Term Soil Productivity (LTSP) Installation near Williams Lake, BC, Canada"
<1..>473
/product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match 93.3%; Score 22.4; DB 1; Length 473;
Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
|||||
Db 21 CAAGTCGAACGGAAGGCGCTTTCG 44
|||||

RESULT 78
DQ136108 474 bp DNA linear ENV 13-AUG-2005
LOCUS Uncultured bacterium clone SC27 16S ribosomal RNA gene, partial
DEFINITION sequence.
ACCESSION DQ136108
VERSION DQ136108.1 GI:71905197
KEYWORDS ENV,
SOURCE uncultured bacterium
ORGANISM uncultured bacterium
Bacteria; environmental samples.
REFERENCE 1 (bases 1 to 474)
AUTHORS Ka,J.-O., Kim,M.-S. and Ahn,J.-H.
TITLE Microbiological remediation studies on diesel-contaminated soil of Baekun Mountain
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 474)
AUTHORS Ka,J.-O., Kim,M.-S. and Ahn,J.-H.
TITLE Direct Submission
JOURNAL Submitted (19-JUL-2005) School of Applied Biology and Chemistry, Seoul National University, San 56-1 Silimdong Kwanakgu 151-921, Korea

FEATURES
source Location/Qualifiers
1..474
/organism="uncultured bacterium"
/mol_type="genomic DNA"
/isolation_source="diesel-contaminated soil"
/db_xref="taxon:77133"
/clone="SC27"
/environmental_sample
<1..>474
/product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match 93.3%; Score 22.4; DB 1; Length 474;
Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
|||||
Db 41 CAAGTCGAACGGAAGGCGCTTTCG 64
|||||

RESULT 79
AY792024 474 bp DNA linear BCT 20-NOV-2004
LOCUS Mycobacterium sp. 6BR15 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION AY792024

VERSION AV792024.1 GI:55740323
KEYWORDS Mycobacterium sp. 6BR15
SOURCE Mycobacterium sp. 6BR15
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 474)
AUTHORS Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.
TITLE Bioremediation of radioactive water with metallic materials
JOURNAL Unpublished
JOURNAL 2 (bases 1 to 474)
AUTHORS Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.
TITLE Direct Submission
JOURNAL Submitted (25-OCT-2004) Dep Ingenieria y Ciencia de los Materiales, Escuela Tecnica Superior de Ingenieros Industriales, Universidad Politecnica de Madrid, Jose Gutierrez Abascal, 2, Madrid, Madrid 28006, Spain
Location/Qualifiers
1..474
/organism="Mycobacterium sp. 6BR15"
/mol_type="genomic DNA"
/isolate="6BR15"
/isolation_source="radioactive water"
/db_xref="taxon:300870"
<1..>474
/product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match 93.3%; Score 22.4; DB 15; Length 474;
Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
|||||
Db 30 CAAGTCGAACGGAAGGCGCTTTCG 53
|||||

RESULT 80
AY559492 476 bp DNA linear BCT 22-MAR-2004
LOCUS Mycobacterium porcinum strain M552 16S ribosomal RNA gene, partial
DEFINITION sequence.
ACCESSION AY559492
VERSION AY559492.1 GI:45511545
KEYWORDS Mycobacterium porcinum
SOURCE Mycobacterium porcinum
ORGANISM Mycobacterium porcinum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 476)
AUTHORS Hontzeas,N., Belimov,A., Safronova,V. and Glick,B.
TITLE Characterization of various plant growth-promoting bacteria
JOURNAL Unpublished
JOURNAL 2 (bases 1 to 476)
AUTHORS Hontzeas,N., Belimov,A., Safronova,V. and Glick,B.
TITLE Direct Submission
JOURNAL Submitted (25-FEB-2004) Biology, University of Waterloo, 200 University Ave. West, Waterloo, ON N2L 3G1, Canada
Location/Qualifiers
1..476
/organism="Mycobacterium porcinum"
/mol_type="genomic DNA"
/strain="M552"
/db_xref="taxon:39693"
<1..>476
/product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match 93.3%; Score 22.4; DB 15; Length 476;
Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24

[illegible]

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TITLE      Direct Submission
JOURNAL    Submitted (04-AUG-2005) Biological Sciences, Purdue University, 915
           West State Street, West Lafayette, IN 47907-2054, USA
FEATURES   Location/Qualifiers
           source
             1..496
             /organism="uncultured soil bacterium"
             /mol_type="genomic DNA"
             /isolation_source="Ross Forest soil"
             /db_xref="taxon:164851"
             /clones="RFS-Cl4"
             /environmental_sample
             <1..>496
             /product="16S ribosomal RNA"

rRNA
ORIGIN
Query Match      93.3%; Score 22.4; DB 1; Length 496;
Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  CAACTCGAAGCGAAGGCTTTTCG 24
        |||||
Db      51 CAACTCGAAGCGAAGGCTTTTCG 74

RESULT 85
LOCUS    AY215287              498 bp      DNA      linear      BCT 08-APR-2003
DEFINITION Mycobacterium mucogenicum isolate N241 16S ribosomal RNA gene,
partial sequence.
ACCESSION AY215287
VERSION   AY215287.1 GI:28274541
KEYWORDS
SOURCE   Mycobacterium mucogenicum
ORGANISM Mycobacterium mucogenicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS  Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
TITLE    Evaluation of the MicroSeq System for Identification of
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
into a Routine Clinical Mycobacteriology Laboratory
JOURNAL  J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
PUBMED   12682128
AUTHORS  Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.
DIRECT SUBMISSION
TITLE    Submitted (08-JAN-2003) Department of Laboratory Medicine and
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
FEATURES   Location/Qualifiers
           source
             1..498
             /organism="Mycobacterium mucogenicum"
             /mol_type="genomic DNA"
             /isolate="N241"
             /db_xref="taxon:56689"
             <1..>498
             /product="16S ribosomal RNA"

rRNA
ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 498;
Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  CAACTCGAAGCGAAGGCTTTTCG 24
        |||||
Db      54 CAACTCGAAGCGAAGGCTTTTCG 77

RESULT 86
LOCUS    AY215324              498 bp      DNA      linear      BCT 08-APR-2003
DEFINITION Mycobacterium sp. N141 16S ribosomal RNA gene, partial sequence.
ACCESSION AY215324
VERSION   AY215324.1 GI:28274578
KEYWORDS
SOURCE   Mycobacterium sp. N141
ORGANISM Mycobacterium sp. N141
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS  Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
TITLE    Evaluation of the MicroSeq System for Identification of
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
into a Routine Clinical Mycobacteriology Laboratory
JOURNAL  J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
PUBMED   12682128
AUTHORS  Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.
DIRECT SUBMISSION
TITLE    Submitted (08-JAN-2003) Department of Laboratory Medicine and
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
FEATURES   Location/Qualifiers
           source
             1..498
             /organism="Mycobacterium sp. N1772T"
             /mol_type="genomic DNA"
             /isolate="N1772T"
             /db_xref="taxon:220014"
             <1..>498
             /product="16S ribosomal RNA"

rRNA
ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 498;
Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  CAACTCGAAGCGAAGGCTTTTCG 24
        |||||
Db      54 CAACTCGAAGCGAAGGCTTTTCG 77

RESULT 87
LOCUS    AY215336              498 bp      DNA      linear      BCT 08-APR-2003
DEFINITION Mycobacterium sp. N1772T 16S ribosomal RNA gene, partial sequence.
ACCESSION AY215336
VERSION   AY215336.1 GI:28274590
KEYWORDS
SOURCE   Mycobacterium sp. N1772T
ORGANISM Mycobacterium sp. N1772T
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS  Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
TITLE    Evaluation of the MicroSeq System for Identification of
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
into a Routine Clinical Mycobacteriology Laboratory
JOURNAL  J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
PUBMED   12682128
AUTHORS  Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.
DIRECT SUBMISSION
TITLE    Submitted (08-JAN-2003) Department of Laboratory Medicine and
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
FEATURES   Location/Qualifiers
           source
             1..498
             /organism="Mycobacterium sp. N1772T"
             /mol_type="genomic DNA"
             /isolate="N1772T"
             /db_xref="taxon:220014"
             <1..>498
             /product="16S ribosomal RNA"

rRNA
ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 498;
Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  CAACTCGAAGCGAAGGCTTTTCG 24
        |||||
Db      54 CAACTCGAAGCGAAGGCTTTTCG 77

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KEYWORDS   Mycobacterium sp. N141
SOURCE     Mycobacterium sp. N141
ORGANISM   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
           Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE  1 (bases 1 to 498)
AUTHORS    Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
TITLE      Evaluation of the MicroSeq System for Identification of
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
into a Routine Clinical Mycobacteriology Laboratory
JOURNAL    J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
PUBMED     12682128
AUTHORS    Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.
DIRECT SUBMISSION
TITLE      Submitted (08-JAN-2003) Department of Laboratory Medicine and
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
FEATURES   Location/Qualifiers
           source
             1..498
             /organism="Mycobacterium sp. N141"
             /mol_type="genomic DNA"
             /isolate="N141"
             /db_xref="taxon:220003"
             <1..>498
             /product="16S ribosomal RNA"

rRNA
ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 498;
Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  CAACTCGAAGCGAAGGCTTTTCG 24
        |||||
Db      54 CAACTCGAAGCGAAGGCTTTTCG 77

RESULT 87
LOCUS    AY215336              498 bp      DNA      linear      BCT 08-APR-2003
DEFINITION Mycobacterium sp. N1772T 16S ribosomal RNA gene, partial sequence.
ACCESSION AY215336
VERSION   AY215336.1 GI:28274590
KEYWORDS
SOURCE     Mycobacterium sp. N1772T
ORGANISM   Mycobacterium sp. N1772T
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE  1 (bases 1 to 498)
AUTHORS    Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
TITLE      Evaluation of the MicroSeq System for Identification of
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
into a Routine Clinical Mycobacteriology Laboratory
JOURNAL    J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
PUBMED     12682128
AUTHORS    Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.
DIRECT SUBMISSION
TITLE      Submitted (08-JAN-2003) Department of Laboratory Medicine and
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
FEATURES   Location/Qualifiers
           source
             1..498
             /organism="Mycobacterium sp. N1772T"
             /mol_type="genomic DNA"
             /isolate="N1772T"
             /db_xref="taxon:220014"
             <1..>498
             /product="16S ribosomal RNA"

rRNA
ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 498;
Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  CAACTCGAAGCGAAGGCTTTTCG 24
        |||||
Db      54 CAACTCGAAGCGAAGGCTTTTCG 77

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Qy 1 CAAAGTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 54 CAAAGTCGAACGGAAGGCGCTTTCG 77

RESULT 88
DQ154566 499 bp DNA linear ENV 27-AUG-2005
LOCUS Uncultured soil bacterium clone RFS-C252 16S ribosomal RNA gene,
DEFINITION partial sequence.
ACCESSION DQ154566
VERSION DQ154566.1 GI:73672356
KEYWORDS ENV.
SOURCE uncultured soil bacterium
ORGANISM uncultured soil bacterium
REFERENCE 1 (bases 1 to 499)
AUTHORS Becker,J.M., Nakatsu,C.H., Turco,R.F. and Konopka,A.
TITLE Low nutrient fluxes result in high cultivation efficiencies of soil
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 499)
AUTHORS Becker,J.M., Nakatsu,C.H., Turco,R.F. and Konopka,A.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-2005) Biological Sciences, Purdue University, 915
WEST State Street, West Lafayette, IN 47907-2054, USA
FEATURES
source
1. 499
/organism="uncultured soil bacterium"
/mol_type="genomic DNA"
/isolation_source="Ross Forest soil"
/db_xref="taxon:164851"
/clone="RFS-C252"
/environmental_sample
<1..>499
/product="16S ribosomal RNA"

rRNA
ORIGIN

Query Match 93.3%; Score 22.4; DB 1; Length 499;
Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 51 CAAAGTCGAACGGAAGGCGCTTTCG 74

RESULT 89
DQ154328 499 bp DNA linear BCT 27-AUG-2005
LOCUS Soil bacterium RFS-1117 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION DQ154328
VERSION DQ154328.1 GI:73672118
KEYWORDS
SOURCE soil bacterium RFS-1117
ORGANISM soil bacterium RFS-1117
REFERENCE 1 (bases 1 to 499)
AUTHORS Becker,J.M., Nakatsu,C.H., Turco,R.F. and Konopka,A.
TITLE Low nutrient fluxes result in high cultivation efficiencies of soil
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 499)
AUTHORS Becker,J.M., Nakatsu,C.H., Turco,R.F. and Konopka,A.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-2005) Biological Sciences, Purdue University, 915
WEST State Street, West Lafayette, IN 47907-2054, USA
FEATURES
source
1. 499
/organism="soil bacterium RFS-1117"
/mol_type="genomic DNA"
/isolate="RFS-1117"
/isolation_source="Ross Forest soil"

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rRNA
ORIGIN

/db_xref="taxon:341511"
<1..>499
/product="16S ribosomal RNA"

Query Match 93.3%; Score 22.4; DB 15; Length 499;
Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 51 CAAAGTCGAACGGAAGGCGCTTTCG 74

RESULT 90
AV215236 499 bp DNA linear BCT 08-APR-2003
LOCUS Mycobacterium abscessus isolate N418 16S ribosomal RNA gene,
DEFINITION partial sequence.
ACCESSION AV215236
VERSION AV215236.1 GI:28274490
KEYWORDS
SOURCE Mycobacterium abscessus
ORGANISM Mycobacterium abscessus
REFERENCE 1 (bases 1 to 499)
AUTHORS Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
TITLE Evaluation of the MicroSeq System for Identification of
JOURNAL Mycobacteria by 16S Ribosomal DNA Sequencing and its Integration
PUBMED 12682128
REFERENCE 2 (bases 1 to 499)
AUTHORS Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-2003) Department of Laboratory Medicine and
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
FEATURES
source
1. 499
/organism="Mycobacterium abscessus"
/mol_type="genomic DNA"
/isolate="N418"
/db_xref="taxon:36809"
<1..>499
/product="16S ribosomal RNA"

rRNA
ORIGIN

Query Match 93.3%; Score 22.4; DB 15; Length 499;
Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 54 CAAAGTCGAACGGAAGGCGCTTTCG 77

RESULT 91
UEU233561 500 bp DNA linear ENV 06-JUN-2003
LOCUS uncultured eubacterium 16S ribosomal RNA, clone WR169.
DEFINITION
ACCESSION UEU233561
VERSION UEU233561.1 GI:5708350
KEYWORDS 16S ribosomal RNA.
SOURCE uncultured eubacterium WR169
ORGANISM uncultured eubacterium WR169
REFERENCE 1 (bases 1 to 500)
AUTHORS Nogales,B., Moore,E.R., Abraham,W.R. and Timmis,K.N.
TITLE Identification of the metabolically active members of a bacterial
JOURNAL community in a polychlorinated biphenyl-polluted moorland soil
PUBMED 11207739

```


REFERENCE 2 (bases 1 to 500)
AUTHORS Nogales B.
TITLE Direct Submission
JOURNAL Submitted (24-SEP-1998) Nogales B., GBF-National Research Centre for Biotechnology, Mascheroder Weg, 1, D-38124 Braunschweig, Germany

FEATURES
source
Location/Qualifiers
1..500
/organism="uncultured eubacterium WR169"
/mol_type="genomic DNA"
/db_xref="taxon:83097"
/clone="WR169"
/note="RT-PCR amplification of 16S ribosomal RNA from soil"
1..500
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 93.3%; Score 22.4; DB 1; Length 500;
Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTCG 24
|||||
Db 50 CAACTCGAACGGAAGGCGCTTTCG 73

RESULT 92
AF498660 500 bp DNA linear BCT 02-DEC-2002
LOCUS Mycobacterium rhodesiae strain K1 16S ribosomal RNA gene, partial sequence.
ACCESSION AF498660
VERSION AF498660.1 GI:21686167
KEYWORDS
SOURCE Mycobacterium rhodesiae
ORGANISM Mycobacterium rhodesiae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1 (bases 1 to 500)
AUTHORS Coleman, N.V., Mattes, T.E., Gossett, J.M. and Spain, J.C.
TITLE Phylogenetic and kinetic diversity of aerobic vinyl chloride-assimilating bacteria from contaminated sites
JOURNAL Appl. Environ. Microbiol. 68 (12), 6162-6171 (2002)
PUBMED 12450841

REFERENCE 2 (bases 1 to 500)
AUTHORS Coleman, N.V.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2002) Air Force Research Laboratory - MLQL, Building 1117, 139 Barnes Dr., Tyndall AFB, FL 32403, USA

FEATURES
source
Location/Qualifiers
1..500
/organism="Mycobacterium rhodesiae"
/mol_type="genomic DNA"
/strain="K1"
/db_xref="taxon:36814"
/note="biodegrades the groundwater pollutant vinyl chloride"
1..500
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 93.3%; Score 22.4; DB 15; Length 500;
Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTCG 24
|||||
Db 54 CAACTCGAACGGAAGGCGCTTTCG 77

RESULT 93
AF498661 500 bp DNA linear BCT 02-DEC-2002
LOCUS Mycobacterium rhodesiae strain TW1 16S ribosomal RNA gene, partial sequence.
ACCESSION AF498661
VERSION AF498661.1 GI:21686168
KEYWORDS
SOURCE Mycobacterium rhodesiae
ORGANISM Mycobacterium rhodesiae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1 (bases 1 to 500)
AUTHORS Coleman, N.V., Mattes, T.E., Gossett, J.M. and Spain, J.C.
TITLE Phylogenetic and kinetic diversity of aerobic vinyl chloride-assimilating bacteria from contaminated sites
JOURNAL Appl. Environ. Microbiol. 68 (12), 6162-6171 (2002)
PUBMED 12450841

REFERENCE 2 (bases 1 to 500)
AUTHORS Coleman, N.V.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2002) Air Force Research Laboratory - MLQL, Building 1117, 139 Barnes Dr., Tyndall AFB, FL 32403, USA

FEATURES
source
Location/Qualifiers
1..500
/organism="Mycobacterium rhodesiae"
/mol_type="genomic DNA"
/strain="K1"
/db_xref="taxon:36814"
/note="biodegrades the groundwater pollutant vinyl chloride"
1..500
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 93.3%; Score 22.4; DB 15; Length 500;
Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTCG 24
|||||
Db 54 CAACTCGAACGGAAGGCGCTTTCG 77

RESULT 94
AY162027 500 bp DNA linear BCT 01-OCT-2003
LOCUS Mycobacterium rhodesiae 16S ribosomal RNA gene, partial sequence.
ACCESSION AY162027
VERSION AY162027.1 GI:24850312
KEYWORDS
SOURCE Mycobacterium rhodesiae
ORGANISM Mycobacterium rhodesiae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1 (bases 1 to 500)
AUTHORS Coleman, N.V. and Spain, J.C.
TITLE Distribution of the Coenzyme M Pathway of Epoxide Metabolism among Ethene- and Vinyl Chloride-Degrading Mycobacterium Strains
JOURNAL Appl. Environ. Microbiol. 69 (10), 6041-6046 (2003)
PUBMED 12450841

REFERENCE 2 (bases 1 to 500)
AUTHORS Coleman, N.V. and Henley, C.M.
TITLE Direct Submission
JOURNAL Submitted (10-OCT-2002) Air Force Research Laboratory - MLQL, Building 1117, 139 Barnes Dr., Tyndall AFB, FL 32403, USA

FEATURES
source
Location/Qualifiers
1..500
/organism="Mycobacterium rhodesiae"
/mol_type="genomic DNA"
/strain="JS622"
/db_xref="taxon:36814"
1..500
/product="16S ribosomal RNA"

rRNA

ORIGIN

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Query Match      93.3%; Score 22.4; DB 15; Length 500;
Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 54 CAAAGTCGAACGGAAGGCGCTTTCG 77

RESULT 95
AV162030
LOCUS Mycobacterium mageritense 500 bp DNA linear BCT 01-OCT-2003
DEFINITION Mycobacterium mageritense 16S ribosomal RNA gene, partial sequence.
ACCESSION AY162030
VERSION AY162030.1 GI:24850315
KEYWORDS
SOURCE
ORGANISM Mycobacterium mageritense
Mycobacterium mageritense
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE
AUTHORS Coleman,N.V. and Spain,J.C.
TITLE Distribution of the Coenzyme M Pathway of Epoxide Metabolism among
Ethene- and Vinyl Chloride-Degrading Mycobacterium Strains
JOURNAL Appl. Environ. Microbiol. 69 (10), 6041-6046 (2003)
REFERENCE
AUTHORS Coleman,N.V. and Henley,C.M.
TITLE Direct Submission
JOURNAL Submitted (10-OCT-2002) Air Force Research Laboratory - MLQ/L,
Building 1117, 119 Barnes Dr., Tyndall AFB, FL 32403, USA
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Mycobacterium sp. N661
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REFERENCE
AUTHORS Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
TITLE Evaluation of the MicroSeq System for Identification of
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
into a Routine Clinical Mycobacteriology Laboratory
JOURNAL J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
REFERENCE
AUTHORS Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-2003) Department of Laboratory Medicine and
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA

Query Match      93.3%; Score 22.4; DB 15; Length 500;
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REFERENCE
AUTHORS Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
TITLE Evaluation of the MicroSeq System for Identification of
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
into a Routine Clinical Mycobacteriology Laboratory
JOURNAL J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
REFERENCE
AUTHORS Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-2003) Department of Laboratory Medicine and
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE
AUTHORS Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
TITLE Evaluation of the MicroSeq System for Identification of
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
into a Routine Clinical Mycobacteriology Laboratory
JOURNAL J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
REFERENCE
AUTHORS Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-2003) Department of Laboratory Medicine and
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
Evaluation of the MicroSeq System for Identification of
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
into a Routine Clinical Mycobacteriology Laboratory
J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
JOURNAL
PUBMED 12682128
REFERENCE 2 (bases 1 to 500)
AUTHORS Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-2003) Department of Laboratory Medicine and
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
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Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
Evaluation of the MicroSeq System for Identification of
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
into a Routine Clinical Mycobacteriology Laboratory
J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
JOURNAL
PUBMED 12682128
REFERENCE 2 (bases 1 to 500)
AUTHORS Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-2003) Department of Laboratory Medicine and
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
Evaluation of the MicroSeq System for Identification of
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
into a Routine Clinical Mycobacteriology Laboratory
J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
JOURNAL
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REFERENCE 2 (bases 1 to 500)
AUTHORS Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-2003) Department of Laboratory Medicine and
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 500)
Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
Evaluation of the MicroSeq System for Identification of
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
into a Routine Clinical Mycobacteriology Laboratory
J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
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REFERENCE 2 (bases 1 to 500)
AUTHORS Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-2003) Department of Laboratory Medicine and
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 02:23:06 ; Search time 769.072 Seconds
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1829.273 Million cell updates/sec

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Scoring table: IDENTITY NUC
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Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

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15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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109	20.4	92.7	499	15	DQ154328	Soil bact	DQ154328	Soil bact	182	20.4	92.7	540	15	AF547936	Mycobacte	AF547936	Mycobacte
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114	20.4	92.7	500	15	AY162027	Mycobacte	AY162027	Mycobacte	187	20.4	92.7	540	15	AF547954	Mycobacte	AF547954	Mycobacte
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119	20.4	92.7	500	15	AY215235	Mycobacte	AY215235	Mycobacte	192	20.4	92.7	540	15	AF547963	Mycobacte	AF547963	Mycobacte
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121	20.4	92.7	500	15	AY215245	Mycobacte	AY215245	Mycobacte	194	20.4	92.7	540	15	AF547972	Mycobacte	AF547972	Mycobacte
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127	20.4	92.7	500	15	AY215285	Mycobacte	AY215285	Mycobacte	200	20.4	92.7	541	15	AY438067	Mycobacte	AY438067	Mycobacte
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132	20.4	92.7	500	15	AY215291	Mycobacte	AY215291	Mycobacte	205	20.4	92.7	542	15	AY438079	Mycobacte	AY438079	Mycobacte
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135	20.4	92.7	500	15	AY215304	Mycobacte	AY215304	Mycobacte	208	20.4	92.7	552	15	AY438074	Mycobacte	AY438074	Mycobacte
136	20.4	92.7	500	15	AY215316	Mycobacte	AY215316	Mycobacte	209	20.4	92.7	558	15	AY039481	Soil bact	AY039481	Soil bact
137	20.4	92.7	500	15	AY215320	Mycobacte	AY215320	Mycobacte	210	20.4	92.7	558	15	AY039481	Soil bact	AY039481	Soil bact
138	20.4	92.7	500	15	AY215323	Mycobacte	AY215323	Mycobacte	211	20.4	92.7	576	15	AY367021	Mycobacte	AY367021	Mycobacte
139	20.4	92.7	500	15	AY215331	Mycobacte	AY215331	Mycobacte	212	20.4	92.7	588	15	AJ627393	Mycobacte	AJ627393	Mycobacte
140	20.4	92.7	500	15	AY215346	Mycobacte	AY215346	Mycobacte	213	20.4	92.7	611	1	DQ149896	Unculture	DQ149896	Unculture
141	20.4	92.7	500	15	AY215348	Mycobacte	AY215348	Mycobacte	214	20.4	92.7	616	1	AY242618	Unculture	AY242618	Unculture
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151	20.4	92.7	503	15	AY215249	Mycobacte	AY215249	Mycobacte	224	20.4	92.7	685	1	AY881659	Unculture	AY881659	Unculture
152	20.4	92.7	503	15	AY215250	Mycobacte	AY215250	Mycobacte	225	20.4	92.7	737	1	AY154573	Unculture	AY154573	Unculture
153	20.4	92.7	508	15	AY148214	Mycobacte	AY148214	Mycobacte	226	20.4	92.7	740	1	AF145831	Metal-con	AF145831	Metal-con
154	20.4	92.7	509	15	AY215212	Mycobacte	AY215212	Mycobacte	227	20.4	92.7	749	15	AJ784807	Mycobacte	AJ784807	Mycobacte
155	20.4	92.7	511	15	AY039467	Earthworm	AY039467	Earthworm	228	20.4	92.7	761	15	AJ746066	Mycobacte	AJ746066	Mycobacte
156	20.4	92.7	512	15	AY215272	Mycobacte	AY215272	Mycobacte	229	20.4	92.7	761	15	AJ746076	Mycobacte	AJ746076	Mycobacte
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162	20.4	92.7	519	15	AY25810	Unculture	AY25810	Unculture	235	20.4	92.7	816	1	AY154519	Unculture	AY154519	Unculture
163	20.4	92.7	530	1	AY039507	Soil bact	AY039507	Soil bact	236	20.4	92.7	817	15	AJ746069	Mycobacte	AJ746069	Mycobacte
164	20.4	92.7	530	15	AY039507	Soil bact	AY039507	Soil bact	237	20.4	92.7	824	15	AJ746060	Mycobacte	AJ746060	Mycobacte

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285 20.4 92.7 1422 15 DQ370010
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299 20.4 92.7 1432 15 DQ372735
300 20.4 92.7 1433 15 DQ370009

ALIGNMENTS

RESULT 1
AR438655
LOCUS AR438655 22 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 23 from patent US 6664081.
ACCESSION AR438655

VERSION AR438655.1 GI:42663579
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Brenzano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and Rodriguez,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: US 6664081-A 23 16-DEC-2003;
FEATURES Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA
source location/Qualifiers
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AR438657
LOCUS AR438657 22 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 23 from Patent WO0144510.
ACCESSION AR438657
VERSION AR438657.1 GI:14596460
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Brenzano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and Rodriguez,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: WO 0144510-A 23 21-JUN-2001;
FEATURES Gen-Probe Incorporated (US) ; Biomerieux S.A. (FR)
source location/Qualifiers
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/db_xref="taxon:32630"
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
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RESULT 3
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LOCUS AF547926 541 bp DNA linear BCT 24-JAN-2006
DEFINITION Mycobacterium gadium strain CIP 105388 16S ribosomal RNA gene, partial sequence.
ACCESSION AF547926
VERSION AF547926.1 GI:27733750
KEYWORDS
SOURCE Mycobacterium gadium
ORGANISM Mycobacterium gadium
REFERENCE 1 (bases 1 to 541)
AUTHORS Devulder,G., de Montclos,M.P. and Flandrois,J.P.

TITLE A multigene approach to phylogenetic analysis using the genus
 JOURNAL Mycobacterium as a model
 PUBMED Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
 REFERENCE 15653990
 2 (bases 1 to 541)
 AUTHORS Devulder,G., Pichat,C. and Flandrois,J.P.
 TITLE Direct Submission
 JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
 Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
 Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

FEATURES
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 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DEFINITION M.gadium 16S ribosomal RNA, part.
 ACCESSION X55594
 VERSION X55594.1 GI:44291
 KEYWORDS 16S ribosomal RNA.
 SOURCE Mycobacterium gadium
 ORGANISM Mycobacterium gadium
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1 (bases 1 to 1456)
 AUTHORS Pitulle,C., Dorsch,M., Kazda,J., Wolters,J. and Stackebrandt,E.
 TITLE Phylogeny of rapidly growing members of the genus Mycobacterium
 JOURNAL Int. J. Syst. Bacteriol. 42 (3), 337-343 (1992)
 PUBMED 1380284
 REFERENCE 2 (bases 1 to 1456)
 AUTHORS Wolters,J.
 TITLE Direct Submission
 JOURNAL Submitted (18-SEP-1990) Wolters J., Institut fuer Allgemeine
 Mikrobiologie der Universitaet, Biologiezentrum, Am Botanischen
 Garten 1-9, 2300 Kiel 1

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 Best Local Similarity 100.0%; Pred. No. 18;
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RESULT 5
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 DEFINITION Mycobacterium cookii partial 16S rRNA.
 ACCESSION X53896
 VERSION X53896.1 GI:44201
 KEYWORDS 16S ribosomal RNA; ribosomal RNA.
 SOURCE Mycobacterium cookii
 ORGANISM Mycobacterium cookii
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1 (bases 1 to 1225)
 AUTHORS Kazda,J., Stackebrandt,E., Smida,J., Minnikin,D.E., Daffe,M.,
 Parlett,J.H. and Pitulle,C.
 TITLE Mycobacterium cookii sp. nov.
 JOURNAL Int. J. Syst. Bacteriol. 40 (3), 217-223 (1990)
 PUBMED 1697763
 REFERENCE 2 (bases 1 to 1459)
 AUTHORS Stackebrandt,E.
 TITLE Direct Submission
 JOURNAL Submitted (01-AUG-1990) Stackebrandt E

FEATURES
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 /mol_type="genomic DNA"
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 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 62 GTCGAACGGAAAGGCCTTTGG 83
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 DEFINITION Sequence 22 from patent US 6664081.
 ACCESSION AR438654
 VERSION AR438654.1 GI:42663578
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 24)
 AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
 Rodrigue,M.
 TITLE Nucleic acid amplification and detection of mycobacterium species
 JOURNAL Patent: US 6664081-A 22 16-DEC-2003;
 Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA

FEATURES
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 Db 4 GTCGAACGGAAAGGCCTTTGG 24
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RESULT 7
 AX166856
 LOCUS AX166856 24 bp DNA linear PAT 04-JUL-2001
 DEFINITION Sequence 22 from Patent WO0144510.

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ACCESSION   AX166856
VERSION     AX166856.1  GI:14596459
KEYWORDS
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
            Rodrigue,M.
TITLE       Nucleic acid amplification and detection of mycobacterium species
JOURNAL
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Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8
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DEFINITION Sequence 21 from patent US 6664081.
ACCESSION   AR438653
VERSION     AR438653.1  GI:42663577
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 25)
AUTHORS     Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
            Rodrigue,M.
TITLE       Nucleic acid amplification and detection of mycobacterium species
JOURNAL
FEATURES
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  GTCGAACGGAAGGCGCTTTCG 21
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RESULT 9
AX166855
LOCUS       AX166855                25 bp      DNA      linear      PAT 04-JUL-2001
DEFINITION Sequence 21 from Patent WO0144510.
ACCESSION   AX166855
VERSION     AX166855.1  GI:14596458
KEYWORDS
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
            Rodrigue,M.

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TITLE       Nucleic acid amplification and detection of mycobacterium species
JOURNAL
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Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  GTCGAACGGAAGGCGCTTTCG 21
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Db   5  GTCGAACGGAAGGCGCTTTCG 25
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RESULT 10
MSGRGDSA
LOCUS       MSGRGDSA                1460 bp      DNA      linear      BCT 21-SEP-1993
DEFINITION Mycobacterium celatum 16S ribosomal RNA gene.
ACCESSION   L08169
VERSION     L08169.1  GI:293249
KEYWORDS    16S ribosomal RNA.
SOURCE      Mycobacterium celatum
ORGANISM    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE   1 (bases 1 to 1460)
AUTHORS     Butler,W.R., O'Connor,S.P., Yakrus,M.A., Smithwick,R.W.,
            Plikaytis,B.B., Moss,C.W., Floyd,M.M., Woodley,C.L., Kilburn,J.O.,
            Vadney,F.S. and Gross,W.M.
TITLE       Mycobacterium celatum sp. nov
JOURNAL     Int. J. Syst. Bacteriol. 43 (3), 539-548 (1993)
PUBMED     8102246
COMMENT     Original source text: Mycobacterium celatum (library: ATCC 51131)
            DNA.
FEATURES
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            /mol_type="genomic DNA"
            /db_xref="taxon:28045"
            /tissue_lib="ATCC 51131"
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            /product="16S ribosomal RNA"
            /note="putative"

rRNA

ORIGIN
Query Match      95.5%; Score 21; DB 15; Length 1460;
Best Local Similarity 95.5%; Pred. No. 53;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1  GTCGAACGGAAGGCGCTTTCG 22
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Db   12 GTCGAACGGAAGGCGCTTNGG 33
      |||||

RESULT 11
MSGRGDSB
LOCUS       MSGRGDSB                1479 bp      DNA      linear      BCT 21-SEP-1993
DEFINITION Mycobacterium celatum 16S ribosomal RNA gene.
ACCESSION   L08170
VERSION     L08170.1  GI:293250
KEYWORDS    16S ribosomal RNA.
SOURCE      Mycobacterium celatum
ORGANISM    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE   1 (bases 1 to 1479)
AUTHORS     Butler,W.R., O'Connor,S.P., Yakrus,M.A., Smithwick,R.W.,

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DEFINITION Mycobacterium fortuitum isolate 60344 16S ribosomal RNA (rrs) gene, partial sequence.
ACCESSION AF059795
VERSION AF059795.1 GI:3132939
KEYWORDS
SOURCE Mycobacterium fortuitum
ORGANISM Mycobacterium fortuitum
REFERENCE 1 (bases 1 to 171)
AUTHORS Gengeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
TITLE Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
JOURNAL Genome Res. 8 (5), 435-448 (1998)
PUBMED 9582189
REFERENCE 2 (bases 1 to 171)
AUTHORS Gengeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
TITLE Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
JOURNAL Genome Res. 8 (5), 435-448 (1998)
PUBMED 9582189
REFERENCE 3 (bases 1 to 171)
AUTHORS Gengeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
TITLE Direct Submission
JOURNAL Submitted (16-APR-1998) Division of Infectious Disease, Affymetrix, 3380 Central Expressway, Santa Clara, CA 95051, USA
FEATURES
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1. .171
/organism="Mycobacterium fortuitum"
/mol_type="rRNA"
/isolate="60344"
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Best Local Similarity 95.5%; Pred. No. 2.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTCGAACGGAAGGCGCTTCGG 22
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Db 2 GTCGAACGGAAGGCGCTTCGG 23
RESULT 15
AF059797
LOCUS Mycobacterium chelonae isolate 95A11814 16S ribosomal RNA (rrs)
DEFINITION gene, partial sequence.
ACCESSION AF059797
VERSION AF059797.1 GI:3132941
KEYWORDS
SOURCE Mycobacterium chelonae
ORGANISM Mycobacterium chelonae
REFERENCE 1 (bases 1 to 171)
AUTHORS Gengeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
TITLE Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
JOURNAL Genome Res. 8 (5), 435-448 (1998)
PUBMED 9582189
REFERENCE 2 (bases 1 to 171)
AUTHORS Gengeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
TITLE Direct Submission
JOURNAL Submitted (16-APR-1998) Division of Infectious Disease, Affymetrix, 3380 Central Expressway, Santa Clara, CA 95051, USA
FEATURES
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/mol_type="rRNA"
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Best Local Similarity 95.5%; Pred. No. 2.8e+02;
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Qy 1 GTCGAACGGAAGGCGCTTCGG 22
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Db 2 GTCGAACGGAAGGCGCTTCGG 23
RESULT 16
AF059808
LOCUS Mycobacterium scrofulaceum isolate 95A3977 16S ribosomal RNA (rrs)
DEFINITION gene, partial sequence.
ACCESSION AF059808
VERSION AF059808.1 GI:3132952
KEYWORDS
SOURCE Mycobacterium scrofulaceum
ORGANISM Mycobacterium scrofulaceum
REFERENCE 1 (bases 1 to 171)
AUTHORS Gengeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
TITLE Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
JOURNAL Genome Res. 8 (5), 435-448 (1998)
PUBMED 9582189
REFERENCE 2 (bases 1 to 171)
AUTHORS Gengeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
TITLE Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
JOURNAL Genome Res. 8 (5), 435-448 (1998)
PUBMED 9582189
REFERENCE 3 (bases 1 to 171)
AUTHORS Gengeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
TITLE Direct Submission
JOURNAL Submitted (16-APR-1998) Division of Infectious Disease, Affymetrix, 3380 Central Expressway, Santa Clara, CA 95051, USA
FEATURES
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REFERENCE 2 (bases 1 to 171)
AUTHORS Gengeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
TITLE Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
JOURNAL Genome Res. 8 (5), 435-448 (1998)
PUBMED 9582189
REFERENCE 3 (bases 1 to 171)
AUTHORS Gengeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
TITLE Direct Submission
JOURNAL Submitted (16-APR-1998) Division of Infectious Disease, Affymetrix, 3380 Central Expressway, Santa Clara, CA 95051, USA
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Best Local Similarity 95.5%; Pred. No. 2.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTCGAACGGAAGGCGCTTCGG 22
|||||
Db 2 GTCGAACGGAAGGCGCTTCGG 23
RESULT 16
AF059808
LOCUS Mycobacterium scrofulaceum isolate 95A3977 16S ribosomal RNA (rrs)
DEFINITION gene, partial sequence.
ACCESSION AF059808
VERSION AF059808.1 GI:3132952
KEYWORDS
SOURCE Mycobacterium scrofulaceum
ORGANISM Mycobacterium scrofulaceum
REFERENCE 1 (bases 1 to 171)
AUTHORS Gengeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
TITLE Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
JOURNAL Genome Res. 8 (5), 435-448 (1998)
PUBMED 9582189
REFERENCE 2 (bases 1 to 171)
AUTHORS Gengeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
TITLE Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
JOURNAL Genome Res. 8 (5), 435-448 (1998)
PUBMED 9582189
REFERENCE 3 (bases 1 to 171)
AUTHORS Gengeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
TITLE Direct Submission
JOURNAL Submitted (16-APR-1998) Division of Infectious Disease, Affymetrix, 3380 Central Expressway, Santa Clara, CA 95051, USA
FEATURES
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/mol_type="rRNA"
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Best Local Similarity 95.5%; Pred. No. 2.8e+02;


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Query Match          92.7%; Score 20.4; DB 15; Length 171;
Best Local Similarity 95.5%; Pred. No. 2.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGCCCTTCGG 22
Db 2 GTCGAACGGAAGCCCTTCGG 23

RESULT 22
AF059841
LOCUS AF059841 171 bp rRNA linear BCT 15-MAY-1998
DEFINITION Mycobacterium chelonae isolate 95A9151 16S ribosomal RNA (rrs)
gene, partial sequence.
ACCESSION AF059841
VERSION AF059841.1 GI:3132985
KEYWORDS
SOURCE Mycobacterium chelonae
ORGANISM Mycobacterium chelonae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 171)
AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,
Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
TITLE Simultaneous genotyping and species identification using
hybridization pattern recognition analysis of generic Mycobacterium
DNA arrays
JOURNAL Genome Res. 8 (5), 435-448 (1998)
PUBMED 9582189
2 (bases 1 to 171)
REFERENCE 2 (bases 1 to 171)
AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,
Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
TITLE Simultaneous genotyping and species identification using
hybridization pattern recognition analysis of generic Mycobacterium
DNA arrays
JOURNAL Genome Res. 8 (5), 435-448 (1998)
PUBMED 9582189
3 (bases 1 to 171)
REFERENCE 3 (bases 1 to 171)
AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,
Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
TITLE Direct Submission
JOURNAL Submitted (16-APR-1998) Division of Infectious Disease, Affymetrix,
3380 Central Expressway, Santa Clara, CA 95051, USA
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/strain="ATCC6841"
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gene
rRNA

ORIGIN
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Best Local Similarity 95.5%; Pred. No. 2.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGCCCTTCGG 22
Db 2 GTCGAACGGAAGCCCTTCGG 23

RESULT 24
AF059852
LOCUS AF059852 171 bp rRNA linear BCT 15-MAY-1998
DEFINITION Mycobacterium chelonae strain ATCC35752 16S ribosomal RNA (rrs)
gene, partial sequence.
ACCESSION AF059852
VERSION AF059852.1 GI:3132996
KEYWORDS
SOURCE Mycobacterium chelonae
ORGANISM Mycobacterium chelonae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 171)
AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,
Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
TITLE Simultaneous genotyping and species identification using
hybridization pattern recognition analysis of generic Mycobacterium
DNA arrays
JOURNAL Genome Res. 8 (5), 435-448 (1998)
PUBMED 9582189
2 (bases 1 to 171)
REFERENCE 2 (bases 1 to 171)

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AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniwski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
TITLE Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
JOURNAL Genome Res. 8 (5), 435-448 (1998)
PUBMED 9582189
REFERENCE 3 (bases 1 to 171)
AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniwski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
TITLE Direct Submission
JOURNAL Submitted (16-APR-1998) Division of Infectious Disease, Affymetrix, 3380 Central Expressway, Santa Clara, CA 95051, USA
FEATURES Location/Qualifiers
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 /organism="Mycobacterium chelonae"
 /mol_type="rRNA"
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 Best Local Similarity 95.5%; Pred. No. 2.8e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GTCGAACGGAAGGCTTTTCGG 22
 |||||
 Db 2 GTCGAACGGAAGGCTTTTCGG 23
 |||||
 RESULT 25
 AF059793 172 bp rRNA linear BCT 15-MAY-1998
 LOCUS Mycobacterium fortuitum isolate 60447 16S ribosomal RNA (rrs) gene,
 DEFINITION partial sequence.
 ACCESSION AF059793
 VERSION AF059793.1 GI:3132937
 KEYWORDS
 SOURCE Mycobacterium fortuitum
 ORGANISM Mycobacterium fortuitum
 Bacteria: Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 REFERENCE
 AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniwski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
 TITLE Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
JOURNAL Genome Res. 8 (5), 435-448 (1998)
PUBMED 9582189
REFERENCE 2 (bases 1 to 172)
AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniwski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
TITLE Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
JOURNAL Genome Res. 8 (5), 435-448 (1998)
PUBMED 9582189
REFERENCE 3 (bases 1 to 172)
AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniwski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
TITLE Direct Submission
JOURNAL Submitted (16-APR-1998) Division of Infectious Disease, Affymetrix, 3380 Central Expressway, Santa Clara, CA 95051, USA
FEATURES Location/Qualifiers
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 /organism="Mycobacterium fortuitum"

gene /mol_type="rRNA"
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rRNA
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 Best Local Similarity 95.5%; Pred. No. 2.8e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GTCGAACGGAAGGCTTTTCGG 22
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 Db 2 GTCGAACGGAAGGCTTTTCGG 23
 |||||
 RESULT 26
 MSGRR16S 268 bp rRNA linear BCT 27-APR-1993
 LOCUS Mycobacterium kansasii 16S ribosomal RNA.
 DEFINITION
 ACCESSION M95469
 VERSION M95469.1 GI:175317
 KEYWORDS 16S ribosomal RNA.
 SOURCE Mycobacterium kansasii
 ORGANISM Mycobacterium kansasii
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 REFERENCE
 AUTHORS Ross,B.C., Jackson,K., Yang,M., Sievers,A. and Dwyer,B.
 TITLE Identification of a genetically distinct sub-species of Mycobacterium kansasii
 JOURNAL Unpublished (1992)
 COMMENT Original source text: Mycobacterium kansasii rRNA.
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 1..268
 /organism="Mycobacterium kansasii"
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gene
rRNA
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 Best Local Similarity 95.5%; Pred. No. 2.3e+02;
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 Qy 1 GTCGAACGGAAGGCTTTTCGG 22
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 Db 42 GTCGAACGGAAGGCTTTTCGG 63
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 RESULT 27
 MSP404591 293 bp DNA linear ENV 06-JUN-2003
 LOCUS Uncultured Mycobacterium MB1 partial 16S rRNA gene.
 DEFINITION
 ACCESSION AJ404591
 VERSION AJ404591.1 GI:8926769
 KEYWORDS 16S ribosomal RNA; 16S rRNA gene.
 SOURCE uncultured Mycobacterium MB1
 ORGANISM uncultured Mycobacterium MB1
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental samples.
 REFERENCE
 AUTHORS Kempell,K.E., Cox,C.J., Hurle,M., Wong,A., Wilkie,S., Zanders,E.D., Gaston,J. and Crowe,J.
 TITLE Reverse Transcriptase-Polymerase Chain Reaction of Bacterial rRNA

for Detection and Characterisation of Bacterial Species in Arthritis Synovial Tissue

Archives Symposia Issue
Unpublished
2 (bases 1 to 293)
Cox, C.J.
Direct Submission
Submitted (05-JUN-2000) Cox C.J., Cancer Research, Sanger Centre,
Wellcome Trust Genome Campus, Hinxton Hall, Hinxton,
Cambridgeshire, CB10 1SA, UNITED KINGDOM

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Best Local Similarity	95.5%	Pred. No. 2.2e+02;
Matches 21; Conservative	0; Mismatches 1;	Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTTTCGG 22
Db 24 GTCGAACGGAAGGCCTTTTCGG 45

RESULT 28			
MF16SRRN			
LOCUS	MF16SRRN	316 bp	DNA
DEFINITION	M.fortuitum 16S rRNA gene, partial.		
		linear	BCT 14-NOV-1996

Y09325.1 GI:1669698
 16S ribosomal RNA; rrn gene.
 Mycobacterium fortuitum
 Mycobacterium fortuitum

REFERENCE
1
AUTHORS
De Smet, K., Kampmann, B., Marshall, B., Kroll, S. and Levin, M.
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

UNPUBLISHED
REFERENCE
AUTHORS
2 (bases 1 to 316)
De Smet, K.A.L.

TITLE Direct Submission
JOURNAL Submitted (08-NOV-1996) K.A.L. De Smet, Imperial College Medical School at St Marys, Medical Microbiology, Norfolk Place, London, W2 1PG, UK

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FEATURES             Location/Qualifiers
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Query Match	92.7%	Score 20.4;	DB 15;	Length 316;
Best Local Similarity	95.5%;	Pred. No. 2.1e+02;		
Matches 21: Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy 1 GTCGAACGGAAAGGCCTTTCGG 22
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Db 49 GTCGAACGGAAAGGCCTTTCGG 70

RESULT 29
DO063127

LOCUS	D063127	384 bp	DNA	linear	BCT 27-JUN-2005
DEFINITION	Actinobacterium BAL187	16S ribosomal RNA gene, partial sequence.			
ACCESSION	D063127				
VERSION	D063127.1	GI:68139160			

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

2 (bases 1 to 384)
Riemann, L., Leitert, C., Pommier, T., Simu, K., Holmfeldt, K. and Hagstrom, A.
Direct Submission
Submitted (16-MAY-2005) Dep. of Biology and Environmental Science
University of Kalmar, Barlastatan 11, Kalmar 39231, Sweden

FEATURES	SOURCE
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/organism="Actinobacterium BAL187"
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rRNA

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Query Match	92.7%	Score 20.4;	DB 15;	Length 384;
Best Local Similarity	95.5%	Pred. No. 1.9e+02;		
Matches 21;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTTCGG 22
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Db 1 GTCGAACGGAAGGCCCTTTCGG 22
|||||

RESULT 30
AY395145

AY395145	388 bp	DNA	linear	ENV 07-SEP-2004
LOCUS	Uncultured bacterium clone D29St	16S ribosomal RNA gene, partial sequence.		
DEFINITION				

ACCESSION	AY395145	
VERSION	AY395145.1	GI:37595660
KEYWORDS	ENV.	
SOURCE	uncultured bacterium	
ORGANISM	uncultured bacterium	
	Bacteria: environmental	samples.

REFERENCE
1 (bases 1 to 386)
AUTHORS
Hackl, E., Zechmeister-Boltenstern, S., Bodrossy, L. and Sessitsch, A.
TITLE
Comparison of diversity and compositions of bacterial populations
inhabiting natural forest soils
JOURNAL
Appl. Environ. Microbiol. 70 (9), 5057-5065 (2004)
PUBMED
15345382

REFERENCE
AUTHORS
2 (bases 1 to 388)
Hackl, E. and Sessitsch, A.

TITLE Direct Submission
JOURNAL Submitted (19-SEP-2003) Environmental and Life Sciences, ARCS
Seibersdorf research GmbH, Seibersdorf A-2444, Austria
FEATURES Location/Qualifiers
source 1. .388

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1.128
204330
/organism="uncultured bacterium"
/mol type="genomic DNA"

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/isolation_source="forest soil"
/db_xref="taxon:77133"
/clone="D29ST"
/environmental_sample
<1..>388
/product="16S ribosomal RNA"

ORIGIN
Query Match          92.7%; Score 20.4; DB 1; Length 388;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTCGG 22
    |||||
Db 54 GTCGAACGGAAGGCCCTTCGG 75

RESULT 31
BSSMK23
LOCUS      BSSMK23          393 bp      DNA      linear      ENV 22-FEB-1995
DEFINITION Bacterium sp. (SMKN23) DNA.
ACCESSION  X78659
VERSION     X78659.1 GI:509728
KEYWORDS   16S ribosomal RNA.
SOURCE      unidentified bacterium
ORGANISM    Bacteria; environmental samples.
REFERENCE   1
AUTHORS     Schuppler,M., Mertens,F., Schon,G. and Gobel,U.B.
TITLE       Molecular characterization of nocardioform actinomycetes in
            activated sludge by 16S rRNA analysis
JOURNAL     Microbiology (Reading, Engl.) 141 (Pt 2), 513-521 (1995)
PUBMED      7704280
AUTHORS     Schuppler,M.
TITLE       Direct Submission
JOURNAL     Submitted (28-MAR-1994) M. Schuppler, Institut fuer Med.
            Mikrobiologie & Hygiene, Universitaet Freiburg, Hermann-Herder-St.
            11, 79104 Freiburg, FRG
FEATURES    Location/Qualifiers
            source
                1..393
                /organism="unidentified bacterium"
                /mol_type="genomic DNA"
                /isolate="SMKN23"
                /db_xref="taxon:2338"
            rRNA
                1..393
                /product="16S ribosomal RNA"

ORIGIN
Query Match          92.7%; Score 20.4; DB 1; Length 393;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTCGG 22
    |||||
Db 11 GTCGAACGGAAGGCCCTTCGG 32

RESULT 32
AY395154
LOCUS      AY395154          394 bp      DNA      linear      ENV 07-SEP-2004
DEFINITION Uncultured actinobacterium clone E02ST 16S ribosomal RNA gene,
            partial sequence.
ACCESSION  AY395154
VERSION     AY395154.1 GI:37595669
KEYWORDS   uncultured actinobacterium
SOURCE      uncultured actinobacterium
ORGANISM    Bacteria; Actinobacteria; environmental samples.
REFERENCE   1 (bases 1 to 394)
AUTHORS     Hackl,E., Zechmeister-Boltenstern,S., Bodrossy,L. and Sessitsch,A.
TITLE       Comparison of diversities and compositions of bacterial populations
            inhabiting natural forest soils

/isolation_source="forest soil"
/db_xref="taxon:77133"
/clone="D29ST"
/environmental_sample
<1..>388
/product="16S ribosomal RNA"

ORIGIN
Query Match          92.7%; Score 20.4; DB 1; Length 388;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTCGG 22
    |||||
Db 54 GTCGAACGGAAGGCCCTTCGG 75

RESULT 33
AY043901
LOCUS      AY043901          395 bp      DNA      linear      ENV 05-MAY-2004
DEFINITION Uncultured actinobacterium clone SMS9.49WL 16S ribosomal RNA gene,
            partial sequence.
ACCESSION  AY043901
VERSION     AY043901.1 GI:22267274
KEYWORDS   uncultured actinobacterium
SOURCE      Bacteria; Actinobacteria; environmental samples.
REFERENCE   1 (bases 1 to 395)
AUTHORS     Axelrood,P.E., Chow,M.L., Radomski,C.C., McDermott,J.M. and
            Davies,J.
TITLE       Molecular characterization of bacterial diversity from British
            Columbia forest soils subjected to disturbance
JOURNAL     Can. J. Microbiol. 48 (7), 655-674 (2002)
PUBMED      1224564
AUTHORS     Axelrood,P.E., Chow,M.L., Radomski,C.C., McDermott,J.M. and
            Davies,J.
TITLE       Direct Submission
JOURNAL     Submitted (20-JUN-2001) BC Research Inc., 3650 Westbrook Mall,
            Vancouver, BC V6S 2L2, Canada
FEATURES    Location/Qualifiers
            source
                1..395
                /organism="uncultured actinobacterium"
                /mol_type="genomic DNA"
                /db_xref="taxon:152507"
                /clone="SMS9.49WL"
                /environmental_sample
                /notes="from forest cut-block mineral soil from the British
                Columbia Ministry of Forests Long-Term Soil Productivity
                (LTSP) installation near Williams Lake, BC, Canada"
            rRNA
                <1..>395
                /product="16S ribosomal RNA"

ORIGIN
Query Match          92.7%; Score 20.4; DB 1; Length 395;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTCGG 22
    |||||
Db 24 GTCGAACGGAAGGCCCTTCGG 45

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JOURNAL     Appl. Environ. Microbiol. 70 (9), 5057-5065 (2004)
PUBMED      15345382
AUTHORS     2 (bases 1 to 394)
            Hackl,E. and Sessitsch,A.
TITLE       Direct Submission
JOURNAL     Submitted (19-SEP-2003) Environmental and Life Sciences, ARC
            Seibersdorf research GmbH, Seibersdorf A-2444, Austria
FEATURES    Location/Qualifiers
            source
                1..394
                /organism="uncultured actinobacterium"
                /mol_type="genomic DNA"
                /isolation_source="forest soil"
                /db_xref="taxon:152507"
                /clone="E02ST"
                /environmental_sample
                <1..>394
                /product="16S ribosomal RNA"
            rRNA
                <1..>394
                /product="16S ribosomal RNA"

ORIGIN
Query Match          92.7%; Score 20.4; DB 1; Length 394;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTCGG 22
    |||||
Db 54 GTCGAACGGAAGGCCCTTCGG 75

RESULT 33
AY043901
LOCUS      AY043901          395 bp      DNA      linear      ENV 05-MAY-2004
DEFINITION Uncultured actinobacterium clone SMS9.49WL 16S ribosomal RNA gene,
            partial sequence.
ACCESSION  AY043901
VERSION     AY043901.1 GI:22267274
KEYWORDS   uncultured actinobacterium
SOURCE      Bacteria; Actinobacteria; environmental samples.
REFERENCE   1 (bases 1 to 395)
AUTHORS     Axelrood,P.E., Chow,M.L., Radomski,C.C., McDermott,J.M. and
            Davies,J.
TITLE       Molecular characterization of bacterial diversity from British
            Columbia forest soils subjected to disturbance
JOURNAL     Can. J. Microbiol. 48 (7), 655-674 (2002)
PUBMED      1224564
AUTHORS     Axelrood,P.E., Chow,M.L., Radomski,C.C., McDermott,J.M. and
            Davies,J.
TITLE       Direct Submission
JOURNAL     Submitted (20-JUN-2001) BC Research Inc., 3650 Westbrook Mall,
            Vancouver, BC V6S 2L2, Canada
FEATURES    Location/Qualifiers
            source
                1..395
                /organism="uncultured actinobacterium"
                /mol_type="genomic DNA"
                /db_xref="taxon:152507"
                /clone="SMS9.49WL"
                /environmental_sample
                /notes="from forest cut-block mineral soil from the British
                Columbia Ministry of Forests Long-Term Soil Productivity
                (LTSP) installation near Williams Lake, BC, Canada"
            rRNA
                <1..>395
                /product="16S ribosomal RNA"

ORIGIN
Query Match          92.7%; Score 20.4; DB 1; Length 395;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTCGG 22
    |||||
Db 24 GTCGAACGGAAGGCCCTTCGG 45

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RESULT 34
LOCUS      AY395151
DEFINITION Uncultured bacterium clone D36ST 16S ribosomal RNA gene, partial
            sequence.
ACCESSION  AY395151
VERSION     AY395151.1 GI:37595666
KEYWORDS   ENV.
SOURCE     uncultured bacterium
ORGANISM   Bacteria; environmental samples.
REFERENCE  1 (bases 1 to 395)
AUTHORS    Hackl,E., Zechmeister-Boltenstern,S., Bodrossy,L. and Sessitsch,A.
TITLE      Comparison of diversities and compositions of bacterial populations
            inhabiting natural forest soils
JOURNAL    Appl. Environ. Microbiol. 70 (9), 5057-5065 (2004)
PUBMED     15345382
AUTHORS    Hackl,E. and Sessitsch,A.
TITLE      Direct Submission
JOURNAL    Submitted (19-SEP-2003) Environmental and Life Sciences, ARC
            Seibersdorf research GmbH, Seibersdorf A-2444, Austria
FEATURES   source
            1..395
            /organism="uncultured bacterium"
            /mol_type="genomic DNA"
            /isolation_source="Forest soil"
            /db_xref="taxon:77133"
            /clone="D36ST"
            /environmental_sample
            <1..>395
            /product="16S ribosomal RNA"

rRNA
ORIGIN
Query Match      92.7%; Score 20.4; DB 1; Length 395;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGCCCTTCGG 22
    |||||
Db 54 GTCGAACGGAAGCCCTTCGG 75

RESULT 35
BSSMKN14
LOCUS      BSSMKN14
DEFINITION Bacterium sp. (SMKN14) DNA.
ACCESSION  X78655
VERSION     X78655.1 GI:509724
KEYWORDS   16S ribosomal RNA.
SOURCE     unidentified bacterium
ORGANISM   Bacteria; environmental samples.
REFERENCE  1
AUTHORS    Schuppler,M., Mertens,F., Schon,G. and Gobel,U.B.
TITLE      Molecular characterization of nocardioform actinomycetes in
            activated sludge by 16S rRNA analysis
JOURNAL    Microbiology (Reading, Engl.) 141 (Pt 2), 513-521 (1995)
PUBMED     7704280
AUTHORS    Schuppler,M.
TITLE      Direct Submission
JOURNAL    Submitted (28-MAR-1994) M. Schuppler, Institut fuer Med.
            Mikrobiologie & Hygiene, Universitaet Freiburg, Hermann-Herder-St.
            11, 79104 Freiburg, FRG
FEATURES   source
            1..396
            /organism="unidentified bacterium"
            /mol_type="genomic DNA"
            /isolate="SMKN14"
            /db_xref="taxon:2338"

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rRNA
ORIGIN
1..396
/product="16S ribosomal RNA"

Query Match      92.7%; Score 20.4; DB 1; Length 396;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGCCCTTCGG 22
    |||||
Db 11 GTCGAACGGAAGCCCTTCGG 32

RESULT 36
DQ063065
LOCUS      DQ063065
DEFINITION Actinobacterium clone BPH3088 16S ribosomal RNA gene, partial
            sequence.
ACCESSION  DQ063065
VERSION     DQ063065.1 GI:80978382
KEYWORDS   ENV.
SOURCE     uncultured bacterium
ORGANISM   Bacteria; environmental samples.
REFERENCE  1 (bases 1 to 400)
AUTHORS    Lambais,M.R., Crowley,D.E., Cury,J.C. and Bull,R.C.
TITLE      Bacterial diversity on leaf surfaces of the Brazilian Atlantic
            Forest
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 400)
AUTHORS    Lambais,M.R., Crowley,D.E., Cury,J.C. and Bull,R.C.
TITLE      Direct Submission
JOURNAL    Submitted (23-SEP-2005) Solos e Nutricao de Plantas, Universidade
            de Sao Paulo, Av. Padua Dias,11, Piracicaba, SP 13418-900, Brazil
FEATURES   source
            1..400
            /organism="uncultured bacterium"
            /mol_type="genomic DNA"
            /isolation_source="Phyllosphere"
            /specific_host="Campomanesia xanthocarpa"
            /db_xref="taxon:77133"
            /clone="BPH3088"
            /environmental_sample
            <1..>400
            /product="16S ribosomal RNA"

rRNA
ORIGIN
Query Match      92.7%; Score 20.4; DB 1; Length 400;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGCCCTTCGG 22
    |||||
Db 19 GTCGAACGGAAGCCCTTCGG 40

RESULT 37
DQ063065
LOCUS      DQ063065
DEFINITION Actinobacterium BAL125 16S ribosomal RNA gene, partial sequence.
ACCESSION  DQ063065
VERSION     DQ063065.1 GI:68139094
KEYWORDS   actinobacterium BAL125
SOURCE     actinobacterium BAL125
ORGANISM   Bacteria; Actinobacteria.
REFERENCE  1 (bases 1 to 401)
AUTHORS    Riemann,L., Leitert,C., Pommier,T., Simu,K., Holmfeldt,K. and
            Hagstrom,A.
TITLE      Bacterial community composition in the central Baltic Sea analyzed
            by cultivation and molecular-based methods
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 401)

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AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
 TITLE Direct Submission
 JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences, University of Kalmar, Bärnäsgratan 11, Kalmar 39031, Sweden
 FEATURES Location/Qualifiers
 source 1..401

/organism="actinobacterium BAL125"
/mol_type="genomic DNA"
/strain="BAL125"
/isolation_source="Baltic Sea, 3m depth, Landsort deep St.
BY31, Zobel/R2A media"
/db_xref="taxon:331783"
/country="Sweden"
/lat_lon="60.42.726N, 05.05.595E"
/collection_date="2 July 2003"
<1..>401
/product="16S ribosomal RNA"

ORIGIN

Query Match 92.7%; Score 20.4; DB 15; Length 401;
 Best Local Similarity 95.5%; Pred. No. 1.9e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTTCGG 22
 |||||
 Db 4 GTCGAACGGAAGGCCTTTCGG 25

RESULT 38

AY234665
 LOCUS Bacterium Ellin6013 403 bp DNA linear BCT 08-DEC-2003
 DEFINITION Bacterium Ellin6013 16S ribosomal RNA gene, partial sequence.
 ACCESSION AY234665
 VERSION AY234665.1 GI:37961822

KEYWORDS

ORGANISM bacterium Ellin6013
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae.

REFERENCE

1 (bases 1 to 403)
 Joseph,S.J., Hugenholtz,P., Sangwan,P., Osborne,C.A. and Janssen,P.H.

AUTHORS

LABORATORY Cultivation of Widespread and Previously Uncultured Soil Bacteria
 Appl. Environ. Microbiol. 69 (12), 7210-7215 (2003)

TITLE

14660368

REFERENCE

2 (bases 1 to 403)
 Joseph,S.J., Hugenholtz,P., Rana,P., Osborne,C.A., Sait,M. and Janssen,P.H.

AUTHORS

Direct Submission
 Submitted (12-FEB-2003) Department of Microbiology and Immunology, University of Melbourne, Parkville, Victoria 3010, Australia

TITLE

Location/Qualifiers

source 1..403

/organism="bacterium Ellin6013"

/mol_type="genomic DNA"

/isolate="Ellin6013"

/db_xref="taxon:234120"

<1..>403

/product="16S ribosomal RNA"

ORIGIN

Query Match 92.7%; Score 20.4; DB 15; Length 403;
 Best Local Similarity 95.5%; Pred. No. 1.9e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTTCGG 22
 |||||
 Db 34 GTCGAACGGAAGGCCTTTCGG 55

RESULT 39

AY792017/c
 LOCUS Mycobacterium sp. 5BR6 407 bp DNA linear BCT 20-NOV-2004
 DEFINITION Mycobacterium sp. 5BR6 16S ribosomal RNA gene, partial sequence.
 ACCESSION AY792017
 VERSION AY792017.1 GI:55740316

KEYWORDS

ORGANISM

Myobacterium sp. 5BR6

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

Corynebacterineae; Mycobacteriaceae; Mycobacterium.

1 (bases 1 to 407)

Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.

Bioremediation of radioactive water with metallic materials

Unpublished

REFERENCE 2 (bases 1 to 407)

Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.

Direct Submission

Submitted (25-OCT-2004) Dep Ingenieria y Ciencia de los Materiales,

Escuela Tecnica Superior de Ingenieros Industriales, Universidad

Politecnica de Madrid, Jose Gutierrez Abascal, 2, Madrid, Madrid

28006, Spain

FEATURES Location/Qualifiers

source 1..407

/organism="Mycobacterium sp. 5BR6"

/mol_type="genomic DNA"

/isolate="5BR6"

/isolation_source="radioactive water"

/db_xref="taxon:300866"

<1..>407

/product="16S ribosomal RNA"

ORIGIN

Query Match 92.7%; Score 20.4; DB 15; Length 407;
 Best Local Similarity 95.5%; Pred. No. 1.9e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTTCGG 22
 |||||

Db 362 GTCGAACGGAAGGCCTTTCGG 341

RESULT 40

BSSMKN12
 LOCUS Bacterium sp. (SMKN12) DNA. 410 bp DNA linear ENV 22-FEB-1995
 DEFINITION Bacterium sp. (SMKN12) DNA.
 ACCESSION X78654
 VERSION X78654.1 GI:509723

16S ribosomal RNA.

unidentified bacterium

unidentified bacterium

Bacteria; environmental samples.

REFERENCE 1

Schuppler,M., Mertens,F., Schon,G. and Gobel,U.B.

Molecular characterization of nocardiform actinomycetes in activated sludge by 16S rRNA analysis

Microbiology (Reading, Engl.) 141 (Pt 2), 513-521 (1995)

7704280

REFERENCE 2 (bases 1 to 410)

Schuppler,M.

Direct Submission

Submitted (28-MAR-1994) M. Schuppler, Institut fuer Med.

Mikrobiologie & Hygiene, Universitaet Freiburg, Hermann-Herder-St.

11, 79104 Freiburg, FRG

FEATURES Location/Qualifiers

source 1..410

/organism="unidentified bacterium"

/mol_type="genomic DNA"

/isolate="SMKN12"

/db_xref="taxon:2338"

1..410

/product="16S ribosomal RNA"

ORIGIN

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Query Match      92.7%; Score 20.4; DB 1; Length 410;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTCGG 22
    |||||
Db 6 GTCGAACGGAAGGCCCTTCGG 27

RESULT 41
DQ063154
LOCUS actinobacterium BAL218 411 bp DNA linear BCT 27-JUN-2005
DEFINITION Actinobacterium BAL218 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ063154
VERSION DQ063154.1 GI:68139192
KEYWORDS .
SOURCE actinobacterium BAL218
ORGANISM actinobacterium BAL218
REFERENCE 1 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE Bacterial community composition in the central Baltic Sea analyzed by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences, University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES
source 1..411
/mol_type="genomic DNA"
/strain="BAL218"
/isolation_source="Baltic Sea, 3m depth, Landsort deep St. BY31, Zobel/R2A media"
/db_xref="taxon:331796"
/country="Sweden"
/lat_lon="60.42.726N, 05.05.595E"
/collection_dates="17 May 2004"
<1..>411
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      92.7%; Score 20.4; DB 15; Length 411;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTCGG 22
    |||||
Db 15 GTCGAACGGAAGGCCCTTCGG 36

RESULT 43
AY792013
LOCUS Mycobacterium sp. 4BR14 16S ribosomal RNA gene, partial sequence.
DEFINITION Mycobacterium sp. 4BR14
ACCESSION AY792013
VERSION AY792013.1 GI:55740312
KEYWORDS .
SOURCE Mycobacterium sp. 4BR14
ORGANISM Mycobacterium sp. 4BR14
REFERENCE 1 (bases 1 to 411)
AUTHORS Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.
TITLE Biorremediation of radioactive water with metallic materials
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 411)
AUTHORS Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.
TITLE Direct Submission
JOURNAL Submitted (25-OCT-2004) Dep Ingenieria y Ciencia de los Materiales, Escuela Tecnica Superior de Ingenieros Industriales, Universidad Politecnica de Madrid, Jose Gutierrez Abascal, 2, Madrid, Madrid 28006, Spain
FEATURES
source 1..411
/mol_type="genomic DNA"
/isolate="4BR14"
/isolation_source="radioactive water"
/db_xref="taxon:300864"
<1..>411
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      92.7%; Score 20.4; DB 15; Length 411;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTCGG 22
    |||||
Db 55 GTCGAACGGAAGGCCCTTCGG 76

RESULT 44
AM085773
LOCUS actinobacterium BAL263 411 bp DNA linear BCT 27-JUN-2005
DEFINITION Actinobacterium BAL263 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ063199
VERSION DQ063199.1 GI:68139237
KEYWORDS .
SOURCE actinobacterium BAL263
ORGANISM actinobacterium BAL263
REFERENCE 1 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE Bacterial community composition in the central Baltic Sea analyzed by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and

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Hagstrom,A.
Direct Submission
Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences, University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
Location/Qualifiers
source 1..411
/organism="actinobacterium BAL263"
/mol_type="genomic DNA"
/strain="BAL263"
/isolation_source="Baltic Sea, 3m depth, Landsort deep St. BY31, Zobel/R2A media"
/db_xref="taxon:331810"
/country="Sweden"
/lat_lon="60.42.726N, 05.05.595E"
/collection_dates="17 May 2004"
<1..>411
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      92.7%; Score 20.4; DB 15; Length 411;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTCGG 22
    |||||
Db 15 GTCGAACGGAAGGCCCTTCGG 36

RESULT 43
AY792013
LOCUS Mycobacterium sp. 4BR14 16S ribosomal RNA gene, partial sequence.
DEFINITION Mycobacterium sp. 4BR14
ACCESSION AY792013
VERSION AY792013.1 GI:55740312
KEYWORDS .
SOURCE Mycobacterium sp. 4BR14
ORGANISM Mycobacterium sp. 4BR14
REFERENCE 1 (bases 1 to 411)
AUTHORS Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.
TITLE Biorremediation of radioactive water with metallic materials
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 411)
AUTHORS Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.
TITLE Direct Submission
JOURNAL Submitted (25-OCT-2004) Dep Ingenieria y Ciencia de los Materiales, Escuela Tecnica Superior de Ingenieros Industriales, Universidad Politecnica de Madrid, Jose Gutierrez Abascal, 2, Madrid, Madrid 28006, Spain
FEATURES
source 1..411
/mol_type="genomic DNA"
/isolate="4BR14"
/isolation_source="radioactive water"
/db_xref="taxon:300864"
<1..>411
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      92.7%; Score 20.4; DB 15; Length 411;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTCGG 22
    |||||
Db 55 GTCGAACGGAAGGCCCTTCGG 76

RESULT 44
AM085773
LOCUS actinobacterium BAL263 411 bp DNA linear ENV 21-SEP-2005
DEFINITION Actinobacterium BAL263 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ063199
VERSION DQ063199.1 GI:68139237
KEYWORDS .
SOURCE actinobacterium BAL263
ORGANISM actinobacterium BAL263
REFERENCE 1 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE Bacterial community composition in the central Baltic Sea analyzed by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and

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DEFINITION Uncultured Mycobacterium sp. partial 16S rRNA gene, clone T6.
ACCESSION AM085773
VERSION ENV; 16S ribosomal RNA; 16S rRNA gene.
KEYWORDS uncultured Mycobacterium sp.
SOURCE uncultured Mycobacterium sp.
ORGANISM uncultured Mycobacterium sp.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental
samples.
REFERENCE 1
AUTHORS Uytendaele, M., Vermeir, S., Wattiau, P., Rynjaert, A. and Springael, D.
TITLE Enrichment and characterization of a bacterial culture utilizing
pyrene at pH 2 and dominated by a slow-growing Mycobacterium sp.
from acidic polycyclic aromatic hydrocarbon contaminated soil
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 414)
AUTHORS Uytendaele, M.
TITLE Direct Submission
JOURNAL Submitted (13-SEP-2005) Uytendaele M., Division Soil and Water
Management, Catholic University of Leuven, Kasteelpark Arenberg 20,
B-3001 Leuven, BELGIUM
FEATURES
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            /isolation_source="PAH-contaminated soil"
            /db_xref="taxon:171292"
            /clone="T6"
            /environmental sample
            /country="Belgium"
            <1..>414
            /gene="16S rRNA"
            <1..>414
            /gene="16S rRNA"
            /product="16S ribosomal RNA"

gene
rRNA

ORIGIN
Query Match 92.7%; Score 20.4; DB 1; Length 414;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTCGG 22
|||||
Db 4 GTCGAACGGAAGGCGCTTCGG 25

RESULT 45
DQ223051 414 bp DNA linear ENV 22-OCT-2005
LOCUS Uncultured bacterium clone H070 16S ribosomal RNA gene, partial
DEFINITION sequence.
ACCESSION DQ223051
VERSION DQ223051.1 GI:77744948
KEYWORDS ENV.
SOURCE uncultured bacterium
ORGANISM uncultured bacterium
Bacteria; environmental samples.
REFERENCE 1 (bases 1 to 414)
AUTHORS Li, H. and Mu, B.
TITLE Phylogenetic diversity and community structure of bacteria in an
oil-storage cavity as detected by 16S rRNA gene library
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 414)
AUTHORS Li, H. and Mu, B.
TITLE Direct Submission
JOURNAL Submitted (26-SEP-2005) Chemical and Pharmaceutical Institution,
East China University of Science and Technology, Meilong Road,
Shanghai 200237, China
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    source
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            /organism="uncultured bacterium"
            /mol_type="genomic DNA"
            /isolation_source="oil-storage cavity"

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rRNA
/db_xref="taxon:77133"
/clones="H070"
/environmental_sample
<1..>414
/product="16S ribosomal RNA"

ORIGIN
Query Match 92.7%; Score 20.4; DB 1; Length 414;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTCGG 22
|||||
Db 54 GTCGAACGGAAGGCGCTTCGG 75

RESULT 46
DQ063108 415 bp DNA linear BCT 27-JUN-2005
LOCUS Actinobacterium BAL168 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION DQ063108
VERSION DQ063108.1 GI:68139141
KEYWORDS actinobacterium BAL168
SOURCE actinobacterium BAL168
ORGANISM Bacteria; Actinobacteria.
REFERENCE 1 (bases 1 to 415)
AUTHORS Riemann, L., Leitert, C., Pommier, T., Simu, K., Holmfeldt, K. and
Hagstrom, A.
TITLE Bacterial community composition in the central Baltic Sea analyzed
by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 415)
AUTHORS Riemann, L., Leitert, C., Pommier, T., Simu, K., Holmfeldt, K. and
Hagstrom, A.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
University of Kalmar, Barlastagan 11, Kalmar 39231, Sweden
FEATURES
    source
        1..415
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            /strain="BAL168"
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            BY31, Zobel/R2A media"
            /db_xref="taxon:331762"
            /country="Sweden"
            /lat_lon="60.42.726N, 05.05.595E"
            /collection_date="8 October 2003"
            <1..>415
            /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 92.7%; Score 20.4; DB 15; Length 415;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTCGG 22
|||||
Db 4 GTCGAACGGAAGGCGCTTCGG 25

RESULT 47
AM085786 416 bp DNA linear ENV 21-SEP-2005
LOCUS Uncultured Mycobacterium sp. partial 16S rRNA gene, clone K11.
DEFINITION
ACCESSION AM085786
VERSION AM085786.1 GI:75754609
KEYWORDS ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE uncultured Mycobacterium sp.
ORGANISM uncultured Mycobacterium sp.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental

```

```

samples.
1
REFERENCE
AUTHORS      Uytendaele, M., Breugelmans, P., Janssen, M., Wattiau, P., Joffe, B.,
              Karlsson, U., Ortega-Calvo, J.J., Bastiaens, L., Rymaert, A. and
              Springael, D.
TITLE        Distribution of the Mycobacterium sp. community and polycyclic
              aromatic hydrocarbons (PAHs) among different size fractions of a
              weathered PAH-contaminated soil
JOURNAL
AUTHORS      Unpublished
              2 (bases 1 to 416)
              Uytendaele, M.
TITLE        Direct Submission
JOURNAL      Submitted (13-SEP-2005) Uytendaele M., Division Soil and Water
              Management, Catholic University of Leuven, Kasteelpark Arenberg 20,
              B-3001 Leuven, BELGIUM
FEATURES
source      Location/Qualifiers
              1. .416
                /organism="uncultured Mycobacterium sp."
                /mol_type="genomic DNA"
                /isolation_source="PAH-contaminated soil"
                /db_xref="taxon:171292"
                /clone="K11"
                /environmental_sample
                /country="Denmark"
                <1. .>416
                /gene="16S rRNA"
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                /gene="16S rRNA"
                /product="16S ribosomal RNA"
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Query Match      92.7%; Score 20.4; DB 1; Length 416;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTCGACGGAAGGCGCTTTCGG 22
      |||||
Db 7 GTCGACGGAAGGCGCTTTCGG 28
      |||||
RESULT 48
LOCUS      DQ063073 417 bp DNA linear BCT 27-JUN-2005
DEFINITION actinobacterium BAL133 16S ribosomal RNA gene, partial sequence.
ACCESSION  DQ063073
VERSION     DQ063073.1 GI:68139102
KEYWORDS   .
SOURCE     actinobacterium BAL133
ORGANISM   actinobacterium BAL133
REFERENCE  1 (bases 1 to 417)
AUTHORS    Riemann, L., Leitert, C., Pommier, T., Simu, K., Holmfeldt, K. and
              Hagsstrom, A.
TITLE      Bacterial community composition in the central Baltic Sea analyzed
              by cultivation and molecular-based methods
JOURNAL
REFERENCE  2 (bases 1 to 417)
AUTHORS    Riemann, L., Leitert, C., Pommier, T., Simu, K., Holmfeldt, K. and
              Hagsstrom, A.
TITLE      Direct Submission
JOURNAL    Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
              University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES
source      Location/Qualifiers
              1. .417
                /organism="actinobacterium BAL133"
                /mol_type="genomic DNA"
                /strain="BAL133"
                /isolation_source="Baltic Sea, 3m depth, Landsort deep St.
                BY31, Zobell/R2A media"
                /db_xref="taxon:331784"
                /country="Sweden"
                /latlon="60.42.726N, 05.05.595E"
                /collection_date="2 July 2003"

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rRNA      <1. .>417
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Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTCGACGGAAGGCGCTTTCGG 22
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Db 1 GTCGACGGAAGGCGCTTTCGG 22
      |||||
RESULT 49
LOCUS      AM085788 418 bp DNA linear ENV 21-SEP-2005
DEFINITION Uncultured Mycobacterium sp. partial 16S rRNA gene, clone K13.
ACCESSION  AM085788
VERSION     AM085788.1 GI:75754611
KEYWORDS   ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE     uncultured Mycobacterium sp.
ORGANISM   uncultured Mycobacterium sp.
REFERENCE  1
AUTHORS    Uytendaele, M., Breugelmans, P., Janssen, M., Wattiau, P., Joffe, B.,
              Karlsson, U., Ortega-Calvo, J.J., Bastiaens, L., Rymaert, A. and
              Springael, D.
TITLE      Distribution of the Mycobacterium sp. community and polycyclic
              aromatic hydrocarbons (PAHs) among different size fractions of a
              weathered PAH-contaminated soil
JOURNAL
REFERENCE  2 (bases 1 to 418)
AUTHORS    Uytendaele, M.
TITLE      Direct Submission
JOURNAL    Submitted (13-SEP-2005) Uytendaele M., Division Soil and Water
              Management, Catholic University of Leuven, Kasteelpark Arenberg 20,
              B-3001 Leuven, BELGIUM
FEATURES
source      Location/Qualifiers
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                /organism="uncultured Mycobacterium sp."
                /mol_type="genomic DNA"
                /isolation_source="PAH-contaminated soil"
                /db_xref="taxon:171292"
                /clone="K13"
                /environmental_sample
                /country="Denmark"
                <1. .>418
                /gene="16S rRNA"
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                /gene="16S rRNA"
                /product="16S ribosomal RNA"
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Query Match      92.7%; Score 20.4; DB 1; Length 418;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTCGACGGAAGGCGCTTTCGG 22
      |||||
Db 7 GTCGACGGAAGGCGCTTTCGG 28
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RESULT 50
LOCUS      AY673261 418 bp DNA linear BCT 20-MAY-2005
DEFINITION Mycobacteriaceae bacterium Ellin7095 16S ribosomal RNA gene,
              partial sequence.
ACCESSION  AY673261
VERSION     AY673261.1 GI:56683118
KEYWORDS   .
SOURCE     Mycobacteriaceae bacterium Ellin7095

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ORGANISM  Mycobacteriaceae bacterium Ellin7095
REFERENCE  1 (bases 1 to 418)
AUTHORS    Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE      Effects of growth medium, inoculum size, and incubation time on
           culturability and isolation of soil bacteria
JOURNAL    Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED     15691937
REFERENCE  2 (bases 1 to 418)
AUTHORS    Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE      Direct Submission
JOURNAL    Submitted (02-JUL-2004) Department of Microbiology and Immunology,
           University of Melbourne, Grattan Street, Parkville, Victoria 3010,
           Australia
FEATURES   Location/Qualifiers
            source
              1..418
              /organism="Mycobacteriaceae bacterium Ellin7095"
              /mol_type="genomic DNA"
              /isolate="Ellin7095"
              /isolation_source="soil"
              /db_xref="taxon:305281"
              <1_>418
              /product="16S ribosomal RNA"
            rRNA
            ORIGIN
              Query Match      92.7%; Score 20.4; DB 15; Length 418;
              Best Local Similarity 95.5%; Pred. No. 1.9e+02;
              Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1  GTCGAACGGAAGGCGCTTTCGG 22
      |||||||||||||||||||
Db  34 GTCGAACGGAAGGCGCTTTCGG 55

RESULT 51
AM085770 LOCUS      421 bp DNA linear ENV 21-SEP-2005
DEFINITION  Uncultured eubacterium partial 16S rRNA gene, clone T3.
ACCESSION   AM085770
VERSION     AM085770.1 GI:75754591
KEYWORDS    ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE      uncultured bacterium
ORGANISM    Bacteria; environmental samples.
REFERENCE   1
AUTHORS     Uytendaele, M., Vermeir, S., Wattiau, P., Ryngaert, A. and Springael, D.
TITLE       Enrichment and characterization of a bacterial culture utilizing
           pyrene at pH 2 and dominated by a slow-growing Mycobacterium sp.
           from acidic polycyclic aromatic hydrocarbon contaminated soil
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 421)
AUTHORS     Uytendaele, M.
TITLE       Direct Submission
JOURNAL     Submitted (13-SEP-2005) Uytendaele M., Division Soil and Water
           Management, Catholic University of Leuven, Kasteelpark Arenberg 20,
           B-3001 Leuven, BELGIUM
FEATURES   Location/Qualifiers
            source
              1..421
              /organism="uncultured bacterium"
              /mol_type="genomic DNA"
              /isolation_source="PAH-contaminated soil"
              /db_xref="taxon:77133"
              /clone="T3"
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              /country="Belgium"
              <1_>421
              /gene="16S rRNA"
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            gene
            rRNA
            ORIGIN

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Query Match      92.7%; Score 20.4; DB 1; Length 421;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1  GTCGAACGGAAGGCGCTTTCGG 22
      |||||||||||||||||||
Db  13 GTCGAACGGAAGGCGCTTTCGG 34

RESULT 52
AJ786807 LOCUS      422 bp DNA linear BCT 29-OCT-2004
DEFINITION  Mycobacterium sp. R-22838 partial 16S rRNA gene, isolate R-22838.
ACCESSION   AJ786807
VERSION     AJ786807.1 GI:54887545
KEYWORDS    16S ribosomal RNA; 16S rRNA gene.
SOURCE      Mycobacterium sp. R-22838
ORGANISM    Mycobacterium sp. R-22838
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE   1
AUTHORS     Vanparrys, B., Heylen, K., Lebbe, L., Boon, N., Wittebolle, L.,
           Verstraete, W. and De Vos, P.
TITLE       The microbial community composition of a commercial nitrifying
           inoculum
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 422)
AUTHORS     Vanparrys, B.
TITLE       Direct Submission
JOURNAL     Submitted (30-JUL-2004) Vanparrys B., Laboratory of Microbiology,
           University of Gent, Ledeganckstraat 35, 9000 Gent, BELGIUM
FEATURES   Location/Qualifiers
            source
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              /organism="Mycobacterium sp. R-22838"
              /mol_type="genomic DNA"
              /isolate="R-22838"
              /isolation_source="commercial nitrifying inoculum"
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              /country="Belgium"
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            rRNA
            ORIGIN
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              Best Local Similarity 95.5%; Pred. No. 1.8e+02;
              Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1  GTCGAACGGAAGGCGCTTTCGG 22
      |||||||||||||||||||
Db  34 GTCGAACGGAAGGCGCTTTCGG 55

RESULT 53
AY673284 LOCUS      422 bp DNA linear BCT 20-MAY-2005
DEFINITION  Micromonosporaceae bacterium Ellin7118 16S ribosomal RNA gene,
           partial sequence.
ACCESSION   AY673284
VERSION     AY673284.1 GI:56683141
KEYWORDS    Micromonosporineae; Micromonosporaceae.
SOURCE      Micromonosporaceae bacterium Ellin7118
ORGANISM    Micromonosporaceae bacterium Ellin7118
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Micromonosporineae; Micromonosporaceae.
REFERENCE   1 (bases 1 to 422)
AUTHORS     Davis, K.E., Joseph, S.J. and Janssen, P.H.
TITLE       Effects of growth medium, inoculum size, and incubation time on
           culturability and isolation of soil bacteria
JOURNAL     Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED     15691937

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REFERENCE 2 (bases 1 to 422)
AUTHORS Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES
source Location/Qualifiers
1..422
/organism="Micromonosporaceae bacterium Ellin7118"
/mol_type="genomic DNA"
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/isolation_source="soil"
/db_xref="taxon:305235"
<1..>422
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rRNA
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Query Match 92.7%; Score 20.4; DB 15; Length 422;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTCGACGGAAAGCCCTTCGG 22
Db 33 GTCGACGGAAAGCCCTTCGG 54
RESULT 54
AY673205
LOCUS Mycobacteriaceae bacterium Ellin7039 BCT 20-MAY-2005
DEFINITION partial sequence.
ACCESSION AY673205.1 GI:56683062
VERSION
KEYWORDS
SOURCE
ORGANISM
Mycobacteriaceae bacterium Ellin7039
Mycobacteriaceae bacterium Ellin7039
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
1 (bases 1 to 423)
Davis,K.E., Joseph,S.J. and Janssen,P.H.
EFFECTS OF growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
JOURNAL
PUBMED 15691937
REFERENCE 2 (bases 1 to 423)
AUTHORS Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES
source Location/Qualifiers
1..423
/organism="Mycobacteriaceae bacterium Ellin7039"
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/isolation_source="soil"
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<1..>423
/product="16S ribosomal RNA"
rRNA
ORIGIN
Query Match 92.7%; Score 20.4; DB 15; Length 423;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTCGACGGAAAGCCCTTCGG 22
Db 34 GTCGACGGAAAGCCCTTCGG 55
RESULT 55
AY673206
LOCUS Mycobacteriaceae bacterium Ellin7041 BCT 20-MAY-2005
DEFINITION partial sequence.
ACCESSION AY673207.1 GI:56683064
VERSION
KEYWORDS
SOURCE
ORGANISM
Mycobacteriaceae bacterium Ellin7041
Mycobacteriaceae bacterium Ellin7041
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
1 (bases 1 to 423)
Davis,K.E., Joseph,S.J. and Janssen,P.H.
EFFECTS OF growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
JOURNAL
PUBMED 15691937
REFERENCE 2 (bases 1 to 423)
AUTHORS Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES
source Location/Qualifiers
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/organism="Mycobacteriaceae bacterium Ellin7041"
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/isolation_source="soil"
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/product="16S ribosomal RNA"
rRNA

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DEFINITION Mycobacteriaceae bacterium Ellin7040 16S ribosomal RNA gene,
partial sequence.
ACCESSION AY673206
VERSION AY673206.1 GI:56683063
KEYWORDS
SOURCE
ORGANISM
Mycobacteriaceae bacterium Ellin7040
Mycobacteriaceae bacterium Ellin7040
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
1 (bases 1 to 423)
Davis,K.E., Joseph,S.J. and Janssen,P.H.
EFFECTS OF growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
JOURNAL
PUBMED 15691937
REFERENCE 2 (bases 1 to 423)
AUTHORS Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES
source Location/Qualifiers
1..423
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/mol_type="genomic DNA"
/isolate="Ellin7040"
/isolation_source="soil"
/db_xref="taxon:305259"
<1..>423
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rRNA
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Query Match 92.7%; Score 20.4; DB 15; Length 423;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTCGACGGAAAGCCCTTCGG 22
Db 34 GTCGACGGAAAGCCCTTCGG 55
RESULT 56
AY673207
LOCUS Mycobacteriaceae bacterium Ellin7041 16S ribosomal RNA gene,
partial sequence.
DEFINITION partial sequence.
ACCESSION AY673207
VERSION AY673207.1 GI:56683064
KEYWORDS
SOURCE
ORGANISM
Mycobacteriaceae bacterium Ellin7041
Mycobacteriaceae bacterium Ellin7041
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
1 (bases 1 to 423)
Davis,K.E., Joseph,S.J. and Janssen,P.H.
EFFECTS OF growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
JOURNAL
PUBMED 15691937
REFERENCE 2 (bases 1 to 423)
AUTHORS Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES
source Location/Qualifiers
1..423
/organism="Mycobacteriaceae bacterium Ellin7041"
/mol_type="genomic DNA"
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/product="16S ribosomal RNA"
rRNA

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/ product="16S ribosomal RNA"

ORIGIN
Query Match          92.7%; Score 20.4; DB 15; Length 423;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTCGG 22
    |||||
Db 34 GTCGAACGGAAGGCGCTTTCGG 55

RESULT 57
DQ063156          424 bp DNA linear BCT 27-JUN-2005
DEFINITION Actinobacterium BAL220 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ063156
VERSION DQ063156.1 GI:68139194
KEYWORDS actinobacterium BAL220
SOURCE actinobacterium BAL220
ORGANISM Bacteria; Actinobacteria.
REFERENCE 1 (bases 1 to 424)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE Bacterial community composition in the central Baltic Sea analyzed by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 424)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences, University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES
source Location/Qualifiers
1..424
/organism="actinobacterium BAL220"
/mol_type="genomic DNA"
/strain="BAL220"
/isolation_source="Baltic Sea, 3m depth, Landsort deep St. BY31, Zobell/R2A media"
/db_xref="taxon:331797"
/country="Sweden"
/lat_lon="60.42.726N, 05.05.595E"
/collection_date="17 May 2004"
<1..>424
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          92.7%; Score 20.4; DB 15; Length 424;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTCGG 22
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Db 18 GTCGAACGGAAGGCGCTTTCGG 39

RESULT 58
AY673287          424 bp DNA linear BCT 20-MAY-2005
DEFINITION Streptoporangiaceae bacterium Ellin7121 16S ribosomal RNA gene, partial sequence.
ACCESSION AY673287
VERSION AY673287.1 GI:56683144
KEYWORDS Streptoporangiaceae bacterium Ellin7121
SOURCE Streptoporangiaceae bacterium Ellin7121
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptoporangineae; Streptoporangaceae.
REFERENCE 1 (bases 1 to 424)
AUTHORS Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE Effects of growth medium, inoculum size, and incubation time on

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culturability and isolation of soil bacteria
Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
15691937
2 (bases 1 to 424)
Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
Direct Submission
Submitted (02-JUL-2004) Department of Microbiology and Immunology, University of Melbourne, Grattan Street, Parkville, Victoria 3010, Australia
FEATURES
source Location/Qualifiers
1..424
/organism="Streptoporangiaceae bacterium Ellin7121"
/mol_type="genomic DNA"
/isolate="Ellin7121"
/isolation_source="soil"
/db_xref="taxon:305348"
<1..>424
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          92.7%; Score 20.4; DB 15; Length 424;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTCGG 22
    |||||
Db 34 GTCGAACGGAAGGCGCTTTCGG 55

RESULT 59
AY756031          424 bp DNA linear BCT 08-APR-2005
DEFINITION Unidentified bacterium TMB805 16S ribosomal RNA gene, partial sequence.
ACCESSION AY756031
VERSION AY756031.1 GI:54299184
KEYWORDS Unidentified bacterium TMB805
SOURCE Unidentified bacterium TMB805
ORGANISM Bacteria.
REFERENCE 1 (bases 1 to 424)
AUTHORS Chapon,V., Benzerara,K., Barakat,M., Achouak,W., Barras,F., Christen,R., Chevenet,F. and Heulin,T.
TITLE Diversity of Bacteria and Archae in the arid desert of Tataouine Unpublished
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 424)
AUTHORS Chapon,V., Benzerara,K., Barakat,M., Achouak,W., Barras,F., Christen,R., Chevenet,F. and Heulin,T.
Direct Submission
Submitted (21-SEP-2004) LEMIR-DEVM-DSV, CEA, Cadarache, Saint Paul Lez Durance 13108, France
FEATURES
source Location/Qualifiers
1..424
/organism="Unidentified bacterium TMB805"
/mol_type="genomic DNA"
/strain="TMB805"
/isolation_source="arid soil"
/db_xref="taxon:297191"
<1..>424
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          92.7%; Score 20.4; DB 15; Length 424;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTCGG 22
    |||||
Db 4 GTCGAACGGAAGGCGCTTTCGG 25

RESULT 60
AY394635

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LOCUS      AY394635                425 bp    DNA        linear    ENV 20-OCT-2003
DEFINITION Uncultured Mycobacterium sp. clone WI-11 16S ribosomal RNA gene,
partial sequence.
ACCESSION  AY394635
VERSION     AY394635.1  GI:37677560
KEYWORDS   ENV.
SOURCE     uncultured Mycobacterium sp.
ORGANISM   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental
samples.
REFERENCE  1 (bases 1 to 425)
AUTHORS   Benson,D.R., Benson,M.J., Gawronski,J.D. and Eveleigh,D.E.
TITLE     Intracellular symbionts and other bacteria associated with deer
ticks (Ixodes scapularis) from Nantucket and Wellfleet, Cape Cod,
Massachusetts
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 425)
AUTHORS   Benson,D.R., Benson,M.J., Gawronski,J.D. and Eveleigh,D.E.
TITLE     Direct Submission
JOURNAL   Submitted (19-SEP-2003) Molecular & Cell Biology, University of
Connecticut, U-3125, North Eagleville Rd., Storrs, CT 06279-3125,
USA
FEATURES   Location/Qualifiers
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            1..425
               /organism="uncultured Mycobacterium sp."
               /mol_type="genomic DNA"
               /specific_host="Ixodes scapularis"
               /db_xref="taxon:171292"
               /clones="WI-11"
               /environmental sample
               /country="USA: Massachusetts, Cape Cod, Nantucket,
               Wellfleet"
               <1..>425
               /product="16S ribosomal RNA"

rRNA

ORIGIN
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      Best Local Similarity 95.5%;   Pred. No. 1.8e+02;
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Qy      1  GTCGAACGGAAAGCCCTTCGG 22
      |||||||||||||||
Db      34  GTCGAACGGAAAGCCCTTCGG 55

RESULT 61
AY673136
LOCUS      AY673136                426 bp    DNA        linear    BCT 22-DEC-2004
DEFINITION Mycobacteriaceae bacterium Ellin5409 16S ribosomal RNA gene,
partial sequence.
ACCESSION  AY673136
VERSION     AY673136.1  GI:56683290
KEYWORDS   Mycobacteriaceae bacterium Ellin5409
SOURCE     Mycobacteriaceae bacterium Ellin5409
ORGANISM   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
REFERENCE  1 (bases 1 to 426)
AUTHORS   Osborne,C.A. and Janssen,P.H.
TITLE     Direct Submission
JOURNAL   Submitted (30-JUN-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES   Location/Qualifiers
            source
            1..426
               /organism="Mycobacteriaceae bacterium Ellin5409"
               /mol_type="genomic DNA"
               /isolate="Ellin5409"
               /isolation_source="soil"
               /db_xref="taxon:305244"
               <1..>426
               /product="16S ribosomal RNA"

rRNA

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ORIGIN
      Query Match      92.7%;   Score 20.4;   DB 15;   Length 426;
      Best Local Similarity 95.5%;   Pred. No. 1.8e+02;
      Matches 21;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy      1  GTCGAACGGAAAGCCCTTCGG 22
      |||||||||||||||
Db      34  GTCGAACGGAAAGCCCTTCGG 55

RESULT 62
AB106918
LOCUS      AB106918                428 bp    DNA        linear    BCT 09-SEP-2003
DEFINITION Gram-positive bacterium 1-6 for 16S ribosomal RNA, partial
sequence.
ACCESSION  AB106918
VERSION     AB106918.1  GI:29421132
KEYWORDS   Gram-positive bacterium 1-6
SOURCE     Gram-positive bacterium 1-6
ORGANISM   Bacteria.
REFERENCE  1
AUTHORS   Amachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
Fujii,T. and Muramatsu,Y.
TITLE     Microbial participation in iodine volatilization from soils
JOURNAL   Environ. Sci. Technol. 37, 3885-3890 (2003)
REFERENCE  2 (bases 1 to 428)
AUTHORS   Amachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
Fujii,T. and Muramatsu,Y.
TITLE     Direct Submission
JOURNAL   Submitted (27-MAR-2003) Seigo Amachi, Chiba University, Dept. of
Bioresources Chem.; 648 Matsudo, Matsudo-shi, Chiba 271-8510, Japan
E-mail:amachi@faculty.chiba-u.jp, Tel:81-47-308-8868,
Fax:81-47-308-8866)
FEATURES   Location/Qualifiers
            source
            1..428
               /organism="Gram-positive bacterium 1-6"
               /mol_type="genomic DNA"
               /strain="1-6"
               /db_xref="taxon:226200"
               <1..>428
               /product="16S ribosomal RNA"

rRNA

ORIGIN
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      Best Local Similarity 95.5%;   Pred. No. 1.8e+02;
      Matches 21;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy      1  GTCGAACGGAAAGCCCTTCGG 22
      |||||||||||||||
Db      34  GTCGAACGGAAAGCCCTTCGG 55

RESULT 63
DQ063058
LOCUS      DQ063058                428 bp    DNA        linear    BCT 27-JUN-2005
DEFINITION Actinobacterium BAL118 16S ribosomal RNA gene, partial sequence.
ACCESSION  DQ063058
VERSION     DQ063058.1  GI:68139087
KEYWORDS   actinobacterium BAL118
SOURCE     actinobacterium BAL118
ORGANISM   Bacteria; Actinobacteria.
REFERENCE  1 (bases 1 to 428)
AUTHORS   Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE     Bacterial community composition in the central Baltic Sea analyzed
by cultivation and molecular-based methods
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 428)
AUTHORS   Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.

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TITLE      Direct Submission
JOURNAL    Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
           University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES   Location/Qualifiers
            source
            1..428
            /organism="actinobacterium BAL118"
            /mol_type="genomic DNA"
            /strain="BAL118"
            /isolation_source="Baltic Sea, 3m depth, Landsort deep St.
            BY31, Zobel1/R2A media"
            /db_xref="taxon:331781"
            /country="Sweden"
            /lat_lon="60.42.726N, 05.05.595E"
            /collection_date="2 July 2003"
            <1..>428
            /product="16S ribosomal RNA"

rRNA
ORIGIN
Query Match      92.7%;   Score 20.4;   DB 15;   Length 428;
Best Local Similarity 95.5%;   Pred. No. 1.8e+02;
Matches 21;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy      1  GTCGAACGGAAGGCGCTTTCGG 22
        |||||
Db      12 GTCGAACGGAAGGCGCTTTCGG 33

RESULT 64
AJ786822
LOCUS      Mycobacterium sp. R-23262 partial 16S rRNA gene, isolate R-23262.
DEFINITION
VERSION     AJ786822.1 GI:54887560
KEYWORDS    16S ribosomal RNA; 16S rRNA gene.
SOURCE      Mycobacterium sp. R-23262
ORGANISM    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE   1  Vanparrys B., Heylen, K., Lebbe, L., Boon, N., Wittebolle, L.,
            Verstraete, W. and De Vos, P.
            The microbial community composition of a commercial nitrifying
            inoculum
JOURNAL    Unpublished
REFERENCE   2  (bases 1 to 430)
AUTHORS    Vanparrys B.
TITLE      Direct Submission
JOURNAL    Submitted (30-JUL-2004) Vanparrys B., Laboratory of Microbiology,
            University of Gent, Ledeganckstraat 35, 9000 Gent, BELGIUM
FEATURES   Location/Qualifiers
            source
            1..430
            /organism="Mycobacterium sp. R-23262"
            /mol_type="genomic DNA"
            /isolate="R-23262"
            /isolation_source="commercial nitrifying inoculum"
            /db_xref="taxon:289008"
            /country="Belgium"
            1..430
            /gene="16S rRNA"
            <1..>430
            /gene="16S rRNA"
            /product="16S ribosomal RNA"

gene
rRNA
ORIGIN
Query Match      92.7%;   Score 20.4;   DB 15;   Length 430;
Best Local Similarity 95.5%;   Pred. No. 1.8e+02;
Matches 21;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy      1  GTCGAACGGAAGGCGCTTTCGG 22
        |||||
Db      34 GTCGAACGGAAGGCGCTTTCGG 55

TITLE      Direct Submission
JOURNAL    Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
            University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES   Location/Qualifiers
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            /strain="BAL118"
            /isolation_source="Baltic Sea, 3m depth, Landsort deep St.
            BY31, Zobel1/R2A media"
            /db_xref="taxon:331781"
            /country="Sweden"
            /lat_lon="60.42.726N, 05.05.595E"
            /collection_date="2 July 2003"
            <1..>428
            /product="16S ribosomal RNA"

rRNA
ORIGIN
Query Match      92.7%;   Score 20.4;   DB 15;   Length 428;
Best Local Similarity 95.5%;   Pred. No. 1.8e+02;
Matches 21;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy      1  GTCGAACGGAAGGCGCTTTCGG 22
        |||||
Db      12 GTCGAACGGAAGGCGCTTTCGG 33

RESULT 65
AJ673202
LOCUS      Mycobacteriaceae bacterium Ellin7036 16S ribosomal RNA gene,
DEFINITION    partial sequence.
VERSION     AJ673202.1 GI:56683059
KEYWORDS    Mycobacteriaceae bacterium Ellin7036
SOURCE      Mycobacteriaceae bacterium Ellin7036
ORGANISM    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae.
REFERENCE   1  (bases 1 to 430)
            Davis, K.E., Joseph, S.J. and Janssen, P.H.
            Effects of growth medium, inoculum size, and incubation time on
            culturability and isolation of soil bacteria
            Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
JOURNAL     15691937
PUBMED
REFERENCE   2  (bases 1 to 430)
            Davis, K.E.R., Joseph, S.J. and Janssen, P.H.
            Direct Submission
            Submitted (02-JUL-2004) Department of Microbiology and Immunology,
            University of Melbourne, Grattan Street, Parkville, Victoria 3010,
            Australia
FEATURES   Location/Qualifiers
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            /organism="Mycobacteriaceae bacterium Ellin7036"
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            /isolation_source="soil"
            /db_xref="taxon:305257"
            <1..>430
            /product="16S ribosomal RNA"

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ORIGIN
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Best Local Similarity 95.5%;   Pred. No. 1.8e+02;
Matches 21;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy      1  GTCGAACGGAAGGCGCTTTCGG 22
        |||||
Db      34 GTCGAACGGAAGGCGCTTTCGG 55

TITLE      Direct Submission
JOURNAL    Submitted (27-MAR-2003) Seigo Anachi, Chiba University, Dept. of
            Bioreources Chem.; 648 Matsudo, Matsudo-shi, Chiba 271-8510, Japan
            (E-mail: anachi@faculty.chiba-u.jp, Tel: 81-47-308-8868,
            Fax: 81-47-308-8866)
FEATURES   Location/Qualifiers
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            1..431
            /organism="Gram-positive bacterium 2-1"
            /mol_type="genomic DNA"
            /strain="2-1"

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RESULT 65
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LOCUS      Mycobacteriaceae bacterium Ellin7036 16S ribosomal RNA gene,
DEFINITION    partial sequence.
VERSION     AJ673202.1 GI:56683059
KEYWORDS    Mycobacteriaceae bacterium Ellin7036
SOURCE      Mycobacteriaceae bacterium Ellin7036
ORGANISM    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae.
REFERENCE   1  (bases 1 to 430)
            Davis, K.E., Joseph, S.J. and Janssen, P.H.
            Effects of growth medium, inoculum size, and incubation time on
            culturability and isolation of soil bacteria
            Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
JOURNAL     15691937
PUBMED
REFERENCE   2  (bases 1 to 430)
            Davis, K.E.R., Joseph, S.J. and Janssen, P.H.
            Direct Submission
            Submitted (02-JUL-2004) Department of Microbiology and Immunology,
            University of Melbourne, Grattan Street, Parkville, Victoria 3010,
            Australia
FEATURES   Location/Qualifiers
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            /isolate="Ellin7036"
            /isolation_source="soil"
            /db_xref="taxon:305257"
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            /product="16S ribosomal RNA"

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Best Local Similarity 95.5%;   Pred. No. 1.8e+02;
Matches 21;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy      1  GTCGAACGGAAGGCGCTTTCGG 22
        |||||
Db      34 GTCGAACGGAAGGCGCTTTCGG 55

TITLE      Direct Submission
JOURNAL    Submitted (27-MAR-2003) Seigo Anachi, Chiba University, Dept. of
            Bioreources Chem.; 648 Matsudo, Matsudo-shi, Chiba 271-8510, Japan
            (E-mail: anachi@faculty.chiba-u.jp, Tel: 81-47-308-8868,
            Fax: 81-47-308-8866)
FEATURES   Location/Qualifiers
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            /strain="2-1"

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/product="16S ribosomal RNA"

ORIGIN
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Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGCCCTTCGG 22
Db 34 GTCGAACGGAAGCCCTTCGG 55

RESULT 67
AF078232
LOCUS      AF078232      432 bp      DNA      linear      ENV 10-MAY-2004
DEFINITION Grassland soil clone saf2_117 16S ribosomal RNA gene, partial
sequence.
ACCESSION  AF078232
VERSION     AF078232.1 GI:4590103
KEYWORDS   ENV.
SOURCE     grassland soil clone saf2_117
ORGANISM   grassland soil clone saf2_117
REFERENCE  1 (bases 1 to 432)
AUTHORS    McCaig,A.E., Glover,L.A. and Prosser,J.I.
TITLE      Molecular analysis of bacterial community structure and diversity
in unimproved and improved upland grass pastures
JOURNAL    Appl. Environ. Microbiol. 65 (4), 1721-1730 (1999)
PUBMED     10103273
REFERENCE  2 (bases 1 to 432)
AUTHORS    McCaig,A.E., Prosser,J.I. and Glover,L.A.
TITLE      Direct Submission
JOURNAL    Submitted (16-JUL-1998) Institute of Medical Sciences, Department
of Molecular and Cell Biology, University of Aberdeen,
Foresterhill, Aberdeen AB25 2ZD, Scotland, UK

FEATURES   Location/Qualifiers
source     1..432
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            /environmental_sample
            <1_>432
            /product="16S ribosomal RNA"

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<1_>432
/product="16S ribosomal RNA"

ORIGIN
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Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGCCCTTCGG 22
Db 12 GTCGAACGGAAGCCCTTCGG 33

RESULT 68
AY673198
LOCUS      AY673198      433 bp      DNA      linear      BCT 20-MAY-2005
DEFINITION Mycobacteriaceae bacterium Ellin7032 16S ribosomal RNA gene,
partial sequence.
ACCESSION  AY673198
VERSION     AY673198.1 GI:56683055
KEYWORDS   Mycobacteriaceae bacterium Ellin7032
SOURCE     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
REFERENCE  1 (bases 1 to 433)
AUTHORS    Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE      Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
JOURNAL    Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED     15691937
REFERENCE  2 (bases 1 to 433)
AUTHORS    Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE      Direct Submission
JOURNAL    Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia

FEATURES   Location/Qualifiers
source     1..433
            /organism="Mycobacteriaceae bacterium Ellin7032"
            /mol_type="genomic DNA"
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            /isolation_source="soil"
            /db_xref="taxon:305283"
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            /product="16S ribosomal RNA"

rRNA
<1_>433
/product="16S ribosomal RNA"

ORIGIN
Query Match      92.7%; Score 20.4; DB 15; Length 433;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGCCCTTCGG 22
Db 34 GTCGAACGGAAGCCCTTCGG 55

RESULT 70

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JOURNAL    Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED     15691937
REFERENCE  2 (bases 1 to 433)
AUTHORS    Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE      Direct Submission
JOURNAL    Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia

FEATURES   Location/Qualifiers
source     1..433
            /organism="Mycobacteriaceae bacterium Ellin7032"
            /mol_type="genomic DNA"
            /isolate="Ellin7032"
            /isolation_source="soil"
            /db_xref="taxon:305255"
            <1_>433
            /product="16S ribosomal RNA"

rRNA
<1_>433
/product="16S ribosomal RNA"

ORIGIN
Query Match      92.7%; Score 20.4; DB 15; Length 433;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGCCCTTCGG 22
Db 34 GTCGAACGGAAGCCCTTCGG 55

RESULT 69
AY673266
LOCUS      AY673266      433 bp      DNA      linear      BCT 20-MAY-2005
DEFINITION Mycobacteriaceae bacterium Ellin7100 16S ribosomal RNA gene,
partial sequence.
ACCESSION  AY673266
VERSION     AY673266.1 GI:56683123
KEYWORDS   Mycobacteriaceae bacterium Ellin7100
SOURCE     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
REFERENCE  1 (bases 1 to 433)
AUTHORS    Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE      Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
JOURNAL    Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED     15691937
REFERENCE  2 (bases 1 to 433)
AUTHORS    Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE      Direct Submission
JOURNAL    Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia

FEATURES   Location/Qualifiers
source     1..433
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            /mol_type="genomic DNA"
            /isolate="Ellin7100"
            /isolation_source="soil"
            /db_xref="taxon:305283"
            <1_>433
            /product="16S ribosomal RNA"

rRNA
<1_>433
/product="16S ribosomal RNA"

ORIGIN
Query Match      92.7%; Score 20.4; DB 15; Length 433;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGCCCTTCGG 22
Db 34 GTCGAACGGAAGCCCTTCGG 55

RESULT 70

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DQ063195
LOCUS      DQ063195          435 bp      DNA          linear      BCT 27-JUN-2005
DEFINITION actinobacterium BAL259 16S ribosomal RNA gene, partial sequence.
ACCESSION  DQ063195
VERSION    DQ063195.1  GI:68139233
KEYWORDS
SOURCE     actinobacterium BAL259
ORGANISM   actinobacterium BAL259
            Bacteria; Actinobacteria.
REFERENCE  1 (bases 1 to 435)
AUTHORS    Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
            Hagstrom,A.
TITLE      Bacterial community composition in the central Baltic Sea analyzed
            by cultivation and molecular-based methods
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 435)
AUTHORS    Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
            Hagstrom,A.
TITLE      Direct Submission
JOURNAL    Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
            University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES   Location/Qualifiers
            source          1..435
                        /organism="actinobacterium BAL259"
                        /mol_type="genomic DNA"
                        /strain="BAL259"
                        /isolation_source="Baltic Sea, 3m depth, Landsort deep St.
                        BY31, Zobel1/R2A media"
                        /db_xref="taxon:331808"
                        /country="Sweden"
                        /lat_lon="60.42.726N, 05.05.595E"
                        /collection_date="17 May 2004"
                        <1..>435
                        /product="16S ribosomal RNA"

rRNA
ORIGIN
Query Match      92.7%; Score 20.4; DB 15; Length 435;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1  GTCGAACGGAAGGCCTTCGG 22
      |||||
Db  19 GTCGAACGGAAGGCCTTCGG 40

RESULT 71
AY234692
LOCUS      AY234692          435 bp      DNA          linear      BCT 08-DEC-2003
DEFINITION Bacterium Ellin6040 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY234692
VERSION    AY234692.1  GI:37961849
KEYWORDS
SOURCE     bacterium Ellin6040
ORGANISM   bacterium Ellin6040
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae.
REFERENCE  1 (bases 1 to 435)
AUTHORS    Joseph,S.J., Hugenholtz,P., Sangwan,P., Osborne,C.A. and
            Janssen,P.H.
TITLE      Laboratory Cultivation of Widespread and Previously Uncultured Soil
            Bacteria
JOURNAL    Appl. Environ. Microbiol. 69 (12), 7210-7215 (2003)
PUBMED    14560368
REFERENCE  2 (bases 1 to 435)
AUTHORS    Joseph,S.J., Hugenholtz,P., Rana,P., Osborne,C.A., Sait,M. and
            Janssen,P.H.
TITLE      Direct Submission
JOURNAL    Submitted (12-FEB-2003) Department of Microbiology and Immunology,
            University of Melbourne, Parkville, Victoria 3010, Australia
FEATURES   Location/Qualifiers
            source          1..435
                        /organism="bacterium Ellin6040"
                        /mol_type="genomic DNA"

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/isolate="Ellin6040"
/db_xref="taxon:234122"
<1..>435
/product="16S ribosomal RNA"

rRNA
ORIGIN
Query Match      92.7%; Score 20.4; DB 15; Length 435;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1  GTCGAACGGAAGGCCTTCGG 22
      |||||
Db  34 GTCGAACGGAAGGCCTTCGG 55

RESULT 72
AY673233
LOCUS      AY673233          435 bp      DNA          linear      BCT 20-MAY-2005
DEFINITION Mycobacteriaceae bacterium Ellin7067 16S ribosomal RNA gene,
            partial sequence.
ACCESSION  AY673233
VERSION    AY673233.1  GI:56683090
KEYWORDS
SOURCE     Mycobacteriaceae bacterium Ellin7067
ORGANISM   Mycobacteriaceae bacterium Ellin7067
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae.
REFERENCE  1 (bases 1 to 435)
AUTHORS    Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE      Effects of growth medium, inoculum size, and incubation time on
            culturability and isolation of soil bacteria
JOURNAL    Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED    15691937
REFERENCE  2 (bases 1 to 435)
AUTHORS    Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE      Direct Submission
JOURNAL    Submitted (02-JUL-2004) Department of Microbiology and Immunology,
            University of Melbourne, Grattan Street, Parkville, Victoria 3010,
            Australia
FEATURES   Location/Qualifiers
            source          1..435
                        /organism="Mycobacteriaceae bacterium Ellin7067"
                        /mol_type="genomic DNA"
                        /isolate="Ellin7067"
                        /isolation_source="soil"
                        /db_xref="taxon:305274"
                        <1..>435
                        /product="16S ribosomal RNA"

rRNA
ORIGIN
Query Match      92.7%; Score 20.4; DB 15; Length 435;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1  GTCGAACGGAAGGCCTTCGG 22
      |||||
Db  34 GTCGAACGGAAGGCCTTCGG 55

RESULT 73
DQ063046
LOCUS      DQ063046          436 bp      DNA          linear      BCT 27-JUN-2005
DEFINITION Actinobacterium BAL106 16S ribosomal RNA gene, partial sequence.
ACCESSION  DQ063046
VERSION    DQ063046.1  GI:68139075
KEYWORDS
SOURCE     actinobacterium BAL106
ORGANISM   actinobacterium BAL106
            Bacteria; Actinobacteria.
REFERENCE  1 (bases 1 to 436)
AUTHORS    Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
            Hagstrom,A.
TITLE      Bacterial community composition in the central Baltic Sea analyzed

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by cultivation and molecular-based methods
 Unpublished
 2 (bases 1 to 436)
 Riemann, U., Letet, C., Pommier, T., Simu, K., Holmfeldt, K. and Hagstrom, A.
 Direct Submission
 Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences, University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
 Location/Qualifiers
 1. .436
 /organism="actinobacterium BAL106"
 /mol_type="genomic DNA"
 /strain="BAL106"
 /isolation_source="Baltic Sea, 3m depth, Landsort deep St. BY31, Zobell/R2A media"
 /db_xref="taxon:331778"
 /country="Sweden"
 /lat_lon="60.42.726N, 05.05.595E"
 /collection_dates="2 July 2003"
 <1. .>436
 /product="16S ribosomal RNA"

FEATURES
 source
 1. .436

ORIGIN
 Query Match 92.7%; Score 20.4; DB 15; Length 436;
 Best Local Similarity 95.5%; Pred. No. 1.8e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCCCTTCGG 22
 |||||

Db 23 GTCGAACGGAAAGCCCTTCGG 44
 |||||

RESULT 74
 AY673199 436 bp DNA linear BCT 20-MAY-2005
 LOCUS
 DEFINITION
 Mycobacteriaceae bacterium Ellin7033 16S ribosomal RNA gene, partial sequence.
 ACCESSION
 AY673199.1 GI:56683056
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mycobacteriaceae bacterium Ellin7033
 Mycobacteriaceae bacterium Ellin7033
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae.
 1 (bases 1 to 436)
 Davis, K.E., Joseph, S.J. and Janssen, P.H.
 Effects of growth medium, inoculum size, and incubation time on culturability and isolation of soil bacteria
 Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
 15691937

REFERENCE
 2 (bases 1 to 436)
 Davis, K.E.R., Joseph, S.J. and Janssen, P.H.
 Direct Submission
 Submitted (02-JUL-2004) Department of Microbiology and Immunology, University of Melbourne, Grattan Street, Parkville, Victoria 3010, Australia
 Location/Qualifiers
 1. .436
 /organism="Mycobacteriaceae bacterium Ellin7033"
 /mol_type="genomic DNA"
 /isolate="Ellin7033"
 /isolation_source="soil"
 /db_xref="taxon:305288"
 <1. .>436
 /product="16S ribosomal RNA"

ORIGIN
 Query Match 92.7%; Score 20.4; DB 15; Length 436;
 Best Local Similarity 95.5%; Pred. No. 1.8e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCCCTTCGG 22
 |||||

Db 23 GTCGAACGGAAAGCCCTTCGG 44
 |||||

RESULT 74
 AY673199 436 bp DNA linear BCT 20-MAY-2005
 LOCUS
 DEFINITION
 Mycobacteriaceae bacterium Ellin7033 16S ribosomal RNA gene, partial sequence.
 ACCESSION
 AY673199.1 GI:56683056
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mycobacteriaceae bacterium Ellin7033
 Mycobacteriaceae bacterium Ellin7033
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae.
 1 (bases 1 to 436)
 Davis, K.E., Joseph, S.J. and Janssen, P.H.
 Effects of growth medium, inoculum size, and incubation time on culturability and isolation of soil bacteria
 Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
 15691937

REFERENCE
 2 (bases 1 to 436)
 Davis, K.E.R., Joseph, S.J. and Janssen, P.H.
 Direct Submission
 Submitted (02-JUL-2004) Department of Microbiology and Immunology, University of Melbourne, Grattan Street, Parkville, Victoria 3010, Australia
 Location/Qualifiers
 1. .436
 /organism="Mycobacteriaceae bacterium Ellin7033"
 /mol_type="genomic DNA"
 /isolate="Ellin7033"
 /isolation_source="soil"
 /db_xref="taxon:305288"
 <1. .>436
 /product="16S ribosomal RNA"

ORIGIN
 Query Match 92.7%; Score 20.4; DB 15; Length 436;
 Best Local Similarity 95.5%; Pred. No. 1.8e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCCCTTCGG 22
 |||||

Db 34 GTCGAACGGAAAGCCCTTCGG 55
 |||||

RESULT 75
 AY673304 436 bp DNA linear BCT 20-MAY-2005
 LOCUS
 DEFINITION
 Mycobacteriaceae bacterium Ellin7138 16S ribosomal RNA gene, partial sequence.
 ACCESSION
 AY673304
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mycobacteriaceae bacterium Ellin7138
 Mycobacteriaceae bacterium Ellin7138
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae.
 1 (bases 1 to 436)
 Davis, K.E., Joseph, S.J. and Janssen, P.H.
 Effects of growth medium, inoculum size, and incubation time on culturability and isolation of soil bacteria
 Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
 15691937

REFERENCE
 2 (bases 1 to 436)
 Davis, K.E.R., Joseph, S.J. and Janssen, P.H.
 Direct Submission
 Submitted (02-JUL-2004) Department of Microbiology and Immunology, University of Melbourne, Grattan Street, Parkville, Victoria 3010, Australia
 Location/Qualifiers
 1. .436
 /organism="Mycobacteriaceae bacterium Ellin7138"
 /mol_type="genomic DNA"
 /isolate="Ellin7138"
 /isolation_source="soil"
 /db_xref="taxon:305288"
 <1. .>436
 /product="16S ribosomal RNA"

ORIGIN
 Query Match 92.7%; Score 20.4; DB 15; Length 436;
 Best Local Similarity 95.5%; Pred. No. 1.8e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCCCTTCGG 22
 |||||

Db 34 GTCGAACGGAAAGCCCTTCGG 55
 |||||

RESULT 76
 AF078419 437 bp DNA linear ENV 10-MAY-2004
 LOCUS
 DEFINITION
 Grassland soil clone sl3_612 16S ribosomal RNA gene, partial sequence.
 ACCESSION
 AF078419
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Grassland soil clone sl3_612
 Grassland soil clone sl3_612
 Bacteria; environmental samples.
 1 (bases 1 to 437)
 McCaig, A.E., Glover, L.A. and Prosser, J.I.
 Molecular analysis of bacterial community structure and diversity in unimproved and improved upland grass pastures
 Appl. Environ. Microbiol. 65 (4), 1721-1730 (1999)
 10103273

REFERENCE
 2 (bases 1 to 437)
 McCaig, A.E., Prosser, J.I. and Glover, L.A.
 Direct Submission
 Submitted (16-JUL-1998) Institute of Medical Sciences, Department of Molecular and Cell Biology, University of Aberdeen, Foresterhill, Aberdeen AB25 2ZD, Scotland, UK
 Location/Qualifiers
 1. .437
 /organism="grassland soil clone sl3_612"

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/mol_type="genomic DNA"
/db_xref="taxon:80115"
/clone_lib="improved grassland soil SL3"
/environmental_sample
<1..>437
/product="16S ribosomal RNA"

ORIGIN
Query Match          92.7%; Score 20.4; DB 1; Length 437;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCGCTTTCCG 22
    ||||| ||||| ||||| |||||
Db 12 GTCGAGCGGAAGGCGCTTTCCG 33

RESULT 77
AB232370          441 bp      DNA      linear      BCT 25-JAN-2006
LOCUS             Mycobacterium kansasii gene for 16S rRNA, partial sequence,
DEFINITION        strain:SA-10.
ACCESSION         AB232370
VERSION           AB232370.1 GI:73589607
KEYWORDS           .
SOURCE            Mycobacterium kansasii
ORGANISM           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                  Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS           Iwamoto, T. and Saito, H.
TITLE             Comparative study of two typing methods, hsp65 PRA and ITS
                  sequencing, revealed a possible evolutionary link between
                  Mycobacterium kansasii type I and II isolates
JOURNAL           FEMS Microbiol. Lett. 254, 129-133 (2006)
AUTHORS           Iwamoto, T.
TITLE             Direct Submission
JOURNAL           Submitted (17-AUG-2005) Tomotada Iwamoto, Kobe Institute of Health,
                  Department of Microbiology; Chuo-ku Minatojima-nakamachi 4-6, Kobe,
                  Hyogo 6500046, Japan (E-mail: kx2t-iwmt@asahi-net.or.jp,
                  URL: http://www.city.kobe.jp/cityoffice/18/menu03/h/kanken/kanken-
                  top, Tel: 81-78-302-6251, Fax: 81-78-302-0894)
FEATURES
source
  1..441
  /organism="Mycobacterium kansasii"
  /mol_type="genomic DNA"
  /strain="SA-10"
  /db_xref="taxon:1768"
  /note="type II"
  <1..>441
  /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          92.7%; Score 20.4; DB 15; Length 441;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCGCTTTCCG 22
    ||||| ||||| ||||| |||||
Db 8 GTCGACGGAAGGCGCTTTCCG 29

RESULT 78
AY306201          442 bp      DNA      linear      BCT 25-JUN-2003
LOCUS             Mycobacterium sp. 1351 16S ribosomal RNA gene, partial sequence.
DEFINITION        AY306201
ACCESSION         AY306201.1 GI:32250950
KEYWORDS           .
SOURCE            Mycobacterium sp. 1351
ORGANISM           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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```
REFERENCE
AUTHORS           Pauls, R.J., Turenne, C.Y., Wolfe, J.N. and Kabani, A.
TITLE             A High Proportion of Novel Mycobacteria Species Identified by 16S
                  rDNA Analysis Among Slowly Growing AccuProbe Negative Strains in a
                  Clinical Setting
JOURNAL           Unpublished
REFERENCE          2 (bases 1 to 442)
AUTHORS           Turenne, C.Y.
TITLE             Direct Submission
JOURNAL           Submitted (26-MAY-2003) National Reference Centre for
                  Mycobacteriology, National Microbiology Laboratory, Health Canada,
                  1015 Arlington Street, Winnipeg, MB R3E 3R2, Canada
FEATURES
source
  1..442
  /organism="Mycobacterium sp. 1351"
  /mol_type="genomic DNA"
  /strain="1351"
  /isolation_source="mouth ulcer"
  /specific_host="Homo sapiens"
  /db_xref="taxon:235254"
  <1..>442
  /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          92.7%; Score 20.4; DB 15; Length 442;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCGCTTTCCG 22
    ||||| ||||| ||||| |||||
Db 8 GTCGACGGAAGGCGCTTTCCG 29

RESULT 79
AY306205          444 bp      DNA      linear      BCT 25-JUN-2003
LOCUS             Mycobacterium sp. HSC507 16S ribosomal RNA gene, partial sequence.
DEFINITION        AY306205
ACCESSION         AY306205.1 GI:32250954
KEYWORDS           .
SOURCE            Mycobacterium sp. HSC507
ORGANISM           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                  Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS           Pauls, R.J., Turenne, C.Y., Wolfe, J.N. and Kabani, A.
TITLE             A High Proportion of Novel Mycobacteria Species Identified by 16S
                  rDNA Analysis Among Slowly Growing AccuProbe Negative Strains in a
                  Clinical Setting
JOURNAL           Unpublished
REFERENCE          2 (bases 1 to 444)
AUTHORS           Turenne, C.Y.
TITLE             Direct Submission
JOURNAL           Submitted (26-MAY-2003) National Reference Centre for
                  Mycobacteriology, National Microbiology Laboratory, Health Canada,
                  1015 Arlington Street, Winnipeg, MB R3E 3R2, Canada
FEATURES
source
  1..444
  /organism="Mycobacterium sp. HSC507"
  /mol_type="genomic DNA"
  /strain="HSC507"
  /isolation_source="sputum"
  /specific_host="Homo sapiens"
  /db_xref="taxon:235258"
  <1..>444
  /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          92.7%; Score 20.4; DB 15; Length 444;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 GTCGAACGGAAGGCGCTTTTCGG 22
|||||
Db 8 GTCGAACGGAAGGCGCTTTTCGG 29

RESULT 80
AB106917
LOCUS
DEFINITION Gram-positive bacterium 1-3 for 16S ribosomal RNA, partial sequence.
ACCESSION AB106917
VERSION AB106917.1 GI:29421131
KEYWORDS Gram-positive bacterium 1-3
SOURCE Gram-positive bacterium 1-3
ORGANISM Bacteria.
REFERENCE 1
AUTHORS Anachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H., Fujii,T. and Muramatsu,Y.
TITLE Microbial participation in iodine volatilization from soils
JOURNAL Environ. Sci. Technol. 37, 3885-3890 (2003)
REFERENCE 2
AUTHORS Anachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H., Fujii,T. and Muramatsu,Y.
TITLE Direct Submission
JOURNAL Submitted (27-MAR-2003) Seigo Anachi, Chiba University, Dept. of Bioreources Chem.: 648 Matsudo, Matsudo-shi, Chiba 271-8510, Japan (E-mail:amachi@faculty.chiba-u.jp, Tel:81-47-308-8868, Fax:81-47-308-8866)
FEATURES
source
1. .445
/organism="Gram-positive bacterium 1-3"
/mol_type="genomic DNA"
/strain="1-3"
/db_xref="taxon:226199"
<1. .>445
/product="16S ribosomal RNA"

rRNA
ORIGIN
Query Match 92.7%; Score 20.4; DB 15; Length 445;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTTCGG 22
|||||
Db 34 GTCGAACGGAAGGCGCTTTTCGG 55

RESULT 81
DQ067466
LOCUS
DEFINITION Mycobacterium sp. F105167 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ067466
VERSION DQ067466.1 GI:67528039
KEYWORDS Unusual mycobacteria isolated from clinical samples
SOURCE Mycobacterium sp. F105167
ORGANISM Mycobacterium sp. F105167
REFERENCE 1
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE Unusual mycobacteria isolated from clinical samples
JOURNAL Unpublished
REFERENCE 2
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-2005) Reg. Reference Center for Mycobacteria, Careggi Hospital, Piastra dei Servizi, Ospedale Careggi, v.le Morgagni 85, Firenze, FI 50134, Italy
FEATURES
source
1. .445
/organism="Mycobacterium sp. F105167"
/mol_type="genomic DNA"

rRNA
ORIGIN
/strain="F105167"
/db_xref="taxon:332013"
<1. .>445
/product="16S ribosomal RNA"

Query Match 92.7%; Score 20.4; DB 15; Length 445;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTTCGG 22
|||||
Db 12 GTCGAACGGAAGGCGCTTTTCGG 33

RESULT 82
AY957708
LOCUS
DEFINITION Uncultured bacterium clone P3DKE08 16S small subunit ribosomal RNA gene, partial sequence.
ACCESSION AY957708
VERSION AY957708.1 GI:62005486
KEYWORDS ENV.
SOURCE uncultured bacterium
ORGANISM Bacteria; environmental samples.
REFERENCE 1
AUTHORS McManus,C.J. and Kelley,S.T.
TITLE Molecular survey of aeroplane bacterial contamination
JOURNAL J. Appl. Microbiol. 99 (3), 502-508 (2005)
PUBMED 16108791
REFERENCE 2
AUTHORS McManus,C.J. and Kelley,S.T.
TITLE Direct Submission
JOURNAL Submitted (09-MAR-2005) Biology, San Diego State University, 5500 Campanile Dr., San Diego, CA 92182, USA
FEATURES
source
1. .447
/organism="uncultured bacterium"
/mol_type="genomic DNA"
/isolation_source="airplane"
/db_xref="taxon:77133"
/clone="P3DKE08"
/environmental_sample
<1. .>447
/product="16S small subunit ribosomal RNA"

rRNA
ORIGIN
Query Match 92.7%; Score 20.4; DB 1; Length 447;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTTCGG 22
|||||
Db 2 GTCGAACGGAAGGCGCTTTTCGG 23

RESULT 83
MS91016SR
LOCUS
DEFINITION Mycobacterium sp.16S rRNA gene, isolate BN910, partial.
ACCESSION Y08205
VERSION Y08205.1 GI:2292948
KEYWORDS 16S ribosomal RNA; 16S rRNA.
SOURCE Mycobacterium sp.
ORGANISM Mycobacterium sp.
REFERENCE 1
AUTHORS Hagenau C., Behringer,K., Naumann,L., Kaiser,R. and Schulze-Roebecke,R.
JOURNAL Unpublished
REFERENCE 2
source
2 (bases 1 to 450)

AUTHORS Hagenau, C.
 TITLE Direct Submission
 JOURNAL Submitted (18-SEP-1996) C. Hagenau, Hygiene-Institute, University of Bonn, Sigmund-Freud-Strasse 25, D-53105 Bonn, FRG
 COMMENT Related sequence M95469
 FEATURES
 source
 Location/Qualifiers
 1..450
 /organism="Mycobacterium sp."
 /mol_type="genomic DNA"
 /isolate="BN910"
 /db_xref="taxon:1785"
 /map=E.coli position 38-503"
 1..450
 /gene="16S rRNA"
 <1..>450
 /gene="16S rRNA"
 /product="16S ribosomal RNA"

gene
 rRNA

ORIGIN
 Query Match 92.7%; Score 20.4; DB 15; Length 450;
 Best Local Similarity 95.5%; Pred. No. 1.8e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTCGG 22
 |||||
 Db 24 GTCGAACGGAAGGCGCTTCGG 45

RESULT 84
 MSP16SR
 LOCUS MSP16SR 450 bp DNA linear BCT 01-AUG-1997
 DEFINITION Mycobacterium sp. 16S rRNA gene.
 ACCESSION Y07954
 VERSION Y07954.1 GI:2292951
 KEYWORDS 16S ribosomal RNA; 16S rRNA gene.
 SOURCE Mycobacterium sp.
 ORGANISM Mycobacterium sp.
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE
 1 Hagenau, C., Behringer, K., Naumann, L., Kaiser, R. and Schulze-Roebebecke, R.
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 450)
 AUTHORS Hagenau, C.
 TITLE Direct Submission
 JOURNAL Submitted (12-SEP-1996) C. Hagenau, Hygiene-Institute, University of Bonn, Sigmund-Freud-Strasse 25, D-53105 Bonn, FRG
 COMMENT Related sequence: M95469.
 FEATURES
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 Location/Qualifiers
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 /isolate="BN737"
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 /map=E.coli 38-503"
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gene
 rRNA

ORIGIN
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 Best Local Similarity 95.5%; Pred. No. 1.8e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTCGG 22
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 Db 24 GTCGAACGGAAGGCGCTTCGG 45

RESULT 85

AY358002
 LOCUS AY358002 450 bp DNA linear BCT 19-AUG-2005
 DEFINITION Actinobacterium irIII7 16S ribosomal RNA gene, partial sequence.
 ACCESSION AY358002
 VERSION AY358002.1 GI:34500643
 KEYWORDS
 SOURCE
 ORGANISM
 actinobacterium irIII7
 actinobacterium irIII7
 Bacteria; Actinobacteria.
 REFERENCE
 1 (bases 1 to 450)
 AUTHORS Idris, R., Trifonova, R., Puschenreiter, M., Wenzel, W. W. and Sessitsch, A.
 TITLE Bacterial Communities Associated with Flowering Plants of the Ni Hyperaccumulator Thlaspi goesingense
 JOURNAL Appl. Environ. Microbiol. 70 (5), 2667-2677 (2004)
 PUBMED 15128517
 REFERENCE 2 (bases 1 to 450)
 AUTHORS Idris, R. and Sessitsch, A.
 TITLE Direct Submission
 JOURNAL Submitted (01-AUG-2003) Environmental and Life Sciences, ARC Seibersdorf Research GmbH, Seibersdorf A-2444, Austria
 FEATURES
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 /db_xref="taxon:244182"
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rRNA

ORIGIN
 Query Match 92.7%; Score 20.4; DB 15; Length 450;
 Best Local Similarity 95.5%; Pred. No. 1.8e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTCGG 22
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 Db 56 GTCGAACGGAAGGCGCTTCGG 77

RESULT 86
 AJ746062
 LOCUS AJ746062 454 bp DNA linear BCT 11-MAR-2005
 DEFINITION Mycobacterium sp. MG5 partial 16S rRNA gene, isolate MG5.
 ACCESSION AJ746062
 VERSION AJ746062.1 GI:61097518
 KEYWORDS 16S ribosomal RNA; 16S rRNA gene.
 SOURCE Mycobacterium sp. MG5
 ORGANISM Mycobacterium sp. MG5
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE
 1 Gomila, M., Gasco, J., Busquets, A., Gil, J., Bernabeu, R., Buades, J. M. and Lalucat, J.
 TITLE Identification of culturable bacteria present in haemodialysis water and fluid
 JOURNAL FEMS Microbiol. Ecol. 52 (1), 101-114 (2005)
 REFERENCE 2 (bases 1 to 454)
 AUTHORS Gomila, M.
 TITLE Direct Submission
 JOURNAL Submitted (07-JUN-2004) Gomila M., Biologia-IMEDEA. Microbiologia, Universitat de les Illes Balears, Ctra. Valldemossa, km. 7.5, 07122 Palma de Mallorca, SPAIN
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 /mol_type="genomic DNA"
 /isolate="MG5"
 /isolation_source="haemodialysis water distribution system"
 /db_xref="taxon:280864"
 /country="Spain:Mallorca"
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gene


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rRNA
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Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCCCTTCGG 22
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Db 27 GTCGAACGGAAAGCCCTTCGG 48

RESULT 87
LOCUS AY358001 456 bp DNA linear BCT 19-AUG-2005
DEFINITION Actinobacterium irIII6 16S ribosomal RNA gene, partial sequence.
ACCESSION AY358001
VERSION AY358001.1 GI:34500642
KEYWORDS actinobacterium irIII6
SOURCE actinobacterium irIII6
ORGANISM actinobacterium irIII6
REFERENCE 1 (bases 1 to 456)
AUTHORS Idris,R., Trifonova,R., Puschenreiter,M., Wenzel,W.W. and Sessitsch,A.
TITLE Bacterial Communities Associated with Flowering Plants of the Ni
JOURNAL Hyperaccumulator Thlaspi goesingense
PUBMED Appl. Environ. Microbiol. 70 (5), 2667-2677 (2004)
15128517
REFERENCE 2 (bases 1 to 456)
AUTHORS Idris,R. and Sessitsch,A.
DIRECT SUBMISSION
TITLE Submitted (01-AUG-2003) Environmental and Life Sciences, ARC
JOURNAL Seibersdorf Research GmbH, Seibersdorf A-2444, Austria
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/db_xref="taxon:244181"
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Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 56 GTCGAACGGAAAGCCCTTCGG 77

RESULT 88
LOCUS AJ609008 459 bp DNA linear ENV 20-JAN-2004
DEFINITION Uncultured bacterium partial 16S rRNA gene, clone 24-9.
ACCESSION AJ609008
VERSION AJ609008.1 GI:41033549
KEYWORDS ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE uncultured bacterium
ORGANISM uncultured bacterium
REFERENCE 1
AUTHORS Schneider,B.A., Huettl,R.F. and Schneider,B.U.
TITLE Evidence for a diverse bacterial consortium specialized to the
degradation of aliphatic and aromatic hydrocarbons in lignite
matter of a forest reclamation site
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 459)

AUTHORS Schneider,B.A.
DIRECT SUBMISSION
SUBMITTED (20-NOV-2003) Schneider B.A., Soil Protection and
Recultivation, Brandenburg Technical University,
Theodor-Neubauer-Str. 6, D-03046 Cottbus, GERMANY
FEATURES
source 1..459
/organism="uncultured bacterium"
/mol_type="genomic DNA"
/isolation_source="lignite matter from the subsurface soil
of a 20 year old Black pine forest"
/db_xref="taxon:77133"
/clone="24-9"
/environmental_sample
/country="Germany:North-eastern Germany, Lusatian lignite
mining area"
1..459
/gene="16S rRNA"
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/gene="16S rRNA"
/product="16S ribosomal RNA"

ORIGIN
Query Match          92.7%; Score 20.4; DB 1; Length 459;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCCCTTCGG 22
    |||||
Db 12 GTCGAACGGTAAGCCCTTCGG 33

RESULT 89
LOCUS AY754884 459 bp DNA linear BCT 17-OCT-2004
DEFINITION Mycobacterium vaccae strain FI04098 16S ribosomal RNA gene, partial
sequence.
ACCESSION AY754884
VERSION AY754884.1 GI:54065968
KEYWORDS Mycobacterium vaccae
SOURCE Mycobacterium vaccae
ORGANISM Mycobacterium vaccae
REFERENCE 1 (bases 1 to 459)
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE Unusual mycobacteria isolated from clinical samples
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 459)
AUTHORS Tortoli,E.
DIRECT SUBMISSION
TITLE Submitted (16-SEP-2004) Microbiology, Careggi Hospital, viale
JOURNAL Morgagni 85, Firenze, FI 50134, Italy
FEATURES
source 1..459
/organism="Mycobacterium vaccae"
/mol_type="genomic DNA"
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/db_xref="taxon:1810"
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/product="16S ribosomal RNA"

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/gene="16S rRNA"
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/gene="16S rRNA"
/product="16S ribosomal RNA"

ORIGIN
Query Match          92.7%; Score 20.4; DB 15; Length 459;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCCCTTCGG 22
    |||||
Db 28 GTCGAACGGAAAGCCCTTCGG 49

RESULT 90

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AY754885
LOCUS AY754885 459 bp DNA linear BCT 17-OCT-2004
DEFINITION Mycobacterium sp. FI02139 16S ribosomal RNA gene, partial sequence.
ACCESSION AY754885
VERSION AY754885.1 GI:54065976
SOURCE
ORGANISM Mycobacterium sp. FI02139
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
Tortoli,E., Mariottini,A. and Mazzarelli,G.
1 (bases 1 to 459)
Unusual mycobacteria isolated from clinical samples
REFERENCE 1 (bases 1 to 459)
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
JOURNAL Unpublished
TITLE Unusual mycobacteria isolated from clinical samples
REFERENCE 2 (bases 1 to 459)
AUTHORS Tortoli,E.
JOURNAL Direct Submission
TITLE Direct Submission
JOURNAL Submitted (16-SEP-2004) Microbiology, Careggi Hospital, viale
Morgagni 85, Firenze, FI 50134, Italy
FEATURES
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/mol_type="genomic DNA"
/strain="FI02139"
/db_xref="taxon:296718"
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/product="16S ribosomal RNA"
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Query Match 92.7%; Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
ORIGIN
1 GTCGAACGGAAGGCGCTTCGG 22
27 GTCGAACGGAAGGCGCTTCGG 48
Query Match 92.7%; Score 20.4; DB 15; Length 459;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
LOCUS AB118817 464 bp DNA linear BCT 01-JUN-2005
DEFINITION Denitrifying bacterium W67a gene for 16S ribosomal RNA, partial
sequence.
ACCESSION AB118817
VERSION AB118817.1 GI:66841148
KEYWORDS denitrifying bacterium W67a
SOURCE denitrifying bacterium W67a
ORGANISM Bacteria; Actinobacteria.
Hashimoto,T., Whang,K.S. and Nagaoka,K.
REFERENCE 1
AUTHORS Hashimoto,T., Whang,K.S. and Nagaoka,K.
TITLE A Quantitative Evaluation and Phylogenetic Characterization of
Oligotrophic Denitrifying Bacteria Harbored in Subsurface Upland
Soil Using Improved Culturability
JOURNAL Biol. Fertil. Soils (2005) In press
REFERENCE 2 (bases 1 to 464)
AUTHORS Hashimoto,T. and Whang,K.
JOURNAL Direct Submission
TITLE Direct Submission
JOURNAL Submitted (29-AUG-2003) Tomovoshi Hashimoto, National Agricultural
Research Center for Kyushu Okinawa Region, Department of
Agro-Environmental Research; Nishigoushi-cho Suya 2421,
Kikuchi-gun, Kumamoto, 861-1192, Japan
(E-mail:hashimoto@affrc.go.jp, Tel:0962427765, Fax:0962491002)
FEATURES
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/mol_type="genomic DNA"
/isolate="W67a"
/db_xref="taxon:245681"
/country="Japan"
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/product="16S ribosomal RNA"
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Query Match 92.7%; Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
ORIGIN
1 GTCGAACGGAAGGCGCTTCGG 22
27 GTCGAACGGAAGGCGCTTCGG 48

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Query Match 92.7%; Score 20.4; DB 15; Length 464;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTCGAACGGAAGGCGCTTCGG 22
DB 50 GTCGAACGGAAGGCGCTTCGG 71
RESULT 92
LOCUS DQ142669 464 bp DNA linear BCT 13-AUG-2005
DEFINITION Mycobacterium sp. FI03023 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ142669
VERSION DQ142669.1 GI:71912648
KEYWORDS
SOURCE Mycobacterium sp. FI03023
ORGANISM Mycobacterium sp. FI03023
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
Tortoli,E., Mariottini,A. and Mazzarelli,G.
1 (bases 1 to 464)
Unusual mycobacteria isolated from clinical specimens
REFERENCE 1 (bases 1 to 464)
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
JOURNAL Unpublished
TITLE Unusual mycobacteria isolated from clinical specimens
REFERENCE 2 (bases 1 to 464)
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
JOURNAL Direct Submission
TITLE Direct Submission
JOURNAL Submitted (18-JUL-2005) Microbiology, Careggi Hospital, viale
Morgagni 85, Firenze, FI 50134, Italy
FEATURES
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/organism="Mycobacterium sp. FI03023"
/mol_type="genomic DNA"
/strain="FI03023"
/db_xref="taxon:339672"
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/product="16S ribosomal RNA"
rRNA
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Score 20.4; DB 15; Length 464;
Query Match 92.7%; Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
ORIGIN
1 GTCGAACGGAAGGCGCTTCGG 22
27 GTCGAACGGAAGGCGCTTCGG 48
Query Match 92.7%; Score 20.4; DB 15; Length 464;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
LOCUS DQ142672 464 bp DNA linear BCT 13-AUG-2005
DEFINITION Mycobacterium sp. FI05244 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ142672
VERSION DQ142672.1 GI:71912651
KEYWORDS
SOURCE Mycobacterium sp. FI05244
ORGANISM Mycobacterium sp. FI05244
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
Tortoli,E., Mariottini,A. and Mazzarelli,G.
1 (bases 1 to 464)
Unusual mycobacteria isolated from clinical specimens
REFERENCE 1 (bases 1 to 464)
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
JOURNAL Unpublished
TITLE Unusual mycobacteria isolated from clinical specimens
REFERENCE 2 (bases 1 to 464)
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
JOURNAL Direct Submission
TITLE Direct Submission
JOURNAL Submitted (25-JUL-2005) Microbiology, Careggi Hospital, viale
Morgagni 85, Firenze, FI 50134, Italy
FEATURES
source
1. .464
/organism="Mycobacterium sp. FI05244"
/mol_type="genomic DNA"

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rRNA      /strain="FI05244"
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Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTTCGG 22
    |||||
Db 27 GTCGAACGGAAGGCCTTTCGG 48
    |||||

RESULT 94
LOCUS      DQ067465          466 bp      DNA      linear      BCT 05-JAN-2006
DEFINITION Mycobacterium sp. FI05038 16S ribosomal RNA gene, partial sequence.
ACCESSION  DQ067465
VERSION     DQ067465.1 GI:67528030
KEYWORDS
SOURCE      Mycobacterium sp. FI05038
ORGANISM    Mycobacterium sp. FI05038
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE   1 (bases 1 to 466)
AUTHORS     Tortoli, E., Mantella, A., Mariottini, A., Mazzarelli, G., Pecile, P.,
            Rogai, P.G., Sterrantino, G., Fantoni, E. and Leoncini, F.
TITLE       Successfully treated spontaneous discitis due to a previously
            unreported mycobacterium
JOURNAL     J. Med. Microbiol. 55 (PT 1), 119-121 (2006)
PUBMED     1638040
REFERENCE   2 (bases 1 to 466)
AUTHORS     Tortoli, E., Mariottini, A. and Mazzarelli, G.
DIRECT SUBMISSION
TITLE       Direct Submission
JOURNAL     Submitted (18-MAY-2005) Reg. Reference Center for Mycobacterias,
            Careggi Hospital, Piastra dei Servizi, Ospedale Careggi, v.le
            Morgagni 85, Firenze, FI 50134, Italy

FEATURES   source
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Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTTCGG 22
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Db 31 GTCGAACGGAAGGCCTTTCGG 52
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RESULT 95
LOCUS      AY524839          466 bp      DNA      linear      BCT 03-FEB-2004
DEFINITION Mycobacterium sp. FI02027 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY524839
VERSION     AY524839.1 GI:41387175
KEYWORDS
SOURCE      Mycobacterium sp. FI02027
ORGANISM    Mycobacterium sp. FI02027
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE   1 (bases 1 to 466)
AUTHORS     Tortoli, E., Mariottini, A. and Mazzarelli, G.
TITLE       Unusual mycobacteria isolated from clinical samples
JOURNAL     Unpublished

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REFERENCE   2 (bases 1 to 466)
AUTHORS     Tortoli, E.
DIRECT SUBMISSION
JOURNAL     Submitted (08-JAN-2004) Microbiology, Careggi Hospital, viale
            Morgagni 85, Firenze, FI 50134, Italy
FEATURES   Location/Qualifiers
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Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTTCGG 22
    |||||
Db 31 GTCGAACGGAAGGCCTTTCGG 52
    |||||

RESULT 96
LOCUS      DQ154332          468 bp      DNA      linear      BCT 27-AUG-2005
DEFINITION Soil bacterium RFS-II28 16S ribosomal RNA gene, partial sequence.
ACCESSION  DQ154332
VERSION     DQ154332.1 GI:73672122
KEYWORDS
SOURCE      soil bacterium RFS-II28
ORGANISM    soil bacterium RFS-II28
            Bacteria.
REFERENCE   1 (bases 1 to 468)
AUTHORS     Becker, J.M., Nakatsu, C.H., Turco, R.F. and Konopka, A.
TITLE       Low nutrient fluxes result in high cultivation efficiencies of soil
            bacteria
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 468)
AUTHORS     Becker, J.M., Nakatsu, C.H., Turco, R.F. and Konopka, A.
DIRECT SUBMISSION
JOURNAL     Submitted (03-AUG-2005) Biological Sciences, Purdue University, 915
            West State Street, West Lafayette, IN 47907-2054, USA

FEATURES   Location/Qualifiers
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            /isolate="RFS-II28"
            /isolation_source="Ross Forest soil"
            /db_xref="taxon:341515"
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            /product="16S ribosomal RNA"

rRNA
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Query Match      92.7%; Score 20.4; DB 15; Length 468;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTTCGG 22
    |||||
Db 23 GTCGAGCGGAAGGCCTTTCGG 44
    |||||

RESULT 97
LOCUS      AY043719          473 bp      DNA      linear      ENV 05-MAY-2004
DEFINITION Uncultured actinobacterium clone NOW2.35WL 16S ribosomal RNA gene,
            partial sequence.
ACCESSION  AY043719
VERSION     AY043719.1 GI:22267092
KEYWORDS    ENV.
SOURCE      uncultured actinobacterium

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ORGANISM uncultured actinobacterium
REFERENCE Bacteria; Actinobacteria; environmental samples.
AUTHORS Axelrood, P.E., Chow, M.L., Radomski, C.C., McDermott, J.M. and Davies, J.
TITLE Molecular characterization of bacterial diversity from British Columbia forest soils subjected to disturbance
JOURNAL Can. J. Microbiol. 48 (7), 655-674 (2002)
PUBMED 12224564
AUTHORS
TITLE
JOURNAL
REFERENCE
2 (bases 1 to 473)
AUTHORS Axelrood, P.E., Chow, M.L., Radomski, C.C., McDermott, J.M. and Davies, J.
TITLE Direct Submission
JOURNAL Submitted (20-JUN-2001) BC Research Inc., 3650 Westbrook Mall, Vancouver, BC V6S 2L2, Canada
FEATURES
LOCATION/Qualifiers
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/organism="uncultured actinobacterium"
/mol_type="genomic DNA"
/db_xref="taxon:152507"
/clones="NOW2.35W1"
/environmental sample
/notes="from forest cut-block surface organic matter from the British Columbia Ministry of Forests Long-Term Soil Productivity (LTSP) Installation near Williams Lake, BC, Canada"
<1. .>473
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 92.7%; Score 20.4; DB 1; Length 473;
Best Local Similarity 95.5%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTTCGG 22
|||||
Db 24 GTCGAACGGTAAGGCTTTTCGG 45

RESULT 98
DQ136108
LOCUS DQ136108 474 bp DNA linear ENV 13-AUG-2005
DEFINITION Uncultured bacterium clone SC27 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ136108
VERSION DQ136108.1 GI:71905197
KEYWORDS ENV, uncultured bacterium
SOURCE uncultured bacterium
ORGANISM Bacteria; environmental samples.
REFERENCE Ka, J.-O., Kim, M.-S. and Ahn, J.-H.
AUTHORS Microbiological remediation studies on diesel-contaminated soil of Baekun Mountain
TITLE Unpublished
JOURNAL
REFERENCE 2 (bases 1 to 474)
AUTHORS Ka, J.-O., Kim, M.-S. and Ahn, J.-H.
TITLE Direct Submission
JOURNAL Submitted (19-JUL-2005) School of Applied Biology and Chemistry, Seoul National University, San 56-1 Sillimdong Kwanakgu 151-921, Korea
FEATURES
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<1. .>474
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rRNA

ORIGIN

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Query Match 92.7%; Score 20.4; DB 1; Length 474;
Best Local Similarity 95.5%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTTCGG 22
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Db 44 GTCGAACGGAAGGCTTTTCGG 65

RESULT 99
AY792024
LOCUS AY792024 474 bp DNA linear BCT 20-NOV-2004
DEFINITION Mycobacterium sp. 6BR15 16S ribosomal RNA gene, partial sequence.
ACCESSION AY792024
VERSION AY792024.1 GI:55740323
KEYWORDS
SOURCE Mycobacterium sp. 6BR15
ORGANISM Mycobacterium sp. 6BR15
REFERENCE Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
AUTHORS Sarro, M.I., Garcia, A.M., Moreno, D.A. and Montero, F.
TITLE Biorremediation of radioactive water with metallic materials
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 474)
AUTHORS Sarro, M.I., Garcia, A.M., Moreno, D.A. and Montero, F.
TITLE Direct Submission
JOURNAL Submitted (25-OCT-2004) Dep Ingenieria y Ciencia de los Materiales, Escuela Tecnica Superior de Ingenieros Industriales, Universidad Politecnica de Madrid, Jose Gutierrez Abascal, 2, Madrid, Madrid 28006, Spain
FEATURES
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DEFINITION Mycobacterium porcinum strain M552 16S ribosomal RNA gene, partial sequence.
ACCESSION AY559492
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KEYWORDS
SOURCE Mycobacterium porcinum
ORGANISM Mycobacterium porcinum
REFERENCE Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
AUTHORS Hontzeas, N., Belimov, A., Safronova, V. and Glick, B.
TITLE Characterization of various plant growth-promoting bacteria
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 476)
AUTHORS Hontzeas, N., Belimov, A., Safronova, V. and Glick, B.
TITLE Direct Submission
JOURNAL Submitted (25-FEB-2004) Biology, University of Waterloo, 200 University Ave. West, Waterloo, ON N2L 3G1, Canada
FEATURES
LOCATION/Qualifiers

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Search completed: May 19, 2006, 04:00:16
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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 02:23:06 ; Search time 769.072 Seconds
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Title: US-10-665-708-25

Perfect score: 22
Sequence: 1 gaaagcccttcgggagtgctc 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

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Post-processing: Minimum Match 0%

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Listing first 300 summaries

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14: gb_cm.*

15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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9	20.4	92.7	1459	15	MC016S
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24	18.8	85.5	424	15	AY756031	Unidentif
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28	18.8	85.5	830	15	AF131455	Nonomurae
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94	18.8	85.5	1414	15	MTU48987	U48987 Microbispor	c 167	17.8	80.9	86571	11	AC151463	AC151463 Xenopus t
95	18.8	85.5	1415	15	MAU48984	U48984 Microbispor	c 168	17.8	80.9	110000	15	CR936257_04	Continuation (5 of
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c 287 16.8 76.4 204287 6 AC126442
c 288 16.8 76.4 214960 12 AC142361
c 289 16.8 76.4 218905 6 AC087772
c 290 16.8 76.4 220893 12 AC106234
c 291 16.8 76.4 231736 12 AC117323
c 292 16.8 76.4 231896 6 AC115116
c 293 16.8 76.4 233440 12 AC094560
c 294 16.8 76.4 233905 12 AC131518
c 295 16.8 76.4 240987 12 AC104055
c 296 16.8 76.4 242531 6 AC108805
c 297 16.8 76.4 249571 6 AC152418
c 298 16.8 76.4 258207 12 AC115279
c 299 16.8 76.4 261093 6 AC027740
c 300 16.8 76.4 285739 12 AC164385

ALIGNMENTS

RESULT 1
AR438657
LOCUS AR438657 22 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 25 from patent US 6664081.
ACCESSION AR438657

VERSION AR438657.1 GI:42663581
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Brentano, S.T., Jucker, M.T., Delgado, F.D., Cleuziat, P. and
Rodrigue, M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent, US 6664081-A 25 16-DEC-2003;
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA
FEATURES
source
1..22
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 22; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAAGGCGCTTCGGGGGTGCTC 22
|||||
Db 1 GAAAGGCGCTTCGGGGGTGCTC 22
RESULT 2
LOCUS AX166859 22 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 25 from Patent WO0144510.
ACCESSION AX166859
VERSION AX166859.1 GI:14596462
KEYWORDS synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Brentano, S.T., Jucker, M.T., Delgado, F.D., Cleuziat, P. and
Rodrigue, M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: WO 0144510-A 25 21-JUN-2001;
Gen-Probe Incorporated (US); Biomerieux S.A. (FR)
FEATURES
source
1..22
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer oligonucleotide"
ORIGIN
Query Match 100.0%; Score 22; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAAGGCGCTTCGGGGGTGCTC 22
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Db 1 GAAAGGCGCTTCGGGGGTGCTC 22
RESULT 3
LOCUS AR438658 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 26 from patent US 6664081.
ACCESSION AR438658
VERSION AR438658.1 GI:42663582
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Brentano, S.T., Jucker, M.T., Delgado, F.D., Cleuziat, P. and
Rodrigue, M.
TITLE Nucleic acid amplification and detection of mycobacterium species

JOURNAL Patent: US 6664081-A 26 16-DEC-2003;
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA
FEATURES
source Location/Qualifiers
1..25
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 22; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGGTGCTC 22
|||||
Db 1 GAAAGGCTTTTCGGGGGTGCTC 22

RESULT 4

AX166860
LOCUS AX166860 25 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 26 from Patent WO0144510.
ACCESSION AX166860
VERSION AX166860.1 GI:14596463
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1.
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
Rodrigue,M.

TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: WO 0144510-A 26 21-JUN-2001;
Gen-Probe Incorporated (US); Biomerieux S.A. (FR)

FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer oligonucleotide"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 42;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGGTGCTC 22
|||||
Db 1 GAAAGGCTTTTCGGGGGTGCTC 22

RESULT 5

MSGRDSB
LOCUS MSGRDSB 1460 bp DNA linear BCT 21-SEP-1993
DEFINITION Mycobacterium celatum 16S ribosomal RNA gene.
ACCESSION L08169
VERSION L08169.1 GI:293249
KEYWORDS
SOURCE Mycobacterium celatum
Mycobacterium celatum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1 (bases 1 to 1460)
AUTHORS Butler,W.R., O'Connor,S.P., Yakus,M.A., Smithwick,R.W.,
Plikaytis,B.B., Moss,C.W., Floyd,M.M., Woodley,C.L., Kilburn,J.O.,
Vadney,F.S. and Gross,W.M.

TITLE Mycobacterium celatum sp. nov
JOURNAL Int. J. Syst. Bacteriol. 43 (3), 539-548 (1993)
PUBMED 8102246

COMMENT Original source text: Mycobacterium celatum (library: ATCC 51131)
DNA.

FEATURES
source Location/Qualifiers
1..1460
/organism="Mycobacterium celatum"

/mol_type="genomic DNA"
/db_xref="taxon:28045"
/tissue_lib="ATCC 51131"
<1..>1460
/product="16S ribosomal RNA"
/note="putative"

ORIGIN

Query Match 95.5%; Score 21; DB 15; Length 1460;
Best Local Similarity 95.5%; Pred. No. 68;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGGTGCTC 22
|||||
Db 20 GAAAGGCTTTTCGGGGGTGCTC 41

RESULT 6

MSGRDSB
LOCUS MSGRDSB 1479 bp DNA linear BCT 21-SEP-1993
DEFINITION Mycobacterium celatum 16S ribosomal RNA gene.
ACCESSION L08170
VERSION L08170.1 GI:293250
KEYWORDS
SOURCE Mycobacterium celatum
Mycobacterium celatum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1 (bases 1 to 1479)
AUTHORS Butler,W.R., O'Connor,S.P., Yakus,M.A., Smithwick,R.W.,
Plikaytis,B.B., Moss,C.W., Floyd,M.M., Woodley,C.L., Kilburn,J.O.,
Vadney,F.S. and Gross,W.M.

TITLE Mycobacterium celatum sp. nov
JOURNAL Int. J. Syst. Bacteriol. 43 (3), 539-548 (1993)
PUBMED 8102246

COMMENT Original source text: Mycobacterium celatum (library: ATCC 51130)
DNA.

FEATURES
source Location/Qualifiers
1..1479
/organism="Mycobacterium celatum"
/mol_type="genomic DNA"
/db_xref="taxon:28045"
/tissue_lib="ATCC 51130"
<1..>1479
/product="16S ribosomal RNA"
/note="putative"

ORIGIN

Query Match 95.5%; Score 21; DB 15; Length 1479;
Best Local Similarity 95.5%; Pred. No. 68;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGGTGCTC 22
|||||
Db 41 GAAAGGCTTTTCGGGGGTGCTC 62

RESULT 7

AF547926
LOCUS AF547926 541 bp DNA linear BCT 24-JAN-2006
DEFINITION Mycobacterium gadium strain CIP 105388 16S ribosomal RNA gene,
partial sequence.

ACCESSION AF547926
VERSION AF547926.1 GI:27733750
KEYWORDS
SOURCE Mycobacterium gadium
Mycobacterium gadium
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1 (bases 1 to 541)
AUTHORS Devilder,G., de Montclos,M.P. and Flandrois,J.P.

TITLE A multigene approach to phylogenetic analysis using the genus
Mycobacterium as a model

JOURNAL Int. J. Syst. Evol. Microbiol. 55 (Pt 1), 293-302 (2005)
 PUBMED 15653890
 REFERENCE 2 (bases 1 to 541)
 AUTHORS Devulder G., Pichat, C. and Flandrois, J.P.
 TITLE Direct Submission
 JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
 Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
 Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
 FEATURES Location/Qualifiers
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 /organism="Mycobacterium gadium"
 /mol_type="genomic DNA"
 /strain="CIP 105388"
 /db_xref="taxon:1794"
 /note="type strain of Mycobacterium gadium"
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 /product="16S ribosomal RNA"
 ORIGIN
 Query Match 92.7%; Score 20.4; DB 15; Length 541;
 Best Local Similarity 95.5%; Pred. No. 1.3e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GAAAGGCTTTCGGGGTGCTC 22
 |||||
 Db 26 GAAAGGCTTTCGGGGTGACTC 47
 |||||
 RESULT 8
 MGAD16S
 LOCUS MGAD16S 1456 bp DNA linear BCT 06-JUN-2003
 DEFINITION M.gadium 16S ribosomal RNA, part.
 ACCESSION X55594
 VERSION X55594.1 GI:44291
 KEYWORDS 16S ribosomal RNA.
 SOURCE Mycobacterium gadium
 ORGANISM Mycobacterium gadium
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 REFERENCE 1 (bases 1 to 1456)
 AUTHORS Pitulle, C., Dorach, M., Karda, J., Wolters, J. and Stackebrandt, E.
 TITLE Phylogeny of rapidly growing members of the genus Mycobacterium
 JOURNAL Int. J. Syst. Bacteriol. 42 (3), 337-343 (1992)
 PUBMED 1380284
 REFERENCE 2 (bases 1 to 1456)
 AUTHORS Wolters, J.
 TITLE Direct Submission
 JOURNAL Submitted (18-SEP-1990) Wolters J., Institut fuer Allgemeine
 Mikrobiologie der Universitaet, Biologiezentrum, Am Botanischen
 Garten 1-9, 2300 Kiel 1
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 1. .1456
 /organism="Mycobacterium gadium"
 /mol_type="genomic DNA"
 /strain="ATCC 27726"
 /db_xref="taxon:1794"
 1. .>1456
 /product="16S ribosomal RNA"
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 Query Match 92.7%; Score 20.4; DB 15; Length 1456;
 Best Local Similarity 95.5%; Pred. No. 1.3e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GAAAGGCTTTCGGGGTGCTC 22
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 Db 70 GAAAGGCTTTCGGGGTGACTC 91
 |||||
 RESULT 9
 MCO16S
 LOCUS MCO16S 1459 bp DNA linear BCT 11-JUN-2003
 DEFINITION Mycobacterium cookii partial 16S rRNA.

X53896
 X53896.1 GI:44201
 16S ribosomal RNA; ribosomal RNA.
 MYCOWORDS Mycobacterium cookii
 SOURCE Mycobacterium cookii
 ORGANISM Mycobacterium cookii
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 REFERENCE 1 (bases 1 to 1225)
 AUTHORS Kazda, J., Stackebrandt, E., Smida, J., Minnikin, D.E., Daffe, M.,
 Parlett, J.H. and Pitulle, C.
 TITLE Mycobacterium cookii sp. nov
 JOURNAL Int. J. Syst. Bacteriol. 40 (3), 217-223 (1990)
 PUBMED 1697763
 REFERENCE 2 (bases 1 to 1459)
 AUTHORS Stackebrandt, E.
 TITLE Direct Submission
 JOURNAL Submitted (01-AUG-1990) Stackebrandt E
 FEATURES Location/Qualifiers
 source
 1. .1459
 /organism="Mycobacterium cookii"
 /mol_type="genomic DNA"
 /strain="ATCC 49103 (T) = N22."
 /db_xref="taxon:1775"
 1. .>1459
 /product="16S ribosomal RNA"
 ORIGIN
 Query Match 92.7%; Score 20.4; DB 15; Length 1459;
 Best Local Similarity 95.5%; Pred. No. 1.3e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GAAAGGCTTTCGGGGTGCTC 22
 |||||
 Db 70 GAAAGGCTTTCGGGGTGACTC 91
 |||||
 RESULT 10
 AB006161
 LOCUS AB006161 1467 bp DNA linear BCT 30-OCT-2001
 DEFINITION Virgosporangium ochraceum gene for 16S rRNA, partial sequence,
 strain:YU794-41.
 ACCESSION AB006161
 VERSION AB006161.1 GI:16519342
 KEYWORDS Virgosporangium ochraceum
 SOURCE Virgosporangium ochraceum
 ORGANISM Virgosporangium ochraceum
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Micromonosporineae; Micromonosporaceae; Virgisporangium.
 REFERENCE 1
 AUTHORS Tamura, T., Hayakawa, M. and Hatano, K.
 TITLE A new genus of the order Actinomycetales, Virgosporangium gen.
 nov., with descriptions of Virgosporangium ochraceum sp. nov. and
 Virgosporangium aurantiacum sp. nov.
 JOURNAL Int. J. Syst. Evol. Microbiol. 51 (Pt 5), 1809-1816 (2001)
 PUBMED 11594613
 REFERENCE 2 (bases 1 to 1467)
 AUTHORS Tamura, T.
 TITLE Direct Submission
 JOURNAL Submitted (31-JUL-1997) Tomohiko Tamura, Institute for
 Fermentation, Osaka, Actinomycetes Group; 17-85, Juso-honmachi
 2-chome, Yodogawa-ku, Osaka, Osaka 532-8686, Japan
 (E-mail: tamura-tomohiko@ifo.or.jp, Tel: 81-6-6300-6555,
 Fax: 81-6-6300-6814)
 FEATURES Sequence updated (24-Jun-1998).
 Location/Qualifiers
 source
 1. .1467
 /organism="Virgisporangium ochraceum"
 /mol_type="genomic DNA"
 /strain="YU794-41"
 /db_xref="taxon:65505"
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 /product="16S ribosomal RNA"
 ORIGIN

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Query Match      92.7%; Score 20.4; DB 15; Length 1467;
Best Local Similarity 95.5%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTCGGGGTGCTC 22
   |||||
Db 42 GAAAGGCCTTCGGGGTGACTC 63

RESULT 11
LOCUS D86946
DEFINITION Pilimelia terevasa 16S rRNA gene, strain IFO15964, partial
sequence.
ACCESSION D86946
VERSION D86946.1 GI:3395635
KEYWORDS 16S ribosomal RNA.
SOURCE Pilimelia terevasa
ORGANISM Pilimelia terevasa
          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Micromonosporineae; Micromonosporaceae; Pilimelia.
REFERENCE 1 (sites)
AUTHORS Tamura,T., Hayakawa,M. and Hatano,K.
TITLE A new genus of the order Actinomycetales, Spirilliplanes gen. nov.,
with description of Spirilliplanes yamanashiensis sp. nov
JOURNAL Int. J. Syst. Bacteriol. 47 (1), 97-102 (1997)
PUBMED 8995810
REFERENCE 2 (bases 1 to 1467)
AUTHORS Tamura,T.
TITLE Direct Submission
JOURNAL Submitted (07-AUG-1996) Tomohiko Tamura, Institute for
Fermentation, Osaka, Actinomycetes group; 17-85, Juso-honnachi
2-chome, Yodogawa-ku, Osaka, Osaka 532, Japan (Tel:06-300-6555,
Fax:06-300-6814)
COMMENT On Aug 5, 1998 this sequence version replaced gi:1902976.
Sequence updated (24-Jun-1998).

FEATURES
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            /note="PCR-amplified 16S rDNA"

rRNA

ORIGIN
Query Match      92.7%; Score 20.4; DB 15; Length 1467;
Best Local Similarity 95.5%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTCGGGGTGCTC 22
   |||||
Db 42 GAAAGGCCTTCGGGGTGACTC 63

RESULT 12
LOCUS AB006162
DEFINITION Virgosporangium ochraceum gene for 16S rRNA, partial sequence,
strain:YU793-41.
ACCESSION AB006162
VERSION AB006162.1 GI:16519343
KEYWORDS Virgosporangium ochraceum
          Virgosporangium ochraceum
          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Micromonosporineae; Micromonosporaceae; Virgosporangium.
REFERENCE 1
AUTHORS Tamura,T., Hayakawa,M. and Hatano,K.
TITLE A new genus of the order Actinomycetales, Virgosporangium gen.
nov., with descriptions of Virgosporangium ochraceum sp. nov. and

```

```

Virgosporangium aurantiacum sp. nov
Int. J. Syst. Evol. Microbiol. 51 (Pt 5), 1809-1816 (2001)
11594613
2 (bases 1 to 1468)
Tamura,T.
Direct Submission
Submitted (31-JUL-1997) Tomohiko Tamura, Institute for
Fermentation, Osaka, Actinomycetes Group; 17-85, Juso-honnachi
2-chome, Yodogawa-ku, Osaka, Osaka 532-8686, Japan
(E-mail:tamura-tomohiko@ifo.or.jp, Tel:81-6-6300-6555,
Fax:81-6-6300-6814)
COMMENT Sequence updated (24-Jun-1998).
Sequence updated (24-Jun-1998).

FEATURES
    source
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            /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      92.7%; Score 20.4; DB 15; Length 1468;
Best Local Similarity 95.5%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTCGGGGTGCTC 22
   |||||
Db 42 GAAAGGCCTTCGGGGTGACTC 63

RESULT 13
LOCUS AC125314/c
DEFINITION Mus musculus BAC clone RP24-361P7 from chromosome 1, complete
sequence.
ACCESSION AC125314
VERSION AC125314.3 GI:29244780
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
          Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 121141)
AUTHORS Holmes,A., Waligorski,J., Meyer,R., Cotton,M. and Bielicki,L.
TITLE The sequence of Mus musculus BAC clone RP24-361P7
JOURNAL Unpublished (2001)
REFERENCE 2 (bases 1 to 121141)
AUTHORS Wilson,R.
TITLE Sequencing of Mus musculus
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 121141)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (22-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
REFERENCE 4 (bases 1 to 121141)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (03-DEC-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
REFERENCE 5 (bases 1 to 121141)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (26-MAR-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
REFERENCE 6 (bases 1 to 121141)
AUTHORS Wilson,R.
TITLE Direct Submission
JOURNAL Submitted (13-NOV-2003) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT On Mar 26, 2003 this sequence version replaced gi:26006669.

```

----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu>
 Contact: submissions@watson.wustl.edu
 ----- Summary Statistics

 Center project name: M_BB0361P07

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

SOURCE INFORMATION:

The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (<http://www.chori.org>) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at <http://www.chori.org>

NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone.

FEATURES

source	Location/Qualifiers
1. .121141	/organism="Mus musculus"
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	/db_xref="taxon:10090"
	/chromosome="1"
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	/clones="RP24-361P7"
	/clone_lib="RPCI-24"
5. .79	
	/rpt_family="L1"
repeat_region	18145..18290 /rpt_family="B2"
repeat_region	18543..18631 /rpt_family="L1"
repeat_region	20980..21293 /rpt_family="MaLR"
repeat_region	21294..22203 /rpt_family="MaLR"
repeat_region	22218..22586 /rpt_family="L1"
repeat_region	22592..23488 /rpt_family="MaLR"
repeat_region	23489..23831 /rpt_family="MaLR"
repeat_region	23992..24456 /rpt_family="L1"
repeat_region	24924..24973 /rpt_family="L1"
repeat_region	25615..25715 /rpt_family="L1"
repeat_region	25723..27499 /rpt_family="L1"
repeat_region	27662..27832 /rpt_family="L1"
repeat_region	28004..28203 /rpt_family="ERVK"
repeat_region	28654..28690 /rpt_family="L1"
repeat_region	28924..29868 /rpt_family="L1"
repeat_region	30667..31205 /rpt_family="L1"
repeat_region	31208..31334 /rpt_family="L1"
repeat_region	31327..31808 /rpt_family="L1"
repeat_region	31808..31919 /rpt_family="L1"
repeat_region	31929..34099 /rpt_family="L1"
repeat_region	34220..34365 /rpt_family="L1"
repeat_region	34364..34582 /rpt_family="L1"
repeat_region	35635..35804 /rpt_family="B4"
repeat_region	36257..37024 /rpt_family="RMER13B"
repeat_region	36343..37200 /rpt_family="ERVK"
repeat_region	38043..38248 /rpt_family="L1"
repeat_region	38258..38440 /rpt_family="RMER13A"
repeat_region	40829..41021 /rpt_family="B2"
repeat_region	41077..41165 /rpt_family="Alu"
repeat_region	42175..42390 /rpt_family="L1"
repeat_region	42676..42812 /rpt_family="Alu"
repeat_region	42876..43552 /rpt_family="L1"
repeat_region	45437..45504 /rpt_family="ERVK"
repeat_region	45565..45676 /rpt_family="L2"
repeat_region	46323..46411 /rpt_family="BC1_MM"
repeat_region	46356..46414 /rpt_family="B4"
repeat_region	46417..46497

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/rpt_family="B4"
48134.48236
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49283.49515
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49548.49703
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49508.50799
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50819.50900
/rpt_family="RMER15"
50944.51508

Query Match 88.2%; Score 19.4; DB 6; Length 121141;
Best Local Similarity 95.2%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGAGCCCTTCGGGGTGCT 21
|||||
Db 108302 GAAGAGCCCTTCGGTGCT 108282

AC015658 177016 bp DNA linear ROD 27-SEP-2003
AC015658/c Mus musculus chromosome 1, clone RP23-130F18, complete sequence.
DEFINITION AC015658
ACCESSION AC015658.11 GI:21306900
VERSION
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 177016)
AUTHORS Birren,B., Nusbaum,C. and Lander,E.
TITLE Mus musculus chromosome 1, clone RP23-130F18
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 177016)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., DeArelilano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Horton,L.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Kann,L.,
Howland,J.C., Johnson,R., Jones,C., Locke,K., Macdonald,P., Marquis,N.,
Lehoczy,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 177016)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,J., Colangelo,M., Collins,S., Collymore,A.,
Cooke,A., Cooke,P., DeArelilano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzGerald,M., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I.,
Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
Lamarez,R., Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K.,
Liu,G., Maclean,C., Macdonald,P., Major,J., Marquis,N.,
Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P.,

O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C.,
Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,
Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (01-JUN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 177016)
AUTHORS Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavsky,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collymore,A., Cooke,A., Cooke,P., Corum,B., DeArelilano,K.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Lui,X., Mabbitt,R., Maclean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (27-SEP-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 1, 2002 this sequence version replaced gi:13958481.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L1249
Center clone name: 130_F18

Location/Qualifiers
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/mol_type="genomic DNA"
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682..816
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complement(1190..1710)
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repeat_region complement(21309..21737)
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Query Match      88.2%; Score 19.4; DB 6; Length 177016;
Best Local Similarity 95.2%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAAGCCTTTCGGGGTGCT 21
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Db 53844 GAAAGCCTTTCGGGGTGCT 53824

RESULT 15
AC148982
LOCUS Mus musculus BAC clone RP23-174122 from 1, complete sequence.
DEFINITION AC148982
ACCESSION AC148982
VERSION AC148982.4 GI:53382933
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 195580)
Deng,S. and Cotton,M.
The sequence of Mus musculus BAC clone RP23-174122
2 (bases 1 to 195580)
Unpublished (2001)
REFERENCE 2 (bases 1 to 195580)
AUTHORS Wilson,R.K.
TITLE Direct Submission
JOURNAL Submitted (30-APR-2004) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 195580)
REFERENCE 3 (bases 1 to 195580)
AUTHORS Wilson,R.K.
TITLE Direct Submission
JOURNAL Submitted (27-JUL-2004) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 195580)
REFERENCE 4 (bases 1 to 195580)
AUTHORS Wilson,R.K.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-2004) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
5 (bases 1 to 195580)
REFERENCE 5 (bases 1 to 195580)
AUTHORS Wilson,R.K.
TITLE Direct Submission
JOURNAL Submitted (28-JAN-2005) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Oct 1, 2004 this sequence version replaced gi:50582872.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: submissions@wustl.edu
----- Summary Statistics
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Center project name: M_BA0174122
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NOTICE:
This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

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MAPPING INFORMATION:
This clone was provided by Dr. Wes Warren,
Department of Genetics, Washington University, St. Louis MO. For
additional information about the map position of this sequence, see
<http://genome.wustl.edu>

SOURCE INFORMATION:

The RPCi-23 BAC Library has been constructed by Kazutoyo Oseawa
and Minako Tateno in the laboratory of Pieter de Jong
(<http://www.chori.org>) from female C57BL/6J mouse kidney and/or
brain genomic DNA. The clone and detailed information can be
obtained from Research Genetics, Inc. (<http://www.resgen.com>) or
Pieter de Jong and coworkers at <http://www.chori.org>

NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone.

FEATURES

Location/Qualifiers

1..195580
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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ORIGIN

Query Match 88.2%; Score 19.4; DB 6; Length 195580;
Best Local Similarity 95.3%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTCGGGGTGCT 21
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DB 28433 GAAAGGCCTTCGGGGTGCT 28453

RESULT 16

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LOCUS Actinomadura viridis strain ATCC27103 16S ribosomal RNA gene,
DEFINITION partial sequence.
ACCESSION AF051385
VERSION AF051385.1 GI:6652697
KEYWORDS Actinomadura viridis
ORGANISM Actinomadura viridis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Thermomonosporaceae; Actinomadura.
REFERENCE 1 (bases 1 to 105)
AUTHORS Rodriguez, V., Parro, V. and Mellado, R.P.
TITLE Molecular Identification of Actinomycetes
JOURNAL Unpublished
AUTHORS Rodriguez, V., Parro, V. and Mellado, R.P.
VERSION 2 (bases 1 to 105)
KEYWORDS Direct Submission
TITLE Submitted (27-FEB-1998) Biotechnology Microbiana, Centro Nacional
JOURNAL de Biotechnology, Campus de la Universidad Autonoma, Cantoblanco,
Madrid 28049, Spain

FEATURES

Location/Qualifiers
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/organism="Actinomadura viridis"
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rRNA

ORIGIN

Query Match 85.5%; Score 18.8; DB 15; Length 105;

Best Local Similarity 90.9%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTCGGGGTGCTC 22
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DB 40 GAAAGGCCTTCGGGGTGCTC 61

RESULT 17

AF051382 108 bp DNA linear BCT 02-JAN-2000
LOCUS Actinomadura livida strain ATCC33578 16S ribosomal RNA gene,
DEFINITION partial sequence.
ACCESSION AF051382
VERSION AF051382.1 GI:6652694
KEYWORDS Actinomadura livida
ORGANISM Actinomadura livida
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Thermomonosporaceae; Actinomadura.
REFERENCE 1 (bases 1 to 108)
AUTHORS Rodriguez, V., Parro, V. and Mellado, R.P.
TITLE Molecular Identification of Actinomycetes
JOURNAL Unpublished
AUTHORS Rodriguez, V., Parro, V. and Mellado, R.P.
VERSION 2 (bases 1 to 108)
KEYWORDS Direct Submission
TITLE Submitted (27-FEB-1998) Biotechnology Microbiana, Centro Nacional
JOURNAL de Biotechnology, Campus de la Universidad Autonoma, Cantoblanco,
Madrid 28049, Spain

FEATURES

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rRNA

ORIGIN

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Best Local Similarity 90.9%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 40 GAAAGGCCTTCGGGGTGCTC 61

RESULT 18

AF051377 117 bp DNA linear BCT 02-JAN-2000
LOCUS Actinomadura citrea strain ATCC27887 16S ribosomal RNA gene,
DEFINITION partial sequence.
ACCESSION AF051377
VERSION AF051377.1 GI:6652689
KEYWORDS Actinomadura citrea
ORGANISM Actinomadura citrea
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Thermomonosporaceae; Actinomadura.
REFERENCE 1 (bases 1 to 117)
AUTHORS Rodriguez, V., Parro, V. and Mellado, R.P.
TITLE Molecular Identification of Actinomycetes
JOURNAL Unpublished
AUTHORS Rodriguez, V., Parro, V. and Mellado, R.P.
VERSION 2 (bases 1 to 117)
KEYWORDS Direct Submission
TITLE Submitted (27-FEB-1998) Biotechnology Microbiana, Centro Nacional
JOURNAL de Biotechnology, Campus de la Universidad Autonoma, Cantoblanco,
Madrid 28049, Spain

FEATURES

Location/Qualifiers

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/product="16S ribosomal RNA"

rRNA

ORIGIN
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Best Local Similarity 90.9%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCGCTTTCGGGGGTGCTC 22
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Db 43 GAAAGGCCCTTCGGGGGTACTC 64

RESULT 19
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LOCUS      117 bp      DNA      linear      BCT 02-JAN-2000
DEFINITION Actinomadura coerulea strain ATCC33576 16S ribosomal RNA gene,
partial sequence.
ACCESSION  AF051378
VERSION     AF051378.1 GI:6652690
KEYWORDS
SOURCE      Actinomadura coerulea
ORGANISM    Actinomadura coerulea
Bacteria; Actinobacteriia; Actinobacteridae; Actinomycetales;
Streptosporangineae; Thermomonosporaceae; Actinomadura.

REFERENCE
AUTHORS    Rodriguez,V., Parro,V. and Mellado,R.P.
TITLE      Molecular Identification of Actinomycetes
JOURNAL    Unpublished
REFERENCE
2 (bases 1 to 117)
Rodriguez,V., Parro,V. and Mellado,R.P.
Direct Submission
Submitted (27-FEB-1998) Biotechnology Microbiana, Centro Nacional
de Biotechnologia, Campus de la Universidad Autonoma, Cantoblanco,
Madrid 28049, Spain
LOCATION/Qualifiers
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/mol_type="genomic DNA"
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/product="16S ribosomal RNA"

rRNA

ORIGIN
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Best Local Similarity 90.9%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCGCTTTCGGGGGTGCTC 22
||||| ||||| ||||| |||||
Db 43 GAAAGGCCCTTCGGGGGTACTC 64

RESULT 20
AF051379
LOCUS      118 bp      DNA      linear      BCT 02-JAN-2000
DEFINITION Actinomadura cremea subsp. cremea strain ATCC33577 16S ribosomal
RNA gene, partial sequence.
ACCESSION  AF051379
VERSION     AF051379.1 GI:6652691
KEYWORDS
SOURCE      Actinomadura cremea subsp. cremea
ORGANISM    Actinomadura cremea subsp. cremea
Bacteria; Actinobacteriia; Actinobacteridae; Actinomycetales;
Streptosporangineae; Thermomonosporaceae; Actinomadura.

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REFERENCE
AUTHORS    Rodriguez,V., Parro,V. and Mellado,R.P.
TITLE      Molecular Identification of Actinomycetes
JOURNAL    Unpublished
REFERENCE
2 (bases 1 to 118)
Rodriguez,V., Parro,V. and Mellado,R.P.
Direct Submission
Submitted (27-FEB-1998) Biotechnology Microbiana, Centro Nacional
de Biotechnologia, Campus de la Universidad Autonoma, Cantoblanco,
Madrid 28049, Spain
LOCATION/Qualifiers
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rRNA

ORIGIN
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Best Local Similarity 90.9%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCGCTTTCGGGGGTGCTC 22
||||| ||||| ||||| |||||
Db 44 GAAAGGCCCTTCGGGGGTACTC 65

RESULT 21
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LOCUS      118 bp      DNA      linear      BCT 02-JAN-2000
DEFINITION Actinomadura spadix strain ATCC27298 16S ribosomal RNA gene,
partial sequence.
ACCESSION  AF051380
VERSION     AF051380.1 GI:6652692
KEYWORDS
SOURCE      Actinomadura spadix
ORGANISM    Actinomadura spadix
Bacteria; Actinobacteriia; Actinobacteridae; Actinomycetales;
Streptosporangineae; Thermomonosporaceae; Actinomadura.

REFERENCE
AUTHORS    Rodriguez,V., Parro,V. and Mellado,R.P.
TITLE      Molecular Identification of Actinomycetes
JOURNAL    Unpublished
REFERENCE
2 (bases 1 to 118)
Rodriguez,V., Parro,V. and Mellado,R.P.
Direct Submission
Submitted (27-FEB-1998) Biotechnology Microbiana, Centro Nacional
de Biotechnologia, Campus de la Universidad Autonoma, Cantoblanco,
Madrid 28049, Spain
LOCATION/Qualifiers
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<1. .>118
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rRNA

ORIGIN
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Best Local Similarity 90.9%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCGCTTTCGGGGGTGCTC 22
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Db 44 GAAAGGCCCTTCGGGGGTACTC 65

RESULT 22

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DEFINITION	AY234506	Bacterium Ellin5089	16S ribosomal RNA	401 bp	linear	BCT 08-DEC-2003
ACCESSION	AY234506	Bacterium Ellin5089	16S ribosomal RNA	401 bp	linear	BCT 08-DEC-2003
VERSION	AY234506.1	GI:37961663				
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
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REFERENCE						
AUTHORS						
TITLE						
JOURNAL						

JOURNAL Submitted (09-APR-2002) Department of Biological and Agricultural Engineering, Department of Microbiology, University of Georgia, Athens, GA 30602, USA

FEATURES
source
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Db 33 GAAAGCCCTTTCGGGGGTACTC 54

RESULT 26
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LOCUS AF131473 829 bp DNA linear BCT 01-MAR-2000
DEFINITION Nonomuraea sp. IM-7031 16S ribosomal RNA gene, partial sequence.
ACCESSION AF131473
VERSION AF131473.1 GI:7109907
KEYWORDS
SOURCE Nonomuraea sp. IM-7031
ORGANISM Nonomuraea sp. IM-7031
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Streptosporangiaceae; Nonomuraea.

REFERENCE
1 (bases 1 to 829)
Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
Investigation of actinomycete diversity in the tropical rainforests of Singapore
J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)

JOURNAL
REFERENCE 2 (bases 1 to 829)
Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
Direct Submission
Submitted (26-FEB-1999) Institute of Molecular and Cell Biology, National University of Singapore, 30 Medical Drive, Singapore 117609, Republic of Singapore

FEATURES
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Db 32 GAAAGCCCTTTCGGGGGTACTC 53

RESULT 27
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DEFINITION Nonomuraea sp. IM-0194 16S ribosomal RNA gene, partial sequence.
ACCESSION AF131452
VERSION AF131452.1 GI:7109886
KEYWORDS
SOURCE Nonomuraea sp. IM-0194
ORGANISM Nonomuraea sp. IM-0194
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Streptosporangiaceae; Nonomuraea.

REFERENCE
1 (bases 1 to 830)
Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
Investigation of actinomycete diversity in the tropical rainforests of Singapore
J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)

JOURNAL
REFERENCE 2 (bases 1 to 830)
Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
Direct Submission
Submitted (26-FEB-1999) Institute of Molecular and Cell Biology, National University of Singapore, 30 Medical Drive, Singapore 117609, Republic of Singapore

FEATURES
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/product="16S ribosomal RNA"

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Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTCGGGGTGCTC 22
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Streptosporangiaceae; Nonomuraea.

REFERENCE
AUTHORS
TITLE
1 (bases 1 to 830)
Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
Investigation of actinomycete diversity in the tropical rainforests of Singapore
J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)

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REFERENCE 2 (bases 1 to 830)
Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
Direct Submission
Submitted (26-FEB-1999) Institute of Molecular and Cell Biology, National University of Singapore, 30 Medical Drive, Singapore 117609, Republic of Singapore

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Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTCGGGGTGCTC 22
||||| ||||||| ||||||| |||||
Db 32 GAAAGCCCTTTCGGGGGTACTC 53

RESULT 28
AF131455
LOCUS AF131455 830 bp DNA linear BCT 01-MAR-2000
DEFINITION Nonomuraea sp. IM-1409 16S ribosomal RNA gene, partial sequence.
ACCESSION AF131455
VERSION AF131455.1 GI:7109889
KEYWORDS
SOURCE Nonomuraea sp. IM-1409
ORGANISM Nonomuraea sp. IM-1409
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Streptosporangiaceae; Nonomuraea.

REFERENCE
AUTHORS
TITLE
1 (bases 1 to 830)
Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
Investigation of actinomycete diversity in the tropical rainforests of Singapore
J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)

JOURNAL
REFERENCE 2 (bases 1 to 830)
Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
Direct Submission
Submitted (26-FEB-1999) Institute of Molecular and Cell Biology, National University of Singapore, 30 Medical Drive, Singapore 117609, Republic of Singapore

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Db 32 GAAAGCCCTTTCGGGGGTACTC 53

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RESULT 29
AF131469
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Nonomuraea sp. IM-6942
Nonomuraea sp. IM-6942
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Streptosporangiaceae; Nonomuraea.
1 (bases 1 to 830)
Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.
Investigation of actinomycete diversity in the tropical rainforests
of Singapore
J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
2 (bases 1 to 830)
Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.
Direct Submission
Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
National University of Singapore, 30 Medical Drive, Singapore
117609, Republic of Singapore
Location/Qualifiers
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QY 1 GAAAGGCCCTTTCGGGGTGCTC 22
||||| ||||| ||||| |||||
Db 32 GAAAGGCCCTTTCGGGGTGACTC 53

RESULT 30
AF131474
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Nonomuraea sp. IM-7062
Nonomuraea sp. IM-7062
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Streptosporangiaceae; Nonomuraea.
1 (bases 1 to 830)
Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.
Investigation of actinomycete diversity in the tropical rainforests
of Singapore
J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
2 (bases 1 to 830)
Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.
Direct Submission
Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
National University of Singapore, 30 Medical Drive, Singapore
117609, Republic of Singapore
Location/Qualifiers
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rRNA

ORIGIN

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Db 32 GAAAGGCCCTTTCGGGGTGACTC 53

RESULT 31
AF131453
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

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Nonomuraea sp. IM-0975
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Streptosporangiaceae; Nonomuraea.
1 (bases 1 to 831)
Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.
Investigation of actinomycete diversity in the tropical rainforests
of Singapore
J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
2 (bases 1 to 831)
Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.
Direct Submission
Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
National University of Singapore, 30 Medical Drive, Singapore
117609, Republic of Singapore
Location/Qualifiers
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rRNA

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Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCCCTTTCGGGGTGCTC 22
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Db 32 GAAAGGCCCTTTCGGGGTGACTC 53

RESULT 32
AF131461
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Nonomuraea sp. IM-2224
Nonomuraea sp. IM-2224
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Streptosporangiaceae; Nonomuraea.
1 (bases 1 to 831)
Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.
Investigation of actinomycete diversity in the tropical rainforests
of Singapore
J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
2 (bases 1 to 831)
Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.
Direct Submission
Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
National University of Singapore, 30 Medical Drive, Singapore
117609, Republic of Singapore
Location/Qualifiers
FEATURES

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Query Match      85.5%; Score 18.8; DB 15; Length 831;
Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTCGGGGTGCTC 22
    |||||
Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 33
AF131463
LOCUS      Nonomuraea sp. IM-3235 831 bp DNA linear BCT 01-MAR-2000
DEFINITION Nonomuraea sp. IM-3235 16S ribosomal RNA gene, partial sequence.
ACCESSION  AF131463
VERSION     AF131463.1 GI:7109897
KEYWORDS
SOURCE      Nonomuraea sp. IM-3235
            Nonomuraea sp. IM-3235
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Streptosporangineae; Streptosporangiaceae; Nonomuraea.
REFERENCE  1 (bases 1 to 831)
AUTHORS    Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE      Investigation of actinomycete diversity in the tropical rainforests
            of Singapore
JOURNAL    J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE  2 (bases 1 to 831)
AUTHORS    Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE      Direct Submission
JOURNAL    Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
            National University of Singapore, 30 Medical Drive, Singapore
            117609, Republic of Singapore
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Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 32 GAAAGGCCCTTCGGGGGTACTC 53

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LOCUS      Actinocorallia sp. IM-5291 832 bp DNA linear BCT 01-MAR-2000
DEFINITION Actinocorallia sp. IM-5291
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ACCESSION  AF131298
VERSION     AF131298.1 GI:7109732
KEYWORDS
SOURCE      Actinocorallia sp. IM-5291
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            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Streptosporangineae; Thermomonosporaceae; Actinocorallia.
REFERENCE  1 (bases 1 to 832)
AUTHORS    Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
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TITLE      Investigation of actinomycete diversity in the tropical rainforests
            of Singapore
JOURNAL    J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE  2 (bases 1 to 832)
AUTHORS    Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE      Direct Submission
JOURNAL    Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
            National University of Singapore, 30 Medical Drive, Singapore
            117609, Republic of Singapore
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Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 35
AF131456
LOCUS      Nonomuraea sp. IM-1682 832 bp DNA linear BCT 01-MAR-2000
DEFINITION Nonomuraea sp. IM-1682 16S ribosomal RNA gene, partial sequence.
ACCESSION  AF131456
VERSION     AF131456.1 GI:7109890
KEYWORDS
SOURCE      Nonomuraea sp. IM-1682
            Nonomuraea sp. IM-1682
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Streptosporangineae; Streptosporangiaceae; Nonomuraea.
REFERENCE  1 (bases 1 to 832)
AUTHORS    Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE      Investigation of actinomycete diversity in the tropical rainforests
            of Singapore
JOURNAL    J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE  2 (bases 1 to 832)
AUTHORS    Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE      Direct Submission
JOURNAL    Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
            National University of Singapore, 30 Medical Drive, Singapore
            117609, Republic of Singapore
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Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 36
AF131465
LOCUS      Nonomuraea sp. IM-6230 16S ribosomal RNA gene, partial sequence.
DEFINITION Nonomuraea sp. IM-6230 16S ribosomal RNA gene, partial sequence.
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ACCESSION AF131465.1 GI:7109899
VERSION AF131465.1
KEYWORDS
SOURCE Nonomuraea sp. IM-6230
ORGANISM Nonomuraea sp. IM-6230
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Streptosporangiaceae; Nonomuraea.
REFERENCE 1 (bases 1 to 832)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Investigation of actinomycete diversity in the tropical rainforests of Singapore
JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE 2 (bases 1 to 832)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology, National University of Singapore, 30 Medical Drive, Singapore 117609, Republic of Singapore
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DEFINITION Nonomuraea sp. IM-6588 16S ribosomal RNA gene, partial sequence.
ACCESSION AF131466
VERSION AF131466.1 GI:7109900
KEYWORDS
SOURCE Nonomuraea sp. IM-6588
ORGANISM Nonomuraea sp. IM-6588
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Streptosporangiaceae; Nonomuraea.
REFERENCE 1 (bases 1 to 832)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Investigation of actinomycete diversity in the tropical rainforests of Singapore
JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE 2 (bases 1 to 832)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology, National University of Singapore, 30 Medical Drive, Singapore 117609, Republic of Singapore
FEATURES
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DEFINITION Nonomuraea sp. IM-6588 16S ribosomal RNA gene, partial sequence.
ACCESSION AF131466
VERSION AF131466.1 GI:7109900
KEYWORDS
SOURCE Nonomuraea sp. IM-6588
ORGANISM Nonomuraea sp. IM-6588
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Streptosporangiaceae; Nonomuraea.
REFERENCE 1 (bases 1 to 832)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Investigation of actinomycete diversity in the tropical rainforests of Singapore
JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE 2 (bases 1 to 832)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology, National University of Singapore, 30 Medical Drive, Singapore 117609, Republic of Singapore
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Db 32 GAAAGGCCTTCGGGGTACTC 53
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LOCUS AF131467 832 bp DNA linear BCT 01-MAR-2000
DEFINITION Nonomuraea sp. IM-6794 16S ribosomal RNA gene, partial sequence.
ACCESSION AF131467
VERSION AF131467.1 GI:7109901
KEYWORDS
SOURCE Nonomuraea sp. IM-6794
ORGANISM Nonomuraea sp. IM-6794
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Streptosporangiaceae; Nonomuraea.
REFERENCE 1 (bases 1 to 832)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Investigation of actinomycete diversity in the tropical rainforests of Singapore
JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE 2 (bases 1 to 832)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology, National University of Singapore, 30 Medical Drive, Singapore 117609, Republic of Singapore
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1. .832
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Db 32 GAAAGGCCTTCGGGGTACTC 53
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AF131468
LOCUS AF131468 832 bp DNA linear BCT 01-MAR-2000
DEFINITION Nonomuraea sp. IM-6911 16S ribosomal RNA gene, partial sequence.
ACCESSION AF131468
VERSION AF131468.1 GI:7109902
KEYWORDS
SOURCE Nonomuraea sp. IM-6911
ORGANISM Nonomuraea sp. IM-6911
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Streptosporangiaceae; Nonomuraea.
REFERENCE 1 (bases 1 to 832)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Investigation of actinomycete diversity in the tropical rainforests of Singapore
JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE 2 (bases 1 to 832)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology, National University of Singapore, 30 Medical Drive, Singapore 117609, Republic of Singapore
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RESULT 40
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LOCUS      832 bp      DNA      linear      BCT 01-MAR-2000
DEFINITION Nonomuraea sp. IM-6943 16S ribosomal RNA gene, partial sequence.
ACCESSION AF131470
VERSION   AF131470.1 GI:7109904
KEYWORDS
SOURCE    Nonomuraea sp. IM-6943
ORGANISM  Nonomuraea sp. IM-6943
          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Streptosporangineae; Streptosporangiaceae; Nonomuraea.
REFERENCE 1 (bases 1 to 832)
AUTHORS   Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE     Investigation of actinomycete diversity in the tropical rainforests
          of Singapore
JOURNAL   J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE 2 (bases 1 to 832)
AUTHORS   Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE     Direct Submission
JOURNAL   Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
          National University of Singapore, 30 Medical Drive, Singapore
          117609, Republic of Singapore

FEATURES
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Db  32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 41
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LOCUS      832 bp      DNA      linear      BCT 01-MAR-2000
DEFINITION Nonomuraea sp. IM-6949 16S ribosomal RNA gene, partial sequence.
ACCESSION AF131471
VERSION   AF131471.1 GI:7109905
KEYWORDS
SOURCE    Nonomuraea sp. IM-6949
ORGANISM  Nonomuraea sp. IM-6949
          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Streptosporangineae; Streptosporangiaceae; Nonomuraea.
REFERENCE 1 (bases 1 to 832)
AUTHORS   Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE     Investigation of actinomycete diversity in the tropical rainforests
          of Singapore
JOURNAL   J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE 2 (bases 1 to 832)
AUTHORS   Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
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Direct Submission
Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
National University of Singapore, 30 Medical Drive, Singapore
117609, Republic of Singapore
Location/Qualifiers
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Db  32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 42
AF131472
LOCUS      832 bp      DNA      linear      BCT 01-MAR-2000
DEFINITION Nonomuraea sp. IM-6966 16S ribosomal RNA gene, partial sequence.
ACCESSION AF131472
VERSION   AF131472.1 GI:7109906
KEYWORDS
SOURCE    Nonomuraea sp. IM-6966
ORGANISM  Nonomuraea sp. IM-6966
          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Streptosporangineae; Streptosporangiaceae; Nonomuraea.
REFERENCE 1 (bases 1 to 832)
AUTHORS   Wang, J., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE     Investigation of actinomycete diversity in the tropical rainforests
          of Singapore
JOURNAL   J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE 2 (bases 1 to 832)
AUTHORS   Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE     Direct Submission
JOURNAL   Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
          National University of Singapore, 30 Medical Drive, Singapore
          117609, Republic of Singapore

FEATURES
source
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Db  32 GAAAGGCCCTTCGGGGGTACTC 53

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LOCUS      832 bp      DNA      linear      BCT 01-MAR-2000
DEFINITION Nonomuraea sp. IM-7078 16S ribosomal RNA gene, partial sequence.
ACCESSION AF131475
VERSION   AF131475.1 GI:7109909
KEYWORDS
SOURCE    Nonomuraea sp. IM-7078
ORGANISM  Nonomuraea sp. IM-7078
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Query Match      85.5%; Score 18.8; DB 15; Length 833;
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    ||||| ||||| ||||| ||||| |||||
Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 47
AF131434
LOCUS Microtetraspora sp. IM-6228 833 bp DNA linear BCT 01-MAR-2000
DEFINITION Microtetraspora sp. IM-6228 16S ribosomal RNA gene, partial
          sequence.
ACCESSION AF131434
VERSION AF131434.1 GI:7109868
KEYWORDS Microtetraspora sp. IM-6228
SOURCE Microtetraspora sp. IM-6228
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Streptosporangineae; Streptosporangiaceae; Microtetraspora.
REFERENCE 1 (bases 1 to 833)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Investigation of actinomycete diversity in the tropical rainforests
          of Singapore
JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE 2 (bases 1 to 833)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
          National University of Singapore, 30 Medical Drive, Singapore
          117609, Republic of Singapore
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rRNA

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QY 1 GAAAGGCCTTCGGGGGTGCTC 22
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Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 48
AF131435
LOCUS Microtetraspora sp. IM-7010 833 bp DNA linear BCT 01-MAR-2000
DEFINITION Microtetraspora sp. IM-7010 16S ribosomal RNA gene, partial
          sequence.
ACCESSION AF131435
VERSION AF131435.1 GI:7109869
KEYWORDS Microtetraspora sp. IM-7010
SOURCE Microtetraspora sp. IM-7010
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Streptosporangineae; Streptosporangiaceae; Microtetraspora.
REFERENCE 1 (bases 1 to 833)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Investigation of actinomycete diversity in the tropical rainforests
          of Singapore
JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE 2 (bases 1 to 833)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
          National University of Singapore, 30 Medical Drive, Singapore,
          117609, Republic of Singapore

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National University of Singapore, 30 Medical Drive, Singapore
117609, Republic of Singapore
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rRNA

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Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 49
AF131436
LOCUS Microtetraspora sp. IM-7249 833 bp DNA linear BCT 01-MAR-2000
DEFINITION Microtetraspora sp. IM-7249 16S ribosomal RNA gene, partial
          sequence.
ACCESSION AF131436
VERSION AF131436.1 GI:7109870
KEYWORDS Microtetraspora sp. IM-7249
SOURCE Microtetraspora sp. IM-7249
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Streptosporangineae; Streptosporangiaceae; Microtetraspora.
REFERENCE 1 (bases 1 to 833)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Investigation of actinomycete diversity in the tropical rainforests
          of Singapore
JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE 2 (bases 1 to 833)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
          National University of Singapore, 30 Medical Drive, Singapore
          117609, Republic of Singapore
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rRNA

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Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 50
AF131454
LOCUS Nonomurea sp. IM-0984 833 bp DNA linear BCT 01-MAR-2000
DEFINITION Nonomurea sp. IM-0984 16S ribosomal RNA gene, partial sequence.
ACCESSION AF131454
VERSION AF131454.1 GI:7109889
KEYWORDS Nonomurea sp. IM-0984
SOURCE Nonomurea sp. IM-0984
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

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Best Local Similarity 90.9%; Pred. No. 8.3e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCCCTTCGGGGGTGCTC 22
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 Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 54
 AF131460
 LOCUS AF131460 833 bp DNA linear BCT 01-MAR-2000
 DEFINITION Nonomuraea sp. IM-2156 16S ribosomal RNA gene, partial sequence.
 ACCESSION AF131460
 VERSION AF131460.1 GI:7109894
 KEYWORDS
 SOURCE Nonomuraea sp. IM-2156
 ORGANISM Nonomuraea sp. IM-2156

REFERENCE 1 (bases 1 to 833)
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Streptosporangineae; Streptosporangiaceae; Nonomuraea.

AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
 TITLE Investigation of actinomycete diversity in the tropical rainforests
 of Singapore

JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
 REFERENCE 2 (bases 1 to 833)
 Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
 TITLE Direct Submission
 JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
 National University of Singapore, 30 Medical Drive, Singapore
 117609, Republic of Singapore

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 Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 55
 AF131462
 LOCUS AF131462 833 bp DNA linear BCT 01-MAR-2000
 DEFINITION Nonomuraea sp. IM-2637 16S ribosomal RNA gene, partial sequence.
 ACCESSION AF131462
 VERSION AF131462.1 GI:7109896
 KEYWORDS
 SOURCE Nonomuraea sp. IM-2637
 ORGANISM Nonomuraea sp. IM-2637

REFERENCE 1 (bases 1 to 833)
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Streptosporangineae; Streptosporangiaceae; Nonomuraea.

AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
 TITLE Investigation of actinomycete diversity in the tropical rainforests
 of Singapore

JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
 REFERENCE 2 (bases 1 to 833)
 Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
 TITLE Direct Submission

JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
 National University of Singapore, 30 Medical Drive, Singapore
 117609, Republic of Singapore

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rRNA
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Query Match 85.5%; Score 18.8; DB 15; Length 833;
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 Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 56
 AF131464
 LOCUS AF131464 833 bp DNA linear BCT 01-MAR-2000
 DEFINITION Nonomuraea sp. IM-3385 16S ribosomal RNA gene, partial sequence.
 ACCESSION AF131464
 VERSION AF131464.1 GI:7109898
 KEYWORDS
 SOURCE Nonomuraea sp. IM-3385
 ORGANISM Nonomuraea sp. IM-3385

REFERENCE 1 (bases 1 to 833)
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Streptosporangineae; Streptosporangiaceae; Nonomuraea.

AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
 TITLE Investigation of actinomycete diversity in the tropical rainforests
 of Singapore

JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
 REFERENCE 2 (bases 1 to 833)
 Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
 TITLE Direct Submission

JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
 National University of Singapore, 30 Medical Drive, Singapore
 117609, Republic of Singapore

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rRNA
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 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 57
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 DEFINITION Microbispora sp. IM-7541 16S ribosomal RNA gene, partial sequence.
 ACCESSION AF131384
 VERSION AF131384.1 GI:7109818
 KEYWORDS
 SOURCE Microbispora sp. IM-7541
 ORGANISM Microbispora sp. IM-7541

REFERENCE 1 (bases 1 to 834)
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Streptosporangineae; Streptosporangiaceae; Microbispora.

AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
 TITLE Investigation of actinomycete diversity in the tropical rainforests
 of Singapore

J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
 REFERENCE 2 (bases 1 to 834)
 AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
 TITLE Direct Submission
 JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
 National University of Singapore, 30 Medical Drive, Singapore
 117609, Republic of Singapore
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 Db 32 GAAAGCCCTTCGGGGGTACTC 53
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 LOCUS AF131641 835 bp DNA linear BCT 01-MAR-2000
 DEFINITION Thermomonosporaceae str. IM-6903 16S ribosomal RNA gene, partial
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 ACCESSION AF131641
 VERSION AF131641.1 GI:7110075
 KEYWORDS Thermomonosporaceae str. IM-6903
 SOURCE Thermomonosporaceae str. IM-6903
 ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Streptosporangineae; Thermomonosporaceae.
 REFERENCE 1 (bases 1 to 835)
 AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
 TITLE Investigation of actinomycete diversity in the tropical rainforests
 of Singapore
 JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
 REFERENCE 2 (bases 1 to 835)
 AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
 TITLE Direct Submission
 JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
 National University of Singapore, 30 Medical Drive, Singapore
 117609, Republic of Singapore
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 Db 32 GAAAGCCCTTCGGGGGTACTC 53
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 LOCUS AF131643 835 bp DNA linear BCT 01-MAR-2000
 DEFINITION Thermomonosporaceae str. IM-6932 16S ribosomal RNA gene, partial
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 ACCESSION AF131643
 VERSION AF131643.1 GI:7110077
 KEYWORDS Thermomonosporaceae str. IM-6932
 SOURCE Thermomonosporaceae str. IM-6932
 ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Streptosporangineae; Thermomonosporaceae.
 REFERENCE 1 (bases 1 to 835)
 AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
 TITLE Investigation of actinomycete diversity in the tropical rainforests
 of Singapore
 JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
 REFERENCE 2 (bases 1 to 835)
 AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
 TITLE Direct Submission
 JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
 National University of Singapore, 30 Medical Drive, Singapore
 117609, Republic of Singapore
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 QY 1 GAAAGCCCTTCGGGGTGCTC 22
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AF131643
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 Thermomonosporaceae str. IM-6932
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Streptosporangineae; Thermomonosporaceae.
 REFERENCE 1 (bases 1 to 835)
 AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
 TITLE Investigation of actinomycete diversity in the tropical rainforests
 of Singapore
 JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
 REFERENCE 2 (bases 1 to 835)
 AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
 TITLE Direct Submission
 JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
 National University of Singapore, 30 Medical Drive, Singapore
 117609, Republic of Singapore
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 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GAAAGCCCTTCGGGGTGCTC 22
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 Db 32 GAAAGCCCTTCGGGGGTACTC 53
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 AF131644
 LOCUS AF131644 835 bp DNA linear BCT 01-MAR-2000
 DEFINITION Thermomonosporaceae str. IM-7042 16S ribosomal RNA gene, partial
 sequence.
 ACCESSION AF131644
 VERSION AF131644.1 GI:7110078
 KEYWORDS Thermomonosporaceae str. IM-7042
 SOURCE Thermomonosporaceae str. IM-7042
 ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Streptosporangineae; Thermomonosporaceae.
 REFERENCE 1 (bases 1 to 835)
 AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
 TITLE Investigation of actinomycete diversity in the tropical rainforests
 of Singapore
 JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
 REFERENCE 2 (bases 1 to 835)
 AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
 TITLE Direct Submission
 JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
 National University of Singapore, 30 Medical Drive, Singapore
 117609, Republic of Singapore
 FEATURES Location/Qualifiers
 source 1..835
 /organism="Thermomonosporaceae str. IM-7042"
 /mol_type="genomic DNA"
 /strain="IM 7042"
 /db_xref="taxon:116546"
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 /product="16S ribosomal RNA"
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 Query Match 85.5%; Score 18.8; DB 15; Length 835;
 Best Local Similarity 90.9%; Pred. No. 8.3e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 GAAAGGCCTTCGGGGGTGCTC 22
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Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 61
AF131646 835 bp DNA linear BCT 01-MAR-2000
LOCUS Thermomonosporaceae str. IM-7209 16S ribosomal RNA gene, partial
DEFINITION sequence.
ACCESSION AF131646
VERSION AF131646.1 GI:7110080
SOURCE Thermomonosporaceae str. IM-7209
ORGANISM Thermomonosporaceae str. IM-7209
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Thermomonosporaceae.
REFERENCE 1 (bases 1 to 835)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Investigation of actinomycete diversity in the tropical rainforests
of Singapore
JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE 2 (bases 1 to 835)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
National University of Singapore, 30 Medical Drive, Singapore
117609, Republic of Singapore
FEATURES
source Location/Qualifiers
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/mol_type="genomic DNA"
/strain="IM 7209"
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<1_>.835
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 85.5%; Score 18.8; DB 15; Length 835;
Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTCGGGGGTGCTC 22
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Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 62
AF131647 835 bp DNA linear BCT 01-MAR-2000
LOCUS Thermomonosporaceae str. IM-7387 16S ribosomal RNA gene, partial
DEFINITION sequence.
ACCESSION AF131647
VERSION AF131647.1 GI:7110081
SOURCE Thermomonosporaceae str. IM-7387
ORGANISM Thermomonosporaceae str. IM-7387
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Thermomonosporaceae.
REFERENCE 1 (bases 1 to 835)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Investigation of actinomycete diversity in the tropical rainforests
of Singapore
JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE 2 (bases 1 to 835)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
National University of Singapore, 30 Medical Drive, Singapore
117609, Republic of Singapore
FEATURES
source Location/Qualifiers
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/organism="Thermomonosporaceae str. IM-7387"
/mol_type="genomic DNA"
/strain="IM 7387"
/db_xref="taxon:116549"
<1_>.835
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 85.5%; Score 18.8; DB 15; Length 836;
Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTCGGGGGTGCTC 22
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Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 63
AF131302 836 bp DNA linear BCT 01-MAR-2000
LOCUS Actinomadura sp. IM-3046 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION AF131302
VERSION AF131302.1 GI:7109736
SOURCE Actinomadura sp. IM-3046
ORGANISM Actinomadura sp. IM-3046
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Thermomonosporaceae; Actinomadura.
REFERENCE 1 (bases 1 to 836)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Investigation of actinomycete diversity in the tropical rainforests
of Singapore
JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE 2 (bases 1 to 836)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
National University of Singapore, 30 Medical Drive, Singapore
117609, Republic of Singapore
FEATURES
source Location/Qualifiers
1. .836
/organism="Actinomadura sp. IM-3046"
/mol_type="genomic DNA"
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<1_>.836
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 85.5%; Score 18.8; DB 15; Length 836;
Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTCGGGGGTGCTC 22
    ||||| ||||| ||||| |||||
Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 64
AF131308 836 bp DNA linear BCT 01-MAR-2000
LOCUS Actinomadura sp. IM-6226 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION AF131308
VERSION AF131308.1 GI:7109742
SOURCE Actinomadura sp. IM-6226
ORGANISM Actinomadura sp. IM-6226
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Thermomonosporaceae; Actinomadura.
REFERENCE 1 (bases 1 to 836)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Investigation of actinomycete diversity in the tropical rainforests
of Singapore
```

J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
 2 (bases 1 to 836)
AUTHORS
 Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE
 Direct Submission
JOURNAL
 Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
 National University of Singapore, 30 Medical Drive, Singapore
 117609, Republic of Singapore
FEATURES
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 /mol_type="genomic DNA"
 /strain="IM 6226"
 /db_xref="taxon:116208"
 <1..>836
 /product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match 85.5%; Score 18.8; DB 15; Length 836;
 Best Local Similarity 90.9%; Pred. No. 8.3e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAGGCGCTTCGGGGGTGC TC 22
 ||||| ||||| ||||| |||||
 Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 65
 AF131309
LOCUS
 AF131309
DEFINITION
 Actinomadura sp. IM-6793 16S ribosomal RNA gene, partial sequence.
ACCESSION
 AF131309
VERSION
 AF131309.1 GI:7109743
KEYWORDS
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SOURCE
 Actinomadura sp. IM-6793
 Actinomadura sp. IM-6793
ORGANISM
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Streptosporangineae; Thermomonosporaceae; Actinomadura.

REFERENCE
 1 (bases 1 to 836)
 Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
AUTHORS
 Investigation of actinomycete diversity in the tropical rainforests
 of Singapore
TITLE
 J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)

JOURNAL
 2 (bases 1 to 836)
AUTHORS
 Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE
 Direct Submission
JOURNAL
 Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
 National University of Singapore, 30 Medical Drive, Singapore
 117609, Republic of Singapore
FEATURES
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 1..836
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 /mol_type="genomic DNA"
 /strain="IM 6793"
 /db_xref="taxon:116209"
 <1..>836
 /product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match 85.5%; Score 18.8; DB 15; Length 836;
 Best Local Similarity 90.9%; Pred. No. 8.3e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAGGCGCTTCGGGGGTGC TC 22
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 Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 66
 AF131330
LOCUS
 AF131330
DEFINITION
 Actinomadura sp. IM-7397 16S ribosomal RNA gene, partial sequence.
ACCESSION
 AF131330
VERSION
 AF131330.1 GI:7109764

KEYWORDS										
SOURCE										
ORGANISM	Actinomadura sp. IM-7397									
	Actinomadura sp. IM-7397									
	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;									
	Streptosporangineae; Thermomonosporaceae; Actinomadura.									
REFERENCE	1 (bases 1 to 836)									
AUTHORS	Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.									
TITLE	Investigation of actinomycete diversity in the tropical rainforests of Singapore									
JOURNAL	J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)									
REFERENCE	2 (bases 1 to 836)									
AUTHORS	Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.									
TITLE	Direct Submission									
JOURNAL	Submitted (26-FEB-1999) Institute of Molecular and Cell Biology, National University of Singapore, 30 Medical Drive, Singapore 117609, Republic of Singapore									
FEATURES	Location/Qualifiers									
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	/mol_type="genomic DNA"									
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	/db_xref="taxon:116230"									
rRNA	<1. .>836									
	/product="16S ribosomal RNA"									
ORIGIN										
Query Match	85.5%; Score 18.8; DB 15; Length 836;									
Best Local Similarity	90.3%; Pred. No. 8.3e+02;									
Matches	20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
QY	1 GAAAGGCCTTTTCGGGGTGCTC 22									
Db	32 GAAAGGCCCTTCGGGGTACTC 53									
RESULT 67										
AF131645										
LOCUS	AF131645 836 bp DNA linear BCT 01-MAR-2000									
DEFINITION	Thermomonosporaceae str. IM-7058 16S ribosomal RNA gene, partial sequence.									
ACCESSION	AF131645									
VERSION	AF131645.1 GI:7110079									
KEYWORDS										
SOURCE	Thermomonosporaceae str. IM-7058									
ORGANISM	Thermomonosporaceae str. IM-7058									
	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;									
	Streptosporangineae; Thermomonosporaceae.									
REFERENCE	1 (bases 1 to 836)									
AUTHORS	Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.									
TITLE	Investigation of actinomycete diversity in the tropical rainforests of Singapore									
JOURNAL	J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)									
REFERENCE	2 (bases 1 to 836)									
AUTHORS	Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.									
TITLE	Direct Submission									
JOURNAL	Submitted (26-FEB-1999) Institute of Molecular and Cell Biology, National University of Singapore, 30 Medical Drive, Singapore 117609, Republic of Singapore									
FEATURES	Location/Qualifiers									
source	1. .836									
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	/mol_type="genomic DNA"									
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	/db_xref="taxon:116547"									
rRNA	<1. .>836									
	/product="16S ribosomal RNA"									
ORIGIN										
Query Match	85.5%; Score 18.8; DB 15; Length 836;									
Best Local Similarity	90.3%; Pred. No. 8.3e+02;									
Matches	20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
QY	1 GAAAGGCCTTTTCGGGGTGCTC 22									

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Db      32 GAAAGGCCCTTCGGGGGTACTC 53
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RESULT 68
AF131642      837 bp      DNA      linear      BCT 01-MAR-2000
LOCUS      Thermomonosporaceae str. IM-6923 16S ribosomal RNA gene, partial
DEFINITION      sequence.
ACCESSION      AF131642
VERSION      AF131642.1 GI:7110076
KEYWORDS      Thermomonosporaceae str. IM-6923
SOURCE      Thermomonosporaceae str. IM-6923
ORGANISM      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Thermomonosporaceae.
REFERENCE      1 (bases 1 to 837)
AUTHORS      Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE      Investigation of actinomycete diversity in the tropical rainforests
of Singapore
JOURNAL      J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE      2 (bases 1 to 837)
AUTHORS      Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE      Direct Submission
JOURNAL      Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
National University of Singapore, 30 Medical Drive, Singapore
117609, Republic of Singapore
FEATURES      Location/Qualifiers
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xrna
ORIGIN

Query Match      85.5%; Score 18.8; DB 15; Length 837;
Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GAAAGGCCCTTCGGGGGTGCTC 22
|||||
Db      32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 69
AF131326      838 bp      DNA      linear      BCT 01-MAR-2000
LOCUS      Actinomadura sp. IM-7213 16S ribosomal RNA gene, partial sequence.
DEFINITION      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
ACCESSION      AF131326
VERSION      AF131326.1 GI:7109760
KEYWORDS      Streptosporangineae; Thermomonosporaceae; Actinomadura.
SOURCE      Actinomadura sp. IM-7213
ORGANISM      Actinomadura sp. IM-7213
REFERENCE      1 (bases 1 to 838)
AUTHORS      Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE      Investigation of actinomycete diversity in the tropical rainforests
of Singapore
JOURNAL      J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE      2 (bases 1 to 838)
AUTHORS      Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE      Direct Submission
JOURNAL      Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
National University of Singapore, 30 Medical Drive, Singapore
117609, Republic of Singapore
FEATURES      Location/Qualifiers
source      1..838
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/strain="IM 7213"

xrna
ORIGIN

Query Match      85.5%; Score 18.8; DB 15; Length 837;
Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GAAAGGCCCTTCGGGGGTGCTC 22
|||||
Db      32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 70
AF131327      838 bp      DNA      linear      BCT 01-MAR-2000
LOCUS      Actinomadura sp. IM-7214 16S ribosomal RNA gene, partial sequence.
DEFINITION      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
ACCESSION      AF131327
VERSION      AF131327.1 GI:7109761
KEYWORDS      Streptosporangineae; Thermomonosporaceae; Actinomadura.
SOURCE      Actinomadura sp. IM-7214
ORGANISM      Actinomadura sp. IM-7214
REFERENCE      1 (bases 1 to 838)
AUTHORS      Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE      Investigation of actinomycete diversity in the tropical rainforests
of Singapore
JOURNAL      J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE      2 (bases 1 to 838)
AUTHORS      Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE      Direct Submission
JOURNAL      Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
National University of Singapore, 30 Medical Drive, Singapore
117609, Republic of Singapore
FEATURES      Location/Qualifiers
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/mol_type="Actinomadura sp. IM-7214"
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/db_xref="taxon:116227"
<1..>838
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xrna
ORIGIN

Query Match      85.5%; Score 18.8; DB 15; Length 838;
Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GAAAGGCCCTTCGGGGGTGCTC 22
|||||
Db      32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 71
AF163338      1013 bp      DNA      linear      BCT 14-DEC-2002
LOCUS      Mycobacterium sp. IP20010664 16S ribosomal RNA gene, partial
DEFINITION      sequence.
ACCESSION      AF163338
VERSION      AF163338.1 GI:26892049
KEYWORDS      Mycobacterium sp. IP20010664
SOURCE      Mycobacterium sp. IP20010664
ORGANISM      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE      1 (bases 1 to 1013)
AUTHORS      Le Dantec, C., Jackson, M., Duguet, J.-P., Montiel, A., Dumoutier, N.,
Dubrou, S. and Vincent, V.
TITLE      Isolation of unusual Mycobacterium species from water supplies
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 1013)

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/db_xref="taxon:116226"
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/product="16S ribosomal RNA"

ORIGIN

Query Match      85.5%; Score 18.8; DB 15; Length 838;
Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GAAAGGCCCTTCGGGGGTGCTC 22
|||||
Db      32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 70
AF131327      838 bp      DNA      linear      BCT 01-MAR-2000
LOCUS      Actinomadura sp. IM-7214 16S ribosomal RNA gene, partial sequence.
DEFINITION      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
ACCESSION      AF131327
VERSION      AF131327.1 GI:7109761
KEYWORDS      Streptosporangineae; Thermomonosporaceae; Actinomadura.
SOURCE      Actinomadura sp. IM-7214
ORGANISM      Actinomadura sp. IM-7214
REFERENCE      1 (bases 1 to 838)
AUTHORS      Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE      Investigation of actinomycete diversity in the tropical rainforests
of Singapore
JOURNAL      J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE      2 (bases 1 to 838)
AUTHORS      Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE      Direct Submission
JOURNAL      Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
National University of Singapore, 30 Medical Drive, Singapore
117609, Republic of Singapore
FEATURES      Location/Qualifiers
source      1..838
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xrna
ORIGIN

Query Match      85.5%; Score 18.8; DB 15; Length 838;
Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GAAAGGCCCTTCGGGGGTGCTC 22
|||||
Db      32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 71
AF163338      1013 bp      DNA      linear      BCT 14-DEC-2002
LOCUS      Mycobacterium sp. IP20010664 16S ribosomal RNA gene, partial
DEFINITION      sequence.
ACCESSION      AF163338
VERSION      AF163338.1 GI:26892049
KEYWORDS      Mycobacterium sp. IP20010664
SOURCE      Mycobacterium sp. IP20010664
ORGANISM      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE      1 (bases 1 to 1013)
AUTHORS      Le Dantec, C., Jackson, M., Duguet, J.-P., Montiel, A., Dumoutier, N.,
Dubrou, S. and Vincent, V.
TITLE      Isolation of unusual Mycobacterium species from water supplies
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 1013)

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AUTHORS TITLE JOURNAL FEATURES source rRNA ORIGIN	Le Dantec,C., Jackson,M., Duguet,J.-P., Montiel,A., Dumoutier,N., Dubrou,S. and Vincent,V. Direct Submission Submitted (15-OCT-2002) Mycobacterie, Institut Pasteur, 25 rue du Docteur Roux, Paris 75015, France Location/Qualifiers 1. .1013 /organism="Mycobacterium sp. IP20010664" /mol_type="genomic DNA" /strain="IP20010664" /db_xref="taxon:215916" <1. .>1013 /product="16S ribosomal RNA"									
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	Best Local Similarity	90.9%;	Pred. No. 8.1e+02;							
	Matches	20;	Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;			
	QY	1	GAAGGCGCTTTCGGGGTGCTC 22							
	Db	63	GAAGGCCCTTCGGGGTACTC 84							
	RESULT 72									
	AEU49004									
	LOCUS	Actinomadura echinospira	1401 bp	DNA	linear	BCT 08-MAY-1996				
REFERENCE AUTHORS TITLE JOURNAL FEATURES source rRNA ORIGIN	Actinomadura echinospira Actinomadura echinospira Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptosporangineae; Thermomonosporaceae; Actinomadura. Wang,Y. Phylogenetic analysis of Actinomadura species Thesis (1996) Institute of Molecular and Cell Biology, National University of Singapore 2 (bases 1 to 1401) Direct Submission Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell Biology, National University of Singapore, 10 Kent Ridge Crescent, Singapore 0511, Singapore Location/Qualifiers 1. .1401 /organism="Actinomadura echinospira" /mol_type="genomic DNA" /strain="IFO 14042" /db_xref="taxon:1992" 1. .1401 /product="16S ribosomal RNA"									
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	Best Local Similarity	90.9%;	Pred. No. 7.7e+02;							
	Matches	20;	Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;			
	QY	1	GAAGGCGCTTTCGGGGTGCTC 22							
	Db	13	GAAGGCCCTTCGGGGTACTC 34							
	RESULT 72									
	AEU49004									
	LOCUS	Actinomadura echinospira	1401 bp	DNA	linear	BCT 08-MAY-1996				
REFERENCE AUTHORS TITLE JOURNAL FEATURES source rRNA ORIGIN	Actinomadura echinospira Actinomadura echinospira Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptosporangineae; Thermomonosporaceae; Actinomadura. Wang,Y. Phylogenetic analysis of Actinomadura species Thesis (1996) Institute of Molecular and Cell Biology, National University of Singapore 2 (bases 1 to 1401) Direct Submission Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell Biology, National University of Singapore, 10 Kent Ridge Crescent, Singapore 0511, Singapore Location/Qualifiers 1. .1401 /organism="Actinomadura echinospira" /mol_type="genomic DNA" /strain="IFO 14042" /db_xref="taxon:1992" 1. .1401 /product="16S ribosomal RNA"									
	Query Match	85.5%;	Score 18.8;	DB 15;	Length 1401;					
	Best Local Similarity	90.9%;	Pred. No. 7.7e+02;							
	Matches	20;	Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;			
	QY	1	GAAGGCGCTTTCGGGGTGCTC 22							
	Db	13	GAAGGCCCTTCGGGGTACTC 34							
	RESULT 73									
	ALU49007									
	LOCUS	Actinomadura libanotica	1404 bp	DNA	linear	BCT 08-MAY-1996				
REFERENCE AUTHORS TITLE JOURNAL FEATURES source rRNA ORIGIN	Actinomadura libanotica Actinomadura libanotica Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptosporangineae; Thermomonosporaceae; Actinomadura. Wang,Y. Phylogenetic analysis of Actinomadura species Thesis (1996) Institute of Molecular and Cell Biology, National University of Singapore 2 (bases 1 to 1406) Direct Submission Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell Biology, National University of Singapore, 10 Kent Ridge Crescent, Singapore 0511, Singapore Location/Qualifiers 1. .1406 /organism="Actinomadura rugatobispora" /mol_type="genomic DNA" /strain="IFO 14382" /db_xref="taxon:1994" 1. .1406 /product="16S ribosomal RNA"									
	Query Match	85.5%;	Score 18.8;	DB 15;	Length 1406;					
	Best Local Similarity	90.9%;	Pred. No. 7.7e+02;							
	Matches	20;	Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;			
	QY	1	GAAGGCGCTTTCGGGGTGCTC 22							
	Db	13	GAAGGCCCTTCGGGGTACTC 34							
	RESULT 74									
	ARU49010									
	LOCUS	Actinomadura rugatobispora	1406 bp	DNA	linear	BCT 08-MAY-1996				
REFERENCE AUTHORS TITLE JOURNAL FEATURES source rRNA ORIGIN	Actinomadura rugatobispora Actinomadura rugatobispora Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptosporangineae; Thermomonosporaceae; Actinomadura. Wang,Y. Phylogenetic analysis of Actinomadura species Thesis (1996) Institute of Molecular and Cell Biology, National University of Singapore 2 (bases 1 to 1406) Direct Submission Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell Biology, National University of Singapore, 10 Kent Ridge Crescent, Singapore 0511, Singapore Location/Qualifiers 1. .1406 /organism="Actinomadura rugatobispora" /mol_type="genomic DNA" /strain="IFO 14382" /db_xref="taxon:1994" 1. .1406 /product="16S ribosomal RNA"									
	Query Match	85.5%;	Score 18.8;	DB 15;	Length 1406;					
	Best Local Similarity	90.9%;	Pred. No. 7.7e+02;							
	Matches	20;	Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;			
	QY	1	GAAGGCGCTTTCGGGGTGCTC 22							
	Db	13	GAAGGCCCTTCGGGGTACTC 34							
	RESULT 75									
	ARU49010									
	LOCUS	Actinomadura rugatobispora	1406 bp	DNA	linear	BCT 08-MAY-1996				

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RESULT 75
ACU49002
LOCUS          ACU49002          1409 bp      DNA          linear      BCT 08-MAY-1996
DEFINITION    Actinomadura coerulea 16S rRNA gene.
ACCESSION    U49002
VERSION      U49002.1  GI:1305434
KEYWORDS
SOURCE
ORGANISM      Actinomadura coerulea
               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
               Streptosporangineae; Thermomonosporaceae; Actinomadura.
REFERENCE
AUTHORS      Wang, Y.
TITLE        Phylogenetic analysis of Actinomadura species
JOURNAL      Thesis (1996) Institute of Molecular and Cell Biology, National
               University of Singapore
REFERENCE
AUTHORS      Wang, Y.
TITLE        Direct Submission
JOURNAL      Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
               Biology, National University of Singapore, 10 Kent Ridge Crescent,
               Singapore 0511, Singapore
FEATURES      source
               1. .1409
               /organism="Actinomadura coerulea"
               /mol_type="genomic DNA"
               /strain="IFO 14679"
               /db_xref="taxon:46159"
               1. .1409
               /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      85.5%; Score 18.8; DB 15; Length 1409;
Best Local Similarity 90.9%; Pred. No. 7.7e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1  GAAAGCCCTTCGGGGGTGCTC 22
      |||||
Db   13  GAAAGCCCTTCGGGGGTACTC 34

RESULT 76
MSU48983
LOCUS          MSU48983          1409 bp      DNA          linear      BCT 09-JUL-1997
DEFINITION    Microtetraspora spiralis 16S rRNA gene.
ACCESSION    U48983
VERSION      U48983.1  GI:2251228
KEYWORDS
SOURCE
ORGANISM      Nonomuraea spiralis
               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
               Streptosporangineae; Streptosporangiaceae; Nonomuraea.
REFERENCE
AUTHORS      Wang, Y.
TITLE        Phylogenetic analysis of Microtetraspora species
JOURNAL      Thesis (1996) Institute of Molecular and Cell Biology, National
               University of Singapore
REFERENCE
AUTHORS      Wang, Y., Zhang, Z., and Ruan, J.
TITLE        Phylogenetic analysis reveals new relationships among members of
               the genera Microtetraspora and Microbispora
JOURNAL      Int. J. Syst. Bacteriol. 46 (3), 658-663 (1996)
PUBMED      8782672
AUTHORS      Wang, Y.
TITLE        Direct Submission
JOURNAL      Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
               Biology, National University of Singapore, 10 Kent Ridge Crescent,
               Singapore 0511, Singapore
FEATURES      source
               1. .1409
               /organism="Nonomuraea spiralis"
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/mol_type="genomic DNA"
/strain="IFO 14097"
/db_xref="taxon:46182"
1. .1409
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      85.5%; Score 18.8; DB 15; Length 1409;
Best Local Similarity 90.9%; Pred. No. 7.7e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1  GAAAGCCCTTCGGGGGTGCTC 22
      |||||
Db   13  GAAAGCCCTTCGGGGGTACTC 34

RESULT 77
AKU49006
LOCUS          AKU49006          1409 bp      DNA          linear      BCT 08-MAY-1996
DEFINITION    Actinomadura kijaniata 16S rRNA gene.
ACCESSION    U49006
VERSION      U49006.1  GI:1305438
KEYWORDS
SOURCE
ORGANISM      Actinomadura kijaniata
               Actinomadura kijaniata
               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
               Streptosporangineae; Thermomonosporaceae; Actinomadura.
REFERENCE
AUTHORS      Wang, Y.
TITLE        Phylogenetic analysis of Actinomadura species
JOURNAL      Thesis (1996) Institute of Molecular and Cell Biology, National
               University of Singapore
REFERENCE
AUTHORS      Wang, Y.
TITLE        Direct Submission
JOURNAL      Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
               Biology, National University of Singapore, 10 Kent Ridge Crescent,
               Singapore 0511, Singapore
FEATURES      source
               1. .1409
               /organism="Actinomadura kijaniata"
               /mol_type="genomic DNA"
               /strain="IFO 14229"
               /db_xref="taxon:46161"
               1. .1409
               /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      85.5%; Score 18.8; DB 15; Length 1409;
Best Local Similarity 90.9%; Pred. No. 7.7e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1  GAAAGCCCTTCGGGGGTGCTC 22
      |||||
Db   13  GAAAGCCCTTCGGGGGTACTC 34

RESULT 78
ALU49008
LOCUS          ALU49008          1409 bp      DNA          linear      BCT 08-MAY-1996
DEFINITION    Actinomadura luteofluorescens 16S rRNA gene.
ACCESSION    U49008
VERSION      U49008.1  GI:1305440
KEYWORDS
SOURCE
ORGANISM      Actinomadura luteofluorescens
               Actinomadura luteofluorescens
               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
               Streptosporangineae; Thermomonosporaceae; Actinomadura.
REFERENCE
AUTHORS      Wang, Y.
TITLE        Phylogenetic analysis of Actinomadura species
JOURNAL      Thesis (1996) Institute of Molecular and Cell Biology, National
               University of Singapore
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REFERENCE 2 (bases 1 to 1409)
AUTHORS Wang, Y.
TITLE Direct Submission
JOURNAL Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
Biology, National University of Singapore, 10 Kent Ridge Crescent,
Singapore 0511, Singapore
FEATURES
source
1. .1409
/organism="Actinomadura luteofluorescens"
/mol_type="genomic DNA"
/strain="IFO 13057"
/db_xref="taxon:46163"
1. .1409
/product="16S ribosomal RNA"
ORIGIN
Query Match 85.5%; Score 18.8; DB 15; Length 1409;
Best Local Similarity 90.9%; Pred. No. 7.7e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GAAAGGCCTTCGGGGGTGCTC 22
|||||
Db 13 GAAAGGCCCTTCGGGGGTACTC 34

RESULT 79
ACU49001
LOCUS Actinomadura citrea 1410 bp DNA linear BCT 08-MAY-1996
DEFINITION Actinomadura citrea 16S rRNA gene.
ACCESSION U49001
VERSION U49001.1 GI:1305433
KEYWORDS
SOURCE
ORGANISM Actinomadura citrea
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Thermomonosporaceae; Actinomadura.
REFERENCE 1 (bases 1 to 1410)
AUTHORS Wang, Y.
TITLE Phylogenetic analysis of Actinomadura species
JOURNAL Thesis (1996) Institute of Molecular and Cell Biology, National
University of Singapore
REFERENCE 2 (bases 1 to 1410)
AUTHORS Wang, Y.
TITLE Direct Submission
JOURNAL Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
Biology, National University of Singapore, 10 Kent Ridge Crescent,
Singapore 0511, Singapore
FEATURES
source
1. .1410
/organism="Actinomadura citrea"
/mol_type="genomic DNA"
/strain="IFO 14678"
/db_xref="taxon:46158"
1. .1410
/product="16S ribosomal RNA"
ORIGIN
Query Match 85.5%; Score 18.8; DB 15; Length 1410;
Best Local Similarity 90.9%; Pred. No. 7.7e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GAAAGGCCTTCGGGGGTGCTC 22
|||||
Db 13 GAAAGGCCCTTCGGGGGTACTC 34

RESULT 80
ACU49003
LOCUS Actinomadura citrea 1410 bp DNA linear BCT 08-MAY-1996
DEFINITION Actinomadura citrea rifamycin 16S rRNA gene.
ACCESSION U49003
VERSION U49003.1 GI:1305435
KEYWORDS
SOURCE
ORGANISM Actinomadura citrea
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Streptosporangiaceae; Nonomuraea.
REFERENCE 1 (bases 1 to 1411)
AUTHORS Wang, Y.
TITLE Phylogenetic analysis of Microtetraspora species
JOURNAL Thesis (1996) Institute of Molecular and Cell Biology, National
University of Singapore
REFERENCE 2 (bases 1 to 1411)
AUTHORS Wang, Y.
TITLE Direct Submission
JOURNAL Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
Biology, National University of Singapore, 10 Kent Ridge Crescent,
Singapore 0511, Singapore
FEATURES
source
1. .1411
/organism="Nonomuraea angiospora"
/mol_type="genomic DNA"
/strain="IFO 13155"
/db_xref="taxon:46172"
1. .1411
/product="16S ribosomal RNA"
ORIGIN
Query Match 85.5%; Score 18.8; DB 15; Length 1411;
Best Local Similarity 90.9%; Pred. No. 7.7e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GAAAGGCCTTCGGGGGTGCTC 22
|||||
Db 13 GAAAGGCCCTTCGGGGGTACTC 34
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Db      13 GAAAGGCCCTTCGGGGTGACTC 34
RESULT 82
MHU48975
LOCUS      1411 bp      DNA      linear      BCT 09-JUL-1997
DEFINITION Microtetraspora helvata 16S rRNA gene.
ACCESSION  U48975
VERSION     U48975.1 GI:2251221
KEYWORDS
SOURCE
ORGANISM   Nonomuraea helvata
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Streptosporangineae; Streptosporangiaceae; Nonomuraea.
REFERENCE
AUTHORS    Wang, Y.
TITLE      Phylogenetic analysis of Microtetraspora species
JOURNAL    Thesis (1996) Institute of Molecular and Cell Biology, National
            University of Singapore
REFERENCE
AUTHORS    Wang, Y., Zhang, Z. and Ruan, J.
TITLE      Phylogenetic analysis reveals new relationships among members of
            the genera Microtetraspora and Microbispora
JOURNAL    Int. J. Syst. Bacteriol. 46 (3), 658-663 (1996)
PUBMED     8782672
REFERENCE
AUTHORS    Wang, Y.
TITLE      Direct Submission
JOURNAL    Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
            Biology, National University of Singapore, 10 Kent Ridge Crescent,
            Singapore 0511, Singapore
FEATURES
source
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            1..1411
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               /mol_type="genomic DNA"
               /strain="IFO 14681"
               /db_xref="taxon:37484"
            1..1411
               /product="16S ribosomal RNA"
ORIGIN
Query Match      85.5%; Score 18.8; DB 15; Length 1411;
Best Local Similarity 90.9%; Pred. No. 7.7e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      1 GAAAGGCCCTTCGGGGTGCTC 22
        ||||| ||||| ||||| |||||
DB      13 GAAAGGCCCTTCGGGGTGACTC 34
RESULT 83
AVU49011
LOCUS      1411 bp      DNA      linear      BCT 08-MAY-1996
DEFINITION Actinomadura verrucospora 16S rRNA gene.
ACCESSION  U49011
VERSION     U49011.1 GI:1305443
KEYWORDS
SOURCE
ORGANISM   Actinomadura verrucospora
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Streptosporangineae; Thermomonosporaceae; Actinomadura.
REFERENCE
AUTHORS    Wang, Y.
TITLE      Phylogenetic analysis of Actinomadura species
JOURNAL    Thesis (1996) Institute of Molecular and Cell Biology, National
            University of Singapore
REFERENCE
AUTHORS    Wang, Y.
TITLE      Direct Submission
JOURNAL    Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
            Biology, National University of Singapore, 10 Kent Ridge Crescent,
            Singapore 0511, Singapore
FEATURES
source
            Location/Qualifiers
            1..1411
               /organism="Actinomadura verrucospora"
               /mol_type="genomic DNA"
               /strain="IFO 14680"
               /db_xref="taxon:46173"
               /clone="16S rRNA gene"
            1..1412
               /product="16S ribosomal RNA"
ORIGIN
Query Match      85.5%; Score 18.8; DB 15; Length 1412;
Best Local Similarity 90.9%; Pred. No. 7.7e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      1 GAAAGGCCCTTCGGGGTGCTC 22
        ||||| ||||| ||||| |||||
DB      13 GAAAGGCCCTTCGGGGTGACTC 34
RESULT 84
MFU48844
LOCUS      1412 bp      DNA      linear      BCT 08-MAY-1996
DEFINITION Microtetraspora fastidiosa 16S rRNA gene.
ACCESSION  U48844
VERSION     U48844.1 GI:1305421
KEYWORDS
SOURCE
ORGANISM   Nonomuraea fastidiosa
            Nonomuraea fastidiosa
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Streptosporangineae; Streptosporangiaceae; Nonomuraea.
REFERENCE
AUTHORS    Wang, Y.
TITLE      Phylogenetic analysis of Microtetraspora species
JOURNAL    Thesis (1996) Institute of Molecular and Cell Biology, National
            University of Singapore
REFERENCE
AUTHORS    Wang, Y.
TITLE      Direct Submission
JOURNAL    Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
            Biology, National University of Singapore, 10 Kent Ridge Crescent,
            Singapore 0511, Singapore
FEATURES
source
            Location/Qualifiers
            1..1412
               /organism="Nonomuraea fastidiosa"
               /mol_type="genomic DNA"
               /strain="IFO 14680"
               /db_xref="taxon:46173"
               /clone="16S rRNA gene"
            1..1412
               /product="16S ribosomal RNA"
ORIGIN
Query Match      85.5%; Score 18.8; DB 15; Length 1411;
Best Local Similarity 90.9%; Pred. No. 7.7e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      1 GAAAGGCCCTTCGGGGTGCTC 22
        ||||| ||||| ||||| |||||
DB      13 GAAAGGCCCTTCGGGGTGACTC 34
RESULT 85
MAU48842
LOCUS      1413 bp      DNA      linear      BCT 08-MAY-1996
DEFINITION Microtetraspora africana 16S rRNA gene.
ACCESSION  U48842
VERSION     U48842.1 GI:1305419
KEYWORDS
SOURCE
ORGANISM   Nonomuraea africana
            Nonomuraea africana
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Streptosporangineae; Streptosporangiaceae; Nonomuraea.
REFERENCE
AUTHORS    Wang, Y.
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TITLE      Phylogenetic analysis of Microtetraspora species
JOURNAL    Thesis (1996) Institute of Molecular and Cell Biology, National
REFERENCE  2 (bases 1 to 1413)
AUTHORS    Wang, Y.
TITLE      Direct Submission
JOURNAL    Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
          Biology, National University of Singapore, 10 Kent Ridge Crescent,
          Singapore 0511, Singapore
FEATURES   Location/Qualifiers
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              1..1413
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              /mol_type="genomic DNA"
              /strain="IFO 14745"
              /db_xref="taxon:46171"
              1..1413
              /product="16S ribosomal RNA"

ORIGIN
Query Match      85.5%; Score 18.8; DB 15; Length 1413;
Best Local Similarity 90.9%; Pred. No. 7.7e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GAAAGGCTTTCGGGGTGCTC 22
        ||||| ||||| ||||| ||||| |||||
Db      13 GAAAGGCTTTCGGGGTGACTC 34

RESULT 86
MDU48990
LOCUS      Microbispora diastatica 1413 bp DNA linear BCT 08-MAY-1996
DEFINITION Microbispora diastatica 16S rRNA gene.
ACCESSION U48990
VERSION   U48990.1 GI:1305428
KEYWORDS
SOURCE    Microbispora rosea subsp. rosea
          Microbispora rosea subsp. rosea
          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Streptosporangiaceae; Streptosporangiaceae; Microbispora.
REFERENCE 1 (bases 1 to 1413)
AUTHORS    Wang, Y.
TITLE      Direct Submission
JOURNAL    Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
          Biology, National University of Singapore, 10 Kent Ridge Crescent,
          Singapore 0511, Singapore
FEATURES   Location/Qualifiers
            source
              1..1413
              /organism="Microbispora rosea subsp. rosea"
              /mol_type="genomic DNA"
              /strain="IFO 14041"
              /db_xref="taxon:58118"
              1..1413
              /product="16S ribosomal RNA"

ORIGIN
Query Match      85.5%; Score 18.8; DB 15; Length 1413;
Best Local Similarity 90.9%; Pred. No. 7.7e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GAAAGGCTTTCGGGGTGCTC 22
        ||||| ||||| ||||| ||||| |||||
Db      13 GAAAGGCTTTCGGGGTGACTC 34

RESULT 87
MPU48977
LOCUS      Microtetraspora polychroma 1413 bp DNA linear BCT 09-JUL-1997
DEFINITION Microtetraspora polychroma 16S rRNA gene.
ACCESSION U48977
VERSION   U48977.1 GI:2251225
KEYWORDS
SOURCE    Nonomuraea recticatena
          Nonomuraea recticatena
          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Streptosporangiaceae; Streptosporangiaceae; Nonomuraea.
REFERENCE 1 (bases 1 to 1413)
AUTHORS    Wang, Y.
TITLE      Phylogenetic analysis of Microtetraspora species
JOURNAL    Thesis (1996) Institute of Molecular and Cell Biology, National
          University of Singapore
          Wang, Y., Zhang, Z. and Ruan, J.
          Phylogenetic analysis reveals new relationships among members of
          the genera Microtetraspora and Microbispora
          Int. J. Syst. Bacteriol. 46 (3), 658-663 (1996)
PUBMED    8782672
AUTHORS    Wang, Y.
TITLE      Direct Submission
JOURNAL    Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
          Biology, National University of Singapore, 10 Kent Ridge Crescent,
          Singapore 0511, Singapore
FEATURES   Location/Qualifiers
            source
              1..1413

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ACCESSION U48977
VERSION   U48977.1 GI:2251223
KEYWORDS
SOURCE    Nonomuraea polychroma
          Nonomuraea polychroma
          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Streptosporangiaceae; Streptosporangiaceae; Nonomuraea.
REFERENCE 1 (bases 1 to 1413)
AUTHORS    Wang, Y.
TITLE      Phylogenetic analysis of Microtetraspora species
JOURNAL    Thesis (1996) Institute of Molecular and Cell Biology, National
          University of Singapore
          Wang, Y., Zhang, Z. and Ruan, J.
          Phylogenetic analysis reveals new relationships among members of
          the genera Microtetraspora and Microbispora
          Int. J. Syst. Bacteriol. 46 (3), 658-663 (1996)
PUBMED    8782672
AUTHORS    Wang, Y.
TITLE      Direct Submission
JOURNAL    Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
          Biology, National University of Singapore, 10 Kent Ridge Crescent,
          Singapore 0511, Singapore
FEATURES   Location/Qualifiers
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              1..1413
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              /mol_type="genomic DNA"
              /strain="IFO 14345"
              /db_xref="taxon:46176"
              1..1413
              /product="16S ribosomal RNA"

ORIGIN
Query Match      85.5%; Score 18.8; DB 15; Length 1413;
Best Local Similarity 90.9%; Pred. No. 7.7e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GAAAGGCTTTCGGGGTGCTC 22
        ||||| ||||| ||||| ||||| |||||
Db      13 GAAAGGCTTTCGGGGTGACTC 34

RESULT 88
MRU48979
LOCUS      Microtetraspora recticatena 1413 bp DNA linear BCT 09-JUL-1997
DEFINITION Microtetraspora recticatena 16S rRNA gene.
ACCESSION U48979
VERSION   U48979.1 GI:2251225
KEYWORDS
SOURCE    Nonomuraea recticatena
          Nonomuraea recticatena
          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Streptosporangiaceae; Streptosporangiaceae; Nonomuraea.
REFERENCE 1 (bases 1 to 1413)
AUTHORS    Wang, Y.
TITLE      Phylogenetic analysis of Microtetraspora species
JOURNAL    Thesis (1996) Institute of Molecular and Cell Biology, National
          University of Singapore
          Wang, Y., Zhang, Z. and Ruan, J.
          Phylogenetic analysis reveals new relationships among members of
          the genera Microtetraspora and Microbispora
          Int. J. Syst. Bacteriol. 46 (3), 658-663 (1996)
PUBMED    8782672
AUTHORS    Wang, Y.
TITLE      Direct Submission
JOURNAL    Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
          Biology, National University of Singapore, 10 Kent Ridge Crescent,
          Singapore 0511, Singapore
FEATURES   Location/Qualifiers
            source
              1..1413

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QY 1 GAAAGGCCTTTCGGGGTGCTC 22
    ||||| ||||| ||||| |||||
Db 13 GAAAGGCCTTTCGGGGTGACTC 34

RESULT 92
MPU48985
LOCUS Microbispora parva 16S rRNA gene. BCT 08-MAY-1996
DEFINITION
ACCESSION U48985
VERSION U48985.1 GI:1305429
KEYWORDS
SOURCE Microbispora rosea subsp. rosea
ORGANISM Microbispora rosea subsp. rosea
          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Streptosporangineae; Streptosporangiaceae; Microbispora.
          Wang, Y.
REFERENCE Phylogenetic analysis of Microbispora species
AUTHORS Thesis (1996) Institute of Molecular and Cell Biology, National
JOURNAL University of Singapore
          2 (bases 1 to 1414)
REFERENCE Wang, Y.
AUTHORS Direct Submission
JOURNAL Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
          Biology, National University of Singapore, 10 Kent Ridge Crescent,
          Singapore 0511, Singapore
FEATURES
    source Location/Qualifiers
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            /mol_type="genomic DNA"
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rRNA

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    Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTCGGGGTGCTC 22
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Db 13 GAAAGGCCTTTCGGGGTGACTC 34

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LOCUS Microbispora thermorosea 16S rRNA gene. linear BCT 08-MAY-1996
DEFINITION
ACCESSION U48987
VERSION U48987.1 GI:1305431
KEYWORDS
SOURCE Microbispora rosea subsp. aerata
ORGANISM Microbispora rosea subsp. aerata
          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Streptosporangineae; Streptosporangiaceae; Microbispora.
          Wang, Y.
REFERENCE Phylogenetic analysis of Microbispora species
AUTHORS Thesis (1996) Institute of Molecular and Cell Biology, National
JOURNAL University of Singapore
          2 (bases 1 to 1414)
REFERENCE Wang, Y.
AUTHORS Direct Submission
JOURNAL Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
          Biology, National University of Singapore, 10 Kent Ridge Crescent,
          Singapore 0511, Singapore
FEATURES
    source Location/Qualifiers
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rRNA

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Db 13 GAAAGGCCTTTCGGGGTGACTC 34

RESULT 95
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LOCUS Microbispora aerata 16S rRNA gene. linear BCT 08-MAY-1996
DEFINITION
ACCESSION U48984
VERSION U48984.1 GI:1305425
KEYWORDS
SOURCE Microbispora rosea subsp. aerata
ORGANISM Microbispora rosea subsp. aerata
          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Streptosporangineae; Streptosporangiaceae; Microbispora.
          Wang, Y.
REFERENCE Phylogenetic analysis of Microbispora species
AUTHORS Thesis (1996) Institute of Molecular and Cell Biology, National
JOURNAL University of Singapore
          2 (bases 1 to 1414)
REFERENCE Wang, Y., Zhang, Z., and Ruan, J.
AUTHORS Phylogenetic analysis reveals new relationships among members of
          the genera Microtetraspora and Microbispora
JOURNAL Int. J. Syst. Bacteriol. 46 (3), 658-663 (1996)
PUBMED 8782672
REFERENCE Wang, Y.
AUTHORS Direct Submission
JOURNAL Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell

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REFERENCE 1 (bases 1 to 1415)
AUTHORS Wang,Y.
TITLE Phylogenetic analysis of Microbispora species
JOURNAL Thesis (1996) Institute of Molecular and Cell Biology, National
University of Singapore
REFERENCE 2 (bases 1 to 1415)
AUTHORS Wang,Y.
TITLE Direct Submission
JOURNAL Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
Biology, National University of Singapore, 10 Kent Ridge Crescent,
Singapore 0511, Singapore
FEATURES
source
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rRNA

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Best Local Similarity 90.9%; Pred. No. 7.7e+02;
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Db 13 GAAAGGCCCTTCGGGGGTACTC 34

RESULT 96
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DEFINITION Microtetraspora ferruginea 16S rRNA gene.
ACCESSION U48845
VERSION U48845.1 GI:1305422
KEYWORDS
SOURCE Nonomuraea ferruginea
ORGANISM Nonomuraea ferruginea
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Streptosporangiaceae; Nonomuraea.
REFERENCE 1 (bases 1 to 1415)
AUTHORS Wang,Y.
TITLE Phylogenetic analysis of Microtetraspora species
JOURNAL Thesis (1996) Institute of Molecular and Cell Biology, National
University of Singapore
REFERENCE 2 (bases 1 to 1415)
AUTHORS Wang,Y.
TITLE Direct Submission
JOURNAL Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
Biology, National University of Singapore, 10 Kent Ridge Crescent,
Singapore 0511, Singapore
FEATURES
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/mol_type="genomic DNA"
/strain="IFO 14094"
/db_xref="taxon:46174"
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/product="16S ribosomal RNA"

rRNA

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Best Local Similarity 90.9%; Pred. No. 7.7e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 97
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DEFINITION Actinomadura fulvescens 16S rRNA gene.
ACCESSION U49005
VERSION U49005.1 GI:1305437
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SOURCE Actinomadura fulvescens
ORGANISM Actinomadura fulvescens
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Thermomonosporaceae; Actinomadura.
REFERENCE 1 (bases 1 to 1415)
AUTHORS Wang,Y.
TITLE Phylogenetic analysis of Actinomadura species
JOURNAL Thesis (1996) Institute of Molecular and Cell Biology, National
University of Singapore
REFERENCE 2 (bases 1 to 1415)
AUTHORS Wang,Y.
TITLE Direct Submission
JOURNAL Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
Biology, National University of Singapore, 10 Kent Ridge Crescent,
Singapore 0511, Singapore
FEATURES
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rRNA

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Db 13 GAAAGGCCCTTCGGGGGTACTC 34

RESULT 98
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DEFINITION Microtetraspora glauca 16S rRNA gene.
ACCESSION U48974
VERSION U48974.1 GI:2251220
KEYWORDS
SOURCE Microtetraspora glauca
ORGANISM Microtetraspora glauca
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Streptosporangiaceae; Microtetraspora.
REFERENCE 1 (bases 1 to 1416)
AUTHORS Wang,Y.
TITLE Phylogenetic analysis of Microtetraspora species
JOURNAL Thesis (1996) Institute of Molecular and Cell Biology, National
University of Singapore
REFERENCE 2 (bases 1 to 1416)
AUTHORS Wang,Y., Zhang,Z. and Ruan,J.
TITLE Phylogenetic analysis reveals new relationships among members of
the genera Microtetraspora and Microbispora
JOURNAL Int. J. Syst. Bacteriol. 46 (3), 658-663 (1996)
PUBMED 8782672
REFERENCE 3 (bases 1 to 1416)
AUTHORS Wang,Y.
TITLE Direct Submission
JOURNAL Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
Biology, National University of Singapore, 10 Kent Ridge Crescent,
Singapore 0511, Singapore
FEATURES
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DEFINITION	Microtetraspora niveoalba 16S rRNA gene.					
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VERSION	U48976.1 GI:2251222					
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ORGANISM	Microtetraspora niveoalba					
REFERENCE	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;					
	Streptosporangiinae; Streptosporangiaceae; Microtetraspora.					
AUTHORS	1 (bases 1 to 1416)					
	Wang, Y.					
TITLE	Phylogenetic analysis of Microtetraspora species					
JOURNAL	Thesis (1996) Institute of Molecular and Cell Biology, National University of Singapore					
REFERENCE	2 (bases 1 to 1416)					
	Wang, Y., Zhang, Z. and Ruan, J.					
AUTHORS	Phylogenetic analysis reveals new relationships among members of the Genera Microtetraspora and Microbispora					
TITLE	Int. J. Syst. Bacteriol. 46 (3), 658-663 (1996)					
JOURNAL	8782672					
PURNED	3 (bases 1 to 1416)					
REFERENCE	Wang, Y.					
	Direct Submission					
AUTHORS	Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell Biology, National University of Singapore, 10 Kent Ridge Crescent, Singapore 0511, Singapore					
JOURNAL	Location/Qualifiers					
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Db						
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DEFINITION	Microbispora thermodiastatica 16S rRNA gene.					
ACCESSION	U48986					
VERSION	U48986.1 GI:1305430					
KEYWORDS						
SOURCE	Microbispora rosea subsp. aerata					
ORGANISM	Microbispora rosea subsp. aerata					
REFERENCE	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;					
	Streptosporangiinae; Streptosporangiaceae; Microbispora.					
AUTHORS	1 (bases 1 to 1417)					
	Wang, Y.					

Phylogenetic analysis of Microbispora species		Thesis (1996) Institute of Molecular and Cell Biology, National University of Singapore		2 (bases 1 to 1417)		
REFERENCE	Wang, Y.		Direct Submission			
TITLE	Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell Biology, National University of Singapore, 10 Kent Ridge Crescent, Singapore 0511, Singapore					
JOURNAL	Location/Qualifiers					
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Db						
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Job time : 785.072 secs						

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 02:23:06 ; Search time 664.199 Seconds
(without alignments)
1829.273 Million cell updates/sec

Title: US-10-665-708-24

Perfect score: 19

Sequence: 1 gaacggaagccttcgg 19

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

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2: gb_pat:*

3: gb_ph:*

4: gb_pl:*

5: gb_pr:*

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12: gb_htg:*

13: gb_in:*

14: gb_cm:*

15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	19	100.0	19	2	AX166858 Sequence
3	19	100.0	22	2	AR438655 Sequence
4	19	100.0	22	2	AX166857 Sequence
5	19	100.0	541	15	AF547926 Mycobacte
6	19	100.0	1456	15	X55594 M.gadium 16
7	19	100.0	1459	15	X53896 Mycobacteri
8	18	94.7	24	2	AR438654 Sequence
9	18	94.7	24	2	AX166856 Sequence
10	18	94.7	25	2	AR438653 Sequence
11	18	94.7	25	2	AX166855 Sequence
12	18	94.7	1460	15	MSGRGDSA L08169 Mycobacteri
13	18	94.7	1479	15	MSGRGDSA L08170 Mycobacteri
14	17.4	91.6	25	2	AX245066 Sequence
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18	17.4	91.6	171	15	AF059795 Mycobacte

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22	17.4	91.6	171	15	AF059833	AF059833 Mycobacte
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26	17.4	91.6	171	15	AF059841	AF059841 Mycobacte
27	17.4	91.6	171	15	AF059851	AF059851 Mycobacte
28	17.4	91.6	171	15	AF059852	AF059852 Mycobacte
29	17.4	91.6	172	15	AF059793	AF059793 Mycobacte
30	17.4	91.6	268	15	MSGRR16S	M95469 Mycobacteri
31	17.4	91.6	283	1	MSP404591	AJ404591 Unculture
32	17.4	91.6	316	15	MF16SRRN	Y09325 M.fortuitum
33	17.4	91.6	384	15	DQ063127	DQ063127 Actinobac
34	17.4	91.6	388	1	AY395145	AY395145 Unculture
35	17.4	91.6	393	1	BSSMKN23	X78659 Bacterium s
36	17.4	91.6	384	1	AY395154	AY395154 Unculture
37	17.4	91.6	395	1	AY043901	AY043901 Unculture
38	17.4	91.6	395	1	AY395151	AY395151 Unculture
39	17.4	91.6	396	1	BSSMKN14	X78655 Bacterium s
40	17.4	91.6	400	1	DQ221681	DQ221681 Unculture
41	17.4	91.6	401	15	DQ063065	DQ063065 Actinobac
42	17.4	91.6	403	15	AY234665	AY234665 Bacterium
43	17.4	91.6	407	15	AY792017	AY792017 Mycobacte
44	17.4	91.6	410	1	BSSMKN12	X78654 Bacterium s
45	17.4	91.6	411	15	DQ063154	DQ063154 Actinobac
46	17.4	91.6	411	15	DQ063199	DQ063199 Actinobac
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49	17.4	91.6	414	1	DQ223051	DQ223051 Unculture
50	17.4	91.6	415	15	DQ063108	DQ063108 Actinobac
51	17.4	91.6	416	1	AM085786	AM085786 Unculture
52	17.4	91.6	416	15	DQ063074	DQ063074 Actinobac
53	17.4	91.6	417	15	DQ063073	DQ063073 Actinobac
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57	17.4	91.6	421	1	AM085770	AM085770 Unculture
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66	17.4	91.6	425	1	AY394635	AY394635 Unculture
67	17.4	91.6	426	15	AY673136	AY673136 Mycobacte
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69	17.4	91.6	428	15	DQ063058	DQ063058 Actinobac
70	17.4	91.6	430	15	AJ786822	AJ786822 Mycobacte
71	17.4	91.6	430	15	AY673202	AY673202 Mycobacte
72	17.4	91.6	431	15	AB106919	AB106919 Gram-posi
73	17.4	91.6	432	1	AF078232	AF078232 Grassland
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75	17.4	91.6	433	15	AY673266	AY673266 Mycobacte
76	17.4	91.6	435	15	DQ063195	DQ063195 Actinobac
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79	17.4	91.6	436	15	DQ063046	DQ063046 Actinobac
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85	17.4	91.6	444	15	AY306205	AY306205 Mycobacte
86	17.4	91.6	445	15	AB106917	AB106917 Gram-posi
87	17.4	91.6	445	15	DQ067466	DQ067466 Mycobacte
88	17.4	91.6	447	1	AY957708	AY957708 Unculture
89	17.4	91.6	450	15	MS91016SR	Y08205 Mycobacteri
90	17.4	91.6	450	15	MSPI6SR	Y07954 Mycobacteri
91	17.4	91.6	450	15	AY358002	AY358002 Actinobac

92	17.4	91.6	454	15	AJ746062	AJ746062 Mycobacte	165	17.4	91.6	512	15	AY215272	AY215272 Mycobacte
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95	17.4	91.6	459	15	AY754884	Mycobacte	168	17.4	91.6	513	15	AY215273	AY215273 Mycobacte
96	17.4	91.6	459	15	AY754885	Mycobacte	169	17.4	91.6	514	15	AY215276	AY215276 Mycobacte
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98	17.4	91.6	464	15	DQ142669	Mycobacte	171	17.4	91.6	519	15	AJ746067	AJ746067 Mycobacte
99	17.4	91.6	464	15	DQ142672	Mycobacte	172	17.4	91.6	530	1	AY725810	AY725810 Unculture
100	17.4	91.6	465	15	DQ067465	Mycobacte	173	17.4	91.6	530	15	AY039507	AY039507 Soil bact
101	17.4	91.6	465	15	AY524839	Mycobacte	174	17.4	91.6	532	15	DQ144114	DQ144114 Mycobacte
102	17.4	91.6	467	15	MF10955	Mycobacte	175	17.4	91.6	532	15	AJ146908	AJ146908 Mycobacte
103	17.4	91.6	468	15	DQ154332	Soil bact	176	17.4	91.6	535	1	AY148216	AY148216 Unculture
104	17.4	91.6	473	1	AY043719	Unculture	177	17.4	91.6	537	15	AY943209	AY943209 Mycobacte
105	17.4	91.6	474	1	DQ136108	Unculture	178	17.4	91.6	540	15	AF547892	AF547892 Mycobacte
106	17.4	91.6	474	15	AY792024	Mycobacte	179	17.4	91.6	540	15	AF547895	AF547895 Mycobacte
107	17.4	91.6	476	15	AY559432	Mycobacte	180	17.4	91.6	540	15	AF547909	AF547909 Mycobacte
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109	17.4	91.6	481	15	MSP413603	Mycobacte	182	17.4	91.6	540	15	AF547911	AF547911 Mycobacte
110	17.4	91.6	495	15	AY943206	Mycobacte	183	17.4	91.6	540	15	AF547912	AF547912 Mycobacte
111	17.4	91.6	496	1	DQ154344	Unculture	184	17.4	91.6	540	15	AF547916	AF547916 Mycobacte
112	17.4	91.6	498	15	AY215287	Mycobacte	185	17.4	91.6	540	15	AF547920	AF547920 Mycobacte
113	17.4	91.6	498	15	AY215334	Mycobacte	186	17.4	91.6	540	15	AF547921	AF547921 Mycobacte
114	17.4	91.6	498	15	AY215336	Mycobacte	187	17.4	91.6	540	15	AF547923	AF547923 Mycobacte
115	17.4	91.6	499	1	DQ154566	Unculture	188	17.4	91.6	540	15	AF547924	AF547924 Mycobacte
116	17.4	91.6	499	15	DQ154328	Soil bact	189	17.4	91.6	540	15	AF547925	AF547925 Mycobacte
117	17.4	91.6	499	15	AY215236	Mycobacte	190	17.4	91.6	540	15	AF547929	AF547929 Mycobacte
118	17.4	91.6	500	1	UEU233561	unculture	191	17.4	91.6	540	15	AF547936	AF547936 Mycobacte
119	17.4	91.6	500	15	AF498660	Mycobacte	192	17.4	91.6	540	15	AF547944	AF547944 Mycobacte
120	17.4	91.6	500	15	AF498661	Mycobacte	193	17.4	91.6	540	15	AF547949	AF547949 Mycobacte
121	17.4	91.6	500	15	AY162027	Mycobacte	194	17.4	91.6	540	15	AF547950	AF547950 Mycobacte
122	17.4	91.6	500	15	AY162030	Mycobacte	195	17.4	91.6	540	15	AF547951	AF547951 Mycobacte
123	17.4	91.6	500	15	AY215218	Mycobacte	196	17.4	91.6	540	15	AF547954	AF547954 Mycobacte
124	17.4	91.6	500	15	AY215228	Mycobacte	197	17.4	91.6	540	15	AF547955	AF547955 Mycobacte
125	17.4	91.6	500	15	AY215234	Mycobacte	198	17.4	91.6	540	15	AF547956	AF547956 Mycobacte
126	17.4	91.6	500	15	AY215235	Mycobacte	199	17.4	91.6	540	15	AF547958	AF547958 Mycobacte
127	17.4	91.6	500	15	AY215237	Mycobacte	200	17.4	91.6	540	15	AF547961	AF547961 Mycobacte
128	17.4	91.6	500	15	AY215240	Mycobacte	201	17.4	91.6	540	15	AF547963	AF547963 Mycobacte
129	17.4	91.6	500	15	AY215245	Mycobacte	202	17.4	91.6	540	15	AF547964	AF547964 Mycobacte
130	17.4	91.6	500	15	AY215247	Mycobacte	203	17.4	91.6	540	15	AF547972	AF547972 Mycobacte
131	17.4	91.6	500	15	AY215251	Mycobacte	204	17.4	91.6	540	15	AF547981	AF547981 Mycobacte
132	17.4	91.6	500	15	AY215252	Mycobacte	205	17.4	91.6	540	15	AY438068	AY438068 Mycobacte
133	17.4	91.6	500	15	AY215266	Mycobacte	206	17.4	91.6	540	15	AY438071	AY438071 Mycobacte
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142	17.4	91.6	500	15	AY215293	Mycobacte	215	17.4	91.6	551	1	AY725804	AY725804 Unculture
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144	17.4	91.6	500	15	AY215316	Mycobacte	217	17.4	91.6	552	15	AY438074	AY438074 Mycobacte
145	17.4	91.6	500	15	AY215320	Mycobacte	218	17.4	91.6	568	15	AY039481	AY039481 Soil bact
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148	17.4	91.6	500	15	AY215346	Mycobacte	221	17.4	91.6	611	1	DQ149896	DQ149896 Unculture
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151	17.4	91.6	501	15	AF498655	Mycobacte	224	17.4	91.6	619	1	AY242619	AY242619 Unculture
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158	17.4	91.6	503	15	AY215227	Mycobacte	231	17.4	91.6	660	1	AY242620	AY242620 Unculture
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160	17.4	91.6	503	15	AY215250	Mycobacte	233	17.4	91.6	685	1	AY881659	AY881659 Unculture
161	17.4	91.6	508	1	DQ154443	Unculture	234	17.4	91.6	737	1	AY154573	AY154573 Unculture
162	17.4	91.6	508	15	AY148214	Mycobacte	235	17.4	91.6	740	1	AF145831	AF145831 Metal-con
163	17.4	91.6	509	15	AY215212	Mycobacte	236	17.4	91.6	749	15	AJ784807	AJ784807 Mycobacte
164	17.4	91.6	511	15	AY039467	Earthworm	237	17.4	91.6	761	15	AJ746066	AJ746066 Mycobacte

238 17.4 91.6 761 15 AJ746076
239 17.4 91.6 773 15 AJ746072
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244 17.4 91.6 815 15 AJ746064
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270 17.4 91.6 1326 15 AF316618
271 17.4 91.6 1331 15 AF054278
272 17.4 91.6 1331 15 AY943386
273 17.4 91.6 1360 15 MSGRDQ
274 17.4 91.6 1362 15 AY897829
275 17.4 91.6 1362 15 AY786470
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288 17.4 91.6 1394 15 AF387803
289 17.4 91.6 1395 15 AF408960
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291 17.4 91.6 1399 15 AF408990
292 17.4 91.6 1399 15 AJ849466
293 17.4 91.6 1400 15 AM056051
294 17.4 91.6 1413 15 AF408993
295 17.4 91.6 1418 15 DQ370011
296 17.4 91.6 1418 15 AF284430
297 17.4 91.6 1420 15 AF409022
298 17.4 91.6 1422 15 DQ370010
299 17.4 91.6 1422 15 MFU441307
300 17.4 91.6 1422 15 AY234735

ALIGNMENTS

RESULT 1
AR438656 AR438656 19 bp DNA linear PAT 20-FEB-2004
LOCUS
DEFINITION Sequence 24 from patent US 6664081.
ACCESSION AR438656

VERSION AR438656.1 GI:42663580
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Brentano, S.T., Jucker, M.T., Delgado, F.D., Cleuziat, P. and
Rodrigue, M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: US 6664081-A 24 16-DEC-2003;
FEATURES Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA
source Location/Qualifiers
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/mol_type="genomic DNA"
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Best Local Similarity 100.0%; Pred. No. 1.5e+03;
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QY 1 GAACGGAAAGGCCTTCGG 19
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Db 1 GAACGGAAAGGCCTTCGG 19
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RESULT 2
LOCUS AX166858 19 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 24 from Patent WO0144510.
ACCESSION AX166858
VERSION AX166858.1 GI:14596461
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Brentano, S.T., Jucker, M.T., Delgado, F.D., Cleuziat, P. and
Rodrigue, M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: WO 0144510-A 24 21-JUN-2001;
FEATURES Gen-Probe Incorporated (US); Biomerieux S.A. (FR)
source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAACGGAAAGGCCTTCGG 19
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Db 1 GAACGGAAAGGCCTTCGG 19
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RESULT 3
LOCUS AR438655 22 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 23 from patent US 6664081.
ACCESSION AR438655
VERSION AR438655.1 GI:42663579
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Brentano, S.T., Jucker, M.T., Delgado, F.D., Cleuziat, P. and
Rodrigue, M.
TITLE Nucleic acid amplification and detection of mycobacterium species

JOURNAL Patent: US 6664081-A 23 16-DEC-2003;
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA

FEATURES
source
Location/Qualifiers
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/mol_type="genomic DNA"

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Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTTCGG 19
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Db 4 GAACGGAAGGCTTTTCGG 22
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RESULT 4
LOCUS AX166857 22 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 23 from Patent WO0144510.
ACCESSION AX166857
VERSION AX166857.1 GI:14596460
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Brenzano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
Rodrigue,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: WO 0144510-A 23 21-JUN-2001;
Gen-Probe Incorporated (US); Biomerieux S.A. (FR)

FEATURES
source
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTTCGG 19
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Db 4 GAACGGAAGGCTTTTCGG 22
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RESULT 5
AF547926 541 bp DNA linear BCT 24-JAN-2006
LOCUS Mycobacterium gadium strain CIP 105388 16S ribosomal RNA gene,
partial sequence.
DEFINITION
ACCESSION AF547926
VERSION AF547926.1 GI:27733750
KEYWORDS
SOURCE Mycobacterium gadium
ORGANISM Mycobacterium gadium
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1
AUTHORS Devulder,G., de Montclos,M.P. and Flandrois,J.P.
TITLE A multigene approach to phylogenetic analysis using the genus
Mycobacterium as a model
JOURNAL Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBMED 15653890
REFERENCE 2 (bases 1 to 541)
AUTHORS Devulder,G., Pichat,C. and Flandrois,J.P.
TITLE Direct Submission
JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,

FEATURES
source
Location/Qualifiers
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QY 1 GAACGGAAGGCTTTTCGG 19
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Db 21 GAACGGAAGGCTTTTCGG 39
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RESULT 6
MGAD16S 1456 bp DNA linear BCT 06-JUN-2003
LOCUS M.gadium 16S ribosomal RNA, part.
DEFINITION
ACCESSION X55594
VERSION X55594.1 GI:44291
KEYWORDS 16S ribosomal RNA.
SOURCE Mycobacterium gadium
ORGANISM Mycobacterium gadium
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1 (bases 1 to 1456)
AUTHORS Pitulle,C., Dorsch,M., Kazda,J., Wolters,J. and Stackebrandt,E.
TITLE Phylogeny of rapidly growing members of the genus Mycobacterium
JOURNAL Int. J. Syst. Bacteriol. 42 (3), 337-343 (1992)
PUBMED 1380284
REFERENCE 2 (bases 1 to 1456)
AUTHORS Wolters,J.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-1990) Wolters J., Institut fuer Allgemeine
Mikrobiologie der Universitaet, Biologiezentrum, Am Botanischen
Garten 1-9, 2300 Kiel 1

FEATURES
source
Location/Qualifiers
1. .1456
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/mol_type="genomic DNA"
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/db_xref="taxon:1794"
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/product="16S ribosomal RNA"

rRNA
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTTCGG 19
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Db 65 GAACGGAAGGCTTTTCGG 83
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RESULT 7
MC016S 1459 bp DNA linear BCT 11-JUN-2003
LOCUS Mycobacterium cookii partial 16S rRNA.
DEFINITION
ACCESSION X53896
VERSION X53896.1 GI:44201
KEYWORDS 16S ribosomal RNA; ribosomal RNA.
SOURCE Mycobacterium cookii
ORGANISM Mycobacterium cookii
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

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REFERENCE 1 (bases 1 to 1225)
AUTHORS Kazda,J., Stackebrandt,E., Smida,J., Minnikin,D.E., Daffe,M.,
          Parlett,J.H. and Pitullie,C.
TITLE Mycobacterium cookii sp. nov
JOURNAL Int. J. Syst. Bacteriol. 40 (3), 217-223 (1990)
PUBMED 1697763
REFERENCE 2 (bases 1 to 1459)
AUTHORS Stackebrandt,E.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-1990) Stackebrandt E
FEATURES
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xrna

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Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTTTCG 19
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Db 65 GAACGGAAGGCGCTTTTCG 83

RESULT 8
LOCUS AR438654 24 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 22 from patent US 6664081.
ACCESSION AR438654
VERSION AR438654.1 GI:42663578
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
          Rodrigue,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: US 6664081-A 22 16-DEC-2003;
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA
FEATURES
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Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTTTCG 18
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Db 7 GAACGGAAGGCGCTTTTCG 24

RESULT 9
LOCUS AX166856 24 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 22 from Patent WO0144510.
ACCESSION AX166856
VERSION AX166856.1 GI:14596459
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
          Rodrigue,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: WO 0144510-A 21 21-JUN-2001;
Gen-Probe Incorporated (US) ; Biomerieux S.A. (FR)
FEATURES
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TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: WO 0144510-A 22 21-JUN-2001;
Gen-Probe Incorporated (US) ; Biomerieux S.A. (FR)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 7 GAACGGAAGGCGCTTTTCG 24

RESULT 10
LOCUS AR438653 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 21 from patent US 6664081.
ACCESSION AR438653
VERSION AR438653.1 GI:42663577
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
          Rodrigue,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: US 6664081-A 21 16-DEC-2003;
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA
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RESULT 11
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DEFINITION Sequence 21 from Patent WO0144510.
ACCESSION AX166855
VERSION AX166855.1 GI:14596458
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
          Rodrigue,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: WO 0144510-A 21 21-JUN-2001;
Gen-Probe Incorporated (US) ; Biomerieux S.A. (FR)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 4.1e+03;
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Qy 1 GAACGGAAGGCGCTTCG 18
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Db 8 GAACGGAAGGCGCTTCG 25

RESULT 12
MSGRDSB
LOCUS MSGRDSB 1460 bp DNA linear BCT 21-SEP-1993
DEFINITION Mycobacterium celatum 16S ribosomal RNA gene.
ACCESSION L08169
VERSION L08169.1 GI:293249
KEYWORDS 16S ribosomal RNA.
SOURCE Mycobacterium celatum
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 1460)
AUTHORS Butler,W.R., O'Connor,S.P., Yakrus,M.A., Smithwick,R.W.,
Plikaytis,B.B., Moss,C.W., Floyd,M.M., Woodley,C.L., Kilburn,J.O.,
Vadney,F.S. and Gross,W.M.
TITLE Mycobacterium celatum sp. nov
JOURNAL Int. J. Syst. Bacteriol. 43 (3), 539-548 (1993)
PUBMED 8102246
COMMENT Original source text: Mycobacterium celatum (library: ATCC 51131)
DNA.
FEATURES
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/db_xref="taxon:28045"
/tissue_lib="ATCC 51131"
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/product="16S ribosomal RNA"
/note="putative"

rRNA

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Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 13
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LOCUS MSGRDSB 1479 bp DNA linear BCT 21-SEP-1993
DEFINITION Mycobacterium celatum 16S ribosomal RNA gene.
ACCESSION L08170
VERSION L08170.1 GI:293250
KEYWORDS 16S ribosomal RNA.
SOURCE Mycobacterium celatum
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 1479)
AUTHORS Butler,W.R., O'Connor,S.P., Yakrus,M.A., Smithwick,R.W.,
Plikaytis,B.B., Moss,C.W., Floyd,M.M., Woodley,C.L., Kilburn,J.O.,
Vadney,F.S. and Gross,W.M.
TITLE Mycobacterium celatum sp. nov
JOURNAL Int. J. Syst. Bacteriol. 43 (3), 539-548 (1993)
PUBMED 8102246
COMMENT Original source text: Mycobacterium celatum (library: ATCC 51130)
DNA.
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source Location/Qualifiers
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/db_xref="taxon:28045"
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rRNA

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Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTCG 19
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Db 36 GAACGGAAGGCGCTTCG 54

RESULT 14
AX245066
LOCUS AX245066 25 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 31 from Patent WO0166797.
ACCESSION AX245066
VERSION AX245066.1 GI:15859740
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Fischer,S.H., Rampal,J.B., Fahle,G.A. and Conville,P.S.
TITLE Multiplex hybridization system for identification of pathogenic
Mycobacterium and method of use
JOURNAL Patent: WO 0166797-A 31 13-SEP-2001;
THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US) ; Beckman Coulter,
Inc. (US)
FEATURES
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DEFINITION Sequence 33 from Patent WO0166797.
ACCESSION AX245068
VERSION AX245068.1 GI:15859742
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Fischer,S.H., Rampal,J.B., Fahle,G.A. and Conville,P.S.
TITLE Multiplex hybridization system for identification of pathogenic
Mycobacterium and method of use
JOURNAL Patent: WO 0166797-A 33 13-SEP-2001;
THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US) ; Beckman Coulter,
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DEFINITION	Mycobacterium chelonae isolate 95A8183 16S ribosomal RNA (rrs)
ACCESSION	AF059812
VERSION	GI:3132956
KEYWORDS	
SOURCE	Mycobacterium chelonae
ORGANISM	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE	1 (bases 1 to 171)
AUTHORS	Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.
TITLE	Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
JOURNAL	Genome Res. 8 (5), 435-448 (1998)
PUBLISHED	9582189
DEFINITION	1 (bases 1 to 171)
ACCESSION	AF059812
VERSION	GI:3132956
KEYWORDS	
SOURCE	Mycobacterium chelonae
ORGANISM	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE	1 (bases 1 to 171)
AUTHORS	Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.
TITLE	Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
JOURNAL	Genome Res. 8 (5), 435-448 (1998)
PUBLISHED	9582189
DEFINITION	2 (bases 1 to 171)
ACCESSION	AF059812
VERSION	GI:3132956
KEYWORDS	
SOURCE	Mycobacterium chelonae
ORGANISM	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE	1 (bases 1 to 171)
AUTHORS	Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.
TITLE	Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
JOURNAL	Genome Res. 8 (5), 435-448 (1998)
PUBLISHED	9582189
DEFINITION	3 (bases 1 to 171)
ACCESSION	AF059812
VERSION	GI:3132956
KEYWORDS	
SOURCE	Mycobacterium chelonae
ORGANISM	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE	1 (bases 1 to 171)
AUTHORS	Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.
TITLE	Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
JOURNAL	Genome Res. 8 (5), 435-448 (1998)
PUBLISHED	9582189
DEFINITION	4 (bases 1 to 171)
ACCESSION	AF059812
VERSION	GI:3132956
KEYWORDS	
SOURCE	Mycobacterium chelonae
ORGANISM	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE	1 (bases 1 to 171)
AUTHORS	Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.
TITLE	Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
JOURNAL	Genome Res. 8 (5), 435-448 (1998)
PUBLISHED	9582189
DEFINITION	5 (bases 1 to 171)
ACCESSION	AF059812
VERSION	GI:3132956
KEYWORDS	
SOURCE	Mycobacterium chelonae
ORGANISM	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE	1 (bases 1 to 171)
AUTHORS	Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.
TITLE	Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
JOURNAL	Genome Res. 8 (5), 435-448 (1998)
PUBLISHED	9582189
DEFINITION	6 (bases 1 to 171)
ACCESSION	AF059812
VERSION	GI:3132956
KEYWORDS	
SOURCE	Mycobacterium chelonae
ORGANISM	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE	1 (bases 1 to 171)
AUTHORS	Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.
TITLE	Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
JOURNAL	Genome Res. 8 (5), 435-448 (1998)
PUBLISHED	9582189
DEFINITION	7 (bases 1 to 171)
ACCESSION	AF059812
VERSION	GI:3132956
KEYWORDS	
SOURCE	Mycobacterium chelonae
ORGANISM	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE	1 (bases 1 to 171)
AUTHORS	Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.
TITLE	Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
JOURNAL	Genome Res. 8 (5), 435-448 (1998)
PUBLISHED	9582189
DEFINITION	8 (bases 1 to 171)
ACCESSION	AF059812
VERSION	GI:3132956
KEYWORDS	
SOURCE	Mycobacterium chelonae
ORGANISM	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE	1 (bases 1 to 171)
AUTHORS	Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.
TITLE	Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
JOURNAL	Genome Res. 8 (5), 435-448 (1998)
PUBLISHED	9582189
DEFINITION	9 (bases 1 to 171)
ACCESSION	AF059812
VERSION	GI:3132956
KEYWORDS	
SOURCE	Mycobacterium chelonae
ORGANISM	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE	1 (bases 1 to 171)
AUTHORS	Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.
TITLE	Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
JOURNAL	Genome Res. 8 (5), 435-448 (1998)
PUBLISHED	9582189
DEFINITION	10 (bases 1 to 171)
ACCESSION	AF059812
VERSION	GI:3132956
KEYWORDS	
SOURCE	Mycobacterium chelonae
ORGANISM	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE	1 (bases 1 to 171)
AUTHORS	Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.
TITLE	Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
JOURNAL	Genome Res. 8 (5), 435-448 (1998)
PUBLISHED	9582189
DEFINITION	11 (bases 1 to 171)
ACCESSION	AF059812
VERSION	GI:3

LOCUS AF059841 171 bp rRNA linear BCT 15-MAY-1998
 DEFINITION Mycobacterium chelonae isolate 95A9151 16S ribosomal RNA (rrs)
 gene, partial sequence.
 ACCESSION AF059841
 VERSION AF059841.1 GI:3132985
 KEYWORDS
 SOURCE Mycobacterium chelonae
 ORGANISM Mycobacterium chelonae
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 REFERENCE 1 (bases 1 to 171)
 AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
 TITLE Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
 JOURNAL Genome Res. 8 (5), 435-448 (1998)
 PUBMED 9582189
 REFERENCE 2 (bases 1 to 171)
 AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
 TITLE Direct Submission
 JOURNAL Submitted (16-APR-1998) Division of Infectious Disease, Affymetrix, 3380 Central Expressway, Santa Clara, CA 95051, USA
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 Qy 1 GAACGGAAGGCTTCGG 19
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 Db 5 GAACGGAAGGCTTCGG 23
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 RESULT 27
 AF059851 171 bp rRNA linear BCT 15-MAY-1998
 LOCUS Mycobacterium fortuitum strain ATCC6841 16S ribosomal RNA (rrs)
 DEFINITION gene, partial sequence.
 ACCESSION AF059851
 VERSION AF059851.1 GI:3132995
 KEYWORDS
 SOURCE Mycobacterium fortuitum
 ORGANISM Mycobacterium fortuitum
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 REFERENCE 1 (bases 1 to 171)
 AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
 TITLE Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
 JOURNAL Genome Res. 8 (5), 435-448 (1998)
 PUBMED 9582189
 REFERENCE 2 (bases 1 to 171)
 AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
 TITLE Direct Submission
 JOURNAL Submitted (16-APR-1998) Division of Infectious Disease, Affymetrix, 3380 Central Expressway, Santa Clara, CA 95051, USA
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 Db 5 GAACGGAAGGCTTCGG 23
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 LOCUS Mycobacterium fortuitum strain ATCC6841 16S ribosomal RNA (rrs)
 DEFINITION gene, partial sequence.
 ACCESSION AF059851
 VERSION AF059851.1 GI:3132995
 KEYWORDS
 SOURCE Mycobacterium fortuitum
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 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 REFERENCE 1 (bases 1 to 171)
 AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
 TITLE Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
 JOURNAL Genome Res. 8 (5), 435-448 (1998)
 PUBMED 9582189
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 AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
 TITLE Direct Submission
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 Db 5 GAACGGAAGGCTTCGG 23
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 RESULT 28
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 LOCUS Mycobacterium chelonae strain ATCC3752 16S ribosomal RNA (rrs)
 DEFINITION gene, partial sequence.
 ACCESSION AF059852
 VERSION AF059852.1 GI:3132996
 KEYWORDS
 SOURCE Mycobacterium chelonae
 ORGANISM Mycobacterium chelonae
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 REFERENCE 1 (bases 1 to 171)
 AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
 TITLE Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
 JOURNAL Genome Res. 8 (5), 435-448 (1998)
 PUBMED 9582189
 REFERENCE 2 (bases 1 to 171)
 AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
 TITLE Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
 JOURNAL Genome Res. 8 (5), 435-448 (1998)
 PUBMED 9582189
 REFERENCE 3 (bases 1 to 171)
 AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
 TITLE Direct Submission
 JOURNAL Submitted (16-APR-1998) Division of Infectious Disease, Affymetrix, 3380 Central Expressway, Santa Clara, CA 95051, USA
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 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GAACGGAAGGCTTCGG 19
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 Db 5 GAACGGAAGGCTTCGG 23
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 RESULT 28
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 LOCUS Mycobacterium chelonae strain ATCC3752 16S ribosomal RNA (rrs)
 DEFINITION gene, partial sequence.
 ACCESSION AF059852
 VERSION AF059852.1 GI:3132996
 KEYWORDS
 SOURCE Mycobacterium chelonae
 ORGANISM Mycobacterium chelonae
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 REFERENCE 1 (bases 1 to 171)
 AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
 TITLE Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
 JOURNAL Genome Res. 8 (5), 435-448 (1998)
 PUBMED 9582189
 REFERENCE 3 (bases 1 to 171)
 AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
 TITLE Direct Submission
 JOURNAL Submitted (16-APR-1998) Division of Infectious Disease, Affymetrix, 3380 Central Expressway, Santa Clara, CA 95051, USA
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PUBMED 9582189
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 AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
 TITLE Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
 JOURNAL Genome Res. 8 (5), 435-448 (1998)
 PUBMED 9582189
 REFERENCE 3 (bases 1 to 171)
 AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
 TITLE Direct Submission
 JOURNAL Submitted (16-APR-1998) Division of Infectious Disease, Affymetrix, 3380 Central Expressway, Santa Clara, CA 95051, USA
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 Best Local Similarity 94.7%; Pred. No. 3e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GAACGGAAGGCTTCGG 19
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 Db 5 GAACGGAAGGCTTCGG 23
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 RESULT 28
 AF059852 171 bp rRNA linear BCT 15-MAY-1998
 LOCUS Mycobacterium chelonae strain ATCC3752 16S ribosomal RNA (rrs)
 DEFINITION gene, partial sequence.
 ACCESSION AF059852
 VERSION AF059852.1 GI:3132996
 KEYWORDS
 SOURCE Mycobacterium chelonae
 ORGANISM Mycobacterium chelonae
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 REFERENCE 1 (bases 1 to 171)
 AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
 TITLE Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
 JOURNAL Genome Res. 8 (5), 435-448 (1998)
 PUBMED 9582189
 REFERENCE 2 (bases 1 to 171)
 AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
 TITLE Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays
 JOURNAL Genome Res. 8 (5), 435-448 (1998)
 PUBMED 9582189
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 AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
 TITLE Direct Submission
 JOURNAL Submitted (16-APR-1998) Division of Infectious Disease, Affymetrix, 3380 Central Expressway, Santa Clara, CA 95051, USA
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ORIGIN
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Best Local Similarity 94.7%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCTTCGG 19
Db 27 GAACGGAAGGCCTTCGG 45

RESULT 32
MF16SRRN
LOCUS      M.fortuitum 16S rRNA gene, partial.          316 bp      DNA      linear      BCT 14-NOV-1996
DEFINITION
ACCESSION  Y09325
VERSION    Y09325.1 GI:1669698
KEYWORDS   16S ribosomal RNA; rrr gene.
SOURCE     Mycobacterium fortuitum
ORGANISM   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE
AUTHORS    De Smet,K., Kampmann,B., Marshall,B., Kroll,S. and Levin,M.
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 316)
AUTHORS    De Smet,K.A.L.
TITLE      Direct Submission
JOURNAL    Submitted (08-NOV-1996) K.A.L. De Smet, Imperial College Medical
School at St Marys, Medical Microbiology, Norfolk Place, London, W2
1PG, UK

FEATURES
source      Location/Qualifiers
1. .316
/organism="Mycobacterium fortuitum"
/mol_type="genomic DNA"
/isolate="36718"
/db_xref="taxon:1766"
1. .316
/gene="rrn"
<1. .>316
/gene="rrn"
/product="16S ribosomal RNA"

gene
rRNA

ORIGIN
Query Match          91.6%; Score 17.4; DB 15; Length 316;
Best Local Similarity 94.7%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCTTCGG 19
Db 52 GAACGGAAGGCCTTCGG 70

RESULT 33
DQ063127
LOCUS      Actinobacterium BAL187 16S ribosomal RNA gene, partial sequence. 384 bp      DNA      linear      BCT 27-JUN-2005
DEFINITION
ACCESSION  DQ063127
VERSION    DQ063127.1 GI:68139160
KEYWORDS   actinobacterium BAL187
SOURCE     actinobacterium BAL187
ORGANISM   Bacteria; Actinobacteria.

REFERENCE
AUTHORS    Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.

/clone="MB1"
/tissue_type="Synovium"
1. .293
/gene="16S rRNA"
<1. .293
/gene="16S rRNA"
/product="16S ribosomal RNA"

ORIGIN
Query Match          91.6%; Score 17.4; DB 1; Length 293;
Best Local Similarity 94.7%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCTTCGG 19
Db 27 GAACGGAAGGCCTTCGG 45

RESULT 34
AY395145
LOCUS      Uncultured bacterium clone D29ST 16S ribosomal RNA gene, partial
sequence.          388 bp      DNA      linear      ENV 07-SEP-2004
DEFINITION
ACCESSION  AY395145
VERSION    AY395145.1 GI:37595660
KEYWORDS   ENV.
SOURCE     uncultured bacterium
ORGANISM   Bacteria; environmental samples.

REFERENCE
AUTHORS    Hackl,E., Zechmeister-Boltenstern,S., Bodrossy,L. and Sessitsch,A.
TITLE      Comparison of diversities and compositions of bacterial populations
inhabiting natural forest soils
JOURNAL    Appl. Environ. Microbiol. 70 (9), 5057-5065 (2004)
PUBMED     15345382

FEATURES
source      Location/Qualifiers
2 (bases 1 to 388)
Hackl,E. and Sessitsch,A.
Direct Submission
Submitted (19-SEP-2003) Environmental and Life Sciences, ARC
Seibersdorf research GmbH, Seibersdorf A-2444, Austria
Location/Qualifiers
1. .388
/organism="uncultured bacterium"
/mol_type="genomic DNA"
/isolation_source="forest soil"
/db_xref="taxon:77133"
/clone="D29ST"
/environmental_sample
<1. .>388
/product="16S ribosomal RNA"

gene
rRNA

ORIGIN
Query Match          91.6%; Score 17.4; DB 1; Length 388;
Best Local Similarity 94.7%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCTTCGG 19
Db 4 GAACGGAAGGCCTTCGG 22

TITLE
JOURNAL
REFERENCE
AUTHORS
JOURNAL
FEATURES
source
1. .384
/organism="actinobacterium BAL187"
/mol_type="genomic DNA"
/strain="BAL187"
/isolation_source="Baltic Sea, 3m depth, Landsort deep St.
BY31, Zobel/R2A media"
/db_xref="taxon:331761"
/country="Sweden"
/lat_lon="60.42.726N, 05.05.595E"
/collection_date="8 October 2003"
<1. .>384
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          91.6%; Score 17.4; DB 15; Length 384;
Best Local Similarity 94.7%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCTTCGG 19
Db 4 GAACGGAAGGCCTTCGG 22

RESULT 34
AY395145
LOCUS      Uncultured bacterium clone D29ST 16S ribosomal RNA gene, partial
sequence.          388 bp      DNA      linear      ENV 07-SEP-2004
DEFINITION
ACCESSION  AY395145
VERSION    AY395145.1 GI:37595660
KEYWORDS   ENV.
SOURCE     uncultured bacterium
ORGANISM   Bacteria; environmental samples.

REFERENCE
AUTHORS    Hackl,E., Zechmeister-Boltenstern,S., Bodrossy,L. and Sessitsch,A.
TITLE      Comparison of diversities and compositions of bacterial populations
inhabiting natural forest soils
JOURNAL    Appl. Environ. Microbiol. 70 (9), 5057-5065 (2004)
PUBMED     15345382

FEATURES
source      Location/Qualifiers
2 (bases 1 to 388)
Hackl,E. and Sessitsch,A.
Direct Submission
Submitted (19-SEP-2003) Environmental and Life Sciences, ARC
Seibersdorf research GmbH, Seibersdorf A-2444, Austria
Location/Qualifiers
1. .388
/organism="uncultured bacterium"
/mol_type="genomic DNA"
/isolation_source="forest soil"
/db_xref="taxon:77133"
/clone="D29ST"
/environmental_sample
<1. .>388
/product="16S ribosomal RNA"

gene
rRNA

ORIGIN
Query Match          91.6%; Score 17.4; DB 1; Length 388;
Best Local Similarity 94.7%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCTTCGG 19
Db 4 GAACGGAAGGCCTTCGG 22

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Db 57 GAACGGAAGGCCCTTCGG 75
/environmental_sample
<1..>394
/product="16S ribosomal RNA"

RESULT 35
LOCUS BSSMKN23
DEFINITION Bacterium sp. (SMKN23) DNA.
ACCESSION X78659
VERSION X78659.1 GI:509728
KEYWORDS 16S ribosomal RNA.
SOURCE unidentified bacterium
ORGANISM unidentified bacterium
Bacteria; environmental samples.

REFERENCE 1
AUTHORS Schuppler, M., Mertens, F., Schon, G. and Gobel, U. B.
TITLE Molecular characterization of nocardioform actinomycetes in
activated sludge by 16S rRNA analysis
JOURNAL Microbiology (Reading, Engl.) 141 (Pt 2), 513-521 (1995)
PUBMED 7704280
REFERENCE 2 (bases 1 to 393)
AUTHORS Schuppler, M.
TITLE Direct Submission
JOURNAL Submitted (28-MAR-1994) M. Schuppler, Institut fuer Med.
Mikrobiologie & Hygiene, Universitaet Freiburg, Hermann-Herder-St.
11, 79104 Freiburg, FRG
FEATURES
source Location/Qualifiers
1..393
/organism="unidentified bacterium"
/mol_type="genomic DNA"
/isolate="SMKN23"
/db_xref="taxon:2338"
1..393
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 91.6%; Score 17.4; DB 1; Length 393;
Best Local Similarity 94.7%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCCTTCGG 19
|||||
Db 14 GAACGGAAGGCCCTTCGG 32
|||||

RESULT 36
LOCUS AY395154
DEFINITION AY395154.1 GI:37595669
ACCESSION AY395154
VERSION AY395154.1
KEYWORDS ENV.
SOURCE uncultured actinobacterium
ORGANISM uncultured actinobacterium
Bacteria; Actinobacteria; environmental samples.

REFERENCE 1 (bases 1 to 394)
AUTHORS Hackl, E., Zechmeister-Boltenstern, S., Bodrossy, L. and Sessitsch, A.
TITLE Comparison of diversities and compositions of bacterial populations
inhabiting natural forest soils
JOURNAL Appl. Environ. Microbiol. 70 (9), 5057-5065 (2004)
PUBMED 15345382
REFERENCE 2 (bases 1 to 394)
AUTHORS Hackl, E. and Sessitsch, A.
TITLE Direct Submission
JOURNAL Submitted (19-SEP-2003) Environmental and Life Sciences, ARC
Seibersdorf research GmbH, Seibersdorf A-2444, Austria
FEATURES
source Location/Qualifiers
1..394
/organism="uncultured actinobacterium"
/mol_type="genomic DNA"
/isolation_source="forest soil"
/db_xref="taxon:152507"
/clone="E02ST"

Db 14 GAACGGAAGGCCCTTCGG 32
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RESULT 37
LOCUS AY043901
DEFINITION AY043901.1 GI:22267274
ACCESSION AY043901
VERSION AY043901.1
KEYWORDS ENV.
SOURCE uncultured actinobacterium
ORGANISM uncultured actinobacterium
Bacteria; Actinobacteria; environmental samples.

REFERENCE 1 (bases 1 to 395)
AUTHORS Axelrood, P. E., Chow, M. L., Radomski, C. C., McDermott, J. M. and
Davies, J.
TITLE Molecular characterization of bacterial diversity from British
Columbia forest soils subjected to disturbance
JOURNAL Can. J. Microbiol. 48 (7), 655-674 (2002)
PUBMED 12224564
REFERENCE 2 (bases 1 to 395)
AUTHORS Axelrood, P. E., Chow, M. L., Radomski, C. C., McDermott, J. M. and
Davies, J.
TITLE Direct Submission
JOURNAL Submitted (20-JUN-2001) BC Research Inc., 3650 Westbrook Mall,
Vancouver, BC V6S 2L2, Canada
FEATURES
source Location/Qualifiers
1..395
/organism="uncultured actinobacterium"
/mol_type="genomic DNA"
/db_xref="taxon:152507"
/clone="SMS9.49WL"
/environmental_sample
/note="from forest cut-block mineral soil from the British
Columbia Ministry of Forests Long-term Soil Productivity
(JTSP) installation near Williams Lake, BC, Canada"
<1..>395
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 91.6%; Score 17.4; DB 1; Length 395;
Best Local Similarity 94.7%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCCTTCGG 19
|||||
Db 27 GAACGGAAGGCCCTTCGG 45
|||||

RESULT 38
LOCUS AY395151
DEFINITION AY395151.1 GI:37595666
ACCESSION AY395151
VERSION AY395151.1
KEYWORDS ENV.
SOURCE uncultured bacterium
ORGANISM uncultured bacterium
Bacteria; environmental samples.

REFERENCE 1 (bases 1 to 395)
```

AUTHORS Hackl,E., Zechmeister-Boltenstern,S., Bodrossy,L. and Sessitsch,A.
 TITLE Comparison of diversities and compositions of bacterial populations
 inhabiting natural forest soils
 JOURNAL Appl. Environ. Microbiol. 70 (9), 5057-5065 (2004)
 PUBMED 15345382

REFERENCE 2 (bases 1 to 395)

AUTHORS Hackl,E. and Sessitsch,A.

TITLE Direct Submission

JOURNAL Submitted (19-SEP-2003) Environmental and Life Sciences, ARC

Seibersdorf research GmbH, Seibersdorf A-2444, Austria

FEATURES

source

1..395 /organism="uncultured bacterium"

/mol_type="genomic DNA"

/isolation_source="forest soil"

/db_xref="taxon:77133"

/clone="D36ST"

/environmental_sample

<1..>395

/product="16S ribosomal RNA"

ORIGIN

Query Match 91.6%; Score 17.4; DB 1; Length 395;

Best Local Similarity 94.7%; Pred. No. 2e+03; 1; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGCCCTTCGG 19

|||||

Db 57 GAACGGAAAGCCCTTCGG 75

RESULT 39

BSSMK14

LOCUS

DEFINITION Bacterium sp.(SMKN14) DNA. 396 bp DNA linear ENV 22-FEB-1995

ACCESSION X78655

VERSION X78655.1 GI:509724

KEYWORDS 16S ribosomal RNA.

SOURCE unidentified bacterium

ORGANISM Bacteria; environmental samples.

REFERENCE 1

AUTHORS Schuppler,M., Mertens,F., Schon,G. and Gobel,U.B.

TITLE Molecular characterization of nocardiform actinomycetes in

activated sludge by 16S rRNA analysis

JOURNAL Microbiology (Reading, Engl.) 141 (Pt 2), 513-521 (1995)

PUBMED 7704280

REFERENCE 2 (bases 1 to 396)

AUTHORS Schuppler,M.

TITLE Direct Submission

Submitted (28-MAR-1994) M. Schuppler, Institut fuer Med.

Mikrobiologie & Hygiene, Universitaet Freiburg, Hermann-Herder-St.

11, 79104 Freiburg FRG

FEATURES

source

1..396

/organism="unidentified bacterium"

/mol_type="genomic DNA"

/isolate="SMKN14"

/db_xref="taxon:2338"

1..396 /product="16S ribosomal RNA"

ORIGIN

Query Match 91.6%; Score 17.4; DB 1; Length 396;

Best Local Similarity 94.7%; Pred. No. 2e+03; 1; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGCCCTTCGG 19

|||||

Db 14 GAACGGAAAGCCCTTCGG 32

RESULT 40

DQ221681

LOCUS

DEFINITION Uncultured bacterium clone BPH3088 16S ribosomal RNA gene, partial
 sequence. 400 bp DNA linear ENV 12-NOV-2005

ACCESSION DQ221681

VERSION DQ221681.1 GI:80978382

KEYWORDS ENV.

SOURCE uncultured bacterium

ORGANISM uncultured bacterium

REFERENCE 1 (bases 1 to 400)

AUTHORS Lambais,M.R., Crowley,D.E., Cury,J.C. and Bull,R.C.

TITLE Bacterial diversity on leaf surfaces of the Brazilian Atlantic

JOURNAL Forest

REFERENCE 2 (bases 1 to 400)

AUTHORS Lambais,M.R., Crowley,D.E., Cury,J.C. and Bull,R.C.

TITLE Direct Submission

JOURNAL Submitted (23-SEP-2005) Solos e Nutricao de Plantas, Universidade

de Sao Paulo, Av. Padua Dias,11, Piracicaba, SP 13418-900, Brazil

FEATURES

source

1..400

/organism="uncultured bacterium"

/mol_type="genomic DNA"

/isolation_source="phyllosphere"

/specific_host="Campomanesia xanthocarpa"

/db_xref="taxon:77133"

/clone="BPH3088"

/environmental_sample

<1..>400

/product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match 91.6%; Score 17.4; DB 1; Length 400;

Best Local Similarity 94.7%; Pred. No. 2e+03; 1; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGCCCTTCGG 19

|||||

Db 22 GAACGGAAAGCCCTTCGG 40

RESULT 41

DQ063065

LOCUS

DEFINITION Actinobacterium BAL125 16S ribosomal RNA gene, partial sequence. 401 bp DNA linear BCT 27-JUN-2005

ACCESSION DQ063065

VERSION DQ063065.1 GI:68139094

KEYWORDS actinobacterium BAL125

SOURCE actinobacterium BAL125

REFERENCE 1 (bases 1 to 401)

AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and

Hagstrom,A.

TITLE Bacterial community composition in the central Baltic Sea analyzed

JOURNAL by cultivation and molecular-based methods

REFERENCE 2 (bases 1 to 401)

AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and

Hagstrom,A.

TITLE Direct Submission

JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,

University of Kalmar, Barlastagan 11, Kalmar 39231, Sweden

FEATURES

source

1..401

/organism="actinobacterium BAL125"

/mol_type="genomic DNA"

/strain="BAL125"

/isolation_source="Baltic Sea, 3m depth, Landsort deep St.

BY31, Zobel/R2A media"

/db_xref="taxon:331783"

/country="Sweden"

rRNA	/lat lon="60.42.726N, 05.05.595E"	
	/collection_date="2 July 2003"	
	<1..>401	
	/product="16S ribosomal RNA"	
ORIGIN	Query Match 91.6%; Score 17.4; DB 15; Length 401;	
	Best Local Similarity 94.7%; Pred. No. 1.9e+03;	
	Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1 GAACGGAAAGCCCTTCGG 19	
	7 GAACGGAAAGCCCTTCGG 25	
Db		
RESULT 42	AY234665 403 bp DNA linear BCT 08-DEC-2003	
	LOCUS Bacterium Ellin6013 16S ribosomal RNA gene, partial sequence.	
	DEFINITION AY234665	
	ACCESSION AY234665	
VERSION	AY234665.1 GI:37961822	
KEYWORDS	Bacterium Ellin6013	
	Bacterium Ellin6013	
	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;	
	Corynebacterineae; Mycobacteriaceae.	
SOURCE	1 (bases 1 to 403)	
	Joseph, S.J., Hugenholtz, P., Sangwan, P., Osborne, C.A. and	
	Janssen, P.H.	
	Laboratory Cultivation of Widespread and Previously Uncultured Soil	
ORGANISM	Bacteria	
	Appl. Environ. Microbiol. 69 (12), 7210-7215 (2003)	
	14660368	
REFERENCE	2 (bases 1 to 403)	
	Joseph, S.J., Hugenholtz, P., Rana, P., Osborne, C.A., Sait, M. and	
	Janssen, P.H.	
	Direct Submission	
AUTHORS	Submitted (12-FEB-2003) Department of Microbiology and Immunology,	
	University of Melbourne, Parkville, Victoria 3010, Australia	
	Location/Qualifiers	
	1..403	
FEATURES	/organism="bacterium Ellin6013"	
	/mol_type="genomic DNA"	
	/isolate="Ellin6013"	
	/db_xref="taxon:234120"	
source	<1..>403	
	/product="16S ribosomal RNA"	
rRNA	Query Match 91.6%; Score 17.4; DB 15; Length 403;	
	Best Local Similarity 94.7%; Pred. No. 1.9e+03;	
	Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1 GAACGGAAAGCCCTTCGG 19	
	37 GAACGGAAAGCCCTTCGG 55	
Db		
RESULT 43	AY792017/c 407 bp DNA linear BCT 20-NOV-2004	
	LOCUS Mycobacterium sp. 5BR6 16S ribosomal RNA gene, partial sequence.	
	DEFINITION AY792017	
	ACCESSION AY792017	
VERSION	AY792017.1 GI:55740316	
KEYWORDS	Mycobacterium sp. 5BR6	
	Mycobacterium sp. 5BR6	
	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;	
	Corynebacterineae; Mycobacteriaceae; Mycobacterium.	
SOURCE	1 (bases 1 to 407)	
	Sarro, M.I., Garcia, A.M., Moreno, D.A. and Montero, F.	
	Blorremediation of radioactive water with metallic materials	
	Unpublished	
ORGANISM		
REFERENCE	2 (bases 1 to 407)	
	Sarro, M.I., Garcia, A.M., Moreno, D.A. and Montero, F.	
	Direct Submission	
	Submitted (25-Oct-2004) Dep Ingenieria y Ciencia de los Materiales,	
AUTHORS	Escuela Tecnica Superior de Ingenieros Industriales, Universidad	
	Politecnica de Madrid, Jose Gutierrez Abascal, 2, Madrid, Madrid	
	28006, Spain	
	Location/Qualifiers	
FEATURES	1..407	
	/organism="Mycobacterium sp. 5BR6"	
	/mol_type="genomic DNA"	
	/isolate="5BR6"	
source	/isolation_source="radioactive water"	
	/db_xref="taxon:300866"	
	<1..>407	
	/product="16S ribosomal RNA"	
ORIGIN	Query Match 91.6%; Score 17.4; DB 15; Length 407;	
	Best Local Similarity 94.7%; Pred. No. 1.9e+03;	
	Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1 GAACGGAAAGCCCTTCGG 19	
	359 GAACGGAAAGCCCTTCGG 341	
Db		
RESULT 44	BSSMKN12 410 bp DNA linear ENV 22-FEB-1995	
	LOCUS Bacterium sp. (SMKN12) DNA.	
	DEFINITION X78654	
	ACCESSION X78654	
VERSION	X78654.1 GI:509723	
KEYWORDS	16S ribosomal RNA.	
	unidentified bacterium	
	unidentified bacterium	
	Bacteria; environmental samples.	
SOURCE	1	
	Schuppler, M., Mertens, F., Schon, G. and Gobel, U.B.	
	Molecular characterization of nocardiform actinomycetes in	
	activated sludge by 16S rRNA analysis	
ORGANISM	Microbiology (Reading, Engl.) 141 (Pt 2), 513-521 (1995)	
	7704280	
	2 (bases 1 to 410)	
	Schuppler, M.	
REFERENCE	Direct Submission	
	Submitted (28-MAR-1994) M. Schuppler, Institut fuer Med.	
	Mikrobiologie & Hygiene, Universitaet Freiburg, Hermann-Herder-St.	
	11, 79104 Freiburg, FRG	
AUTHORS	Location/Qualifiers	
	1..410	
	/organism="unidentified bacterium"	
	/mol_type="genomic DNA"	
TITLE	/isolate="SMKN12"	
	/db_xref="taxon:2338"	
	1..410	
	/product="16S ribosomal RNA"	
JOURNAL	Query Match 91.6%; Score 17.4; DB 1; Length 410;	
	Best Local Similarity 94.7%; Pred. No. 1.9e+03;	
	Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
PUBMED	1 GAACGGAAAGCCCTTCGG 19	
	9 GAACGGAAAGCCCTTCGG 27	
LOCUS	DO063154	
	DEFINITION Actinobacterium BAL218 16S ribosomal RNA gene, partial sequence.	
	ACCESSION DO063154	

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VERSION DQ063154.1 GI:68139192
KEYWORDS
SOURCE actinobacterium BAL218
ORGANISM actinobacterium BAL218
Bacteria; Actinobacteria.
REFERENCE 1 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE Bacterial community composition in the central Baltic Sea analyzed by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences, University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES
    source
        1..411
            /organism="actinobacterium BAL218"
            /mol_type="genomic DNA"
            /strain="BAL218"
            /isolation_source="Baltic Sea, 3m depth, Landsort deep St. BY31, Zobell/R2A media"
            /db_xref="taxon:331796"
            /country="Sweden"
            /lat_lon="60.42.726N, 05.05.595E"
            /collection_dates="17 May 2004"
            <1..>411
            /product="16S ribosomal RNA"

    rRNA

    ORIGIN
        Query Match          91.6%; Score 17.4; DB 15; Length 411;
        Best Local Similarity 94.7%; Pred. No. 1.9e+03;
        Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTCGG 19
Db 17 GAACGGAAGGCGCTTCGG 35

RESULT 46
DQ063199
LOCUS actinobacterium BAL263 411 bp DNA linear BCT 27-JUN-2005
DEFINITION Actinobacterium BAL263 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ063199
VERSION DQ063199.1 GI:68139237
KEYWORDS
SOURCE actinobacterium BAL263
ORGANISM actinobacterium BAL263
Bacteria; Actinobacteria.
REFERENCE 1 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE Bacterial community composition in the central Baltic Sea analyzed by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences, University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES
    source
        1..411
            /organism="actinobacterium BAL263"
            /mol_type="genomic DNA"
            /strain="BAL263"
            /isolation_source="Baltic Sea, 3m depth, Landsort deep St. BY31, Zobell/R2A media"
            /db_xref="taxon:331810"
            /country="Sweden"
            /lat_lon="60.42.726N, 05.05.595E"

    rRNA

    ORIGIN
        Query Match          91.6%; Score 17.4; DB 15; Length 411;
        Best Local Similarity 94.7%; Pred. No. 1.9e+03;
        Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTCGG 19
Db 17 GAACGGAAGGCGCTTCGG 35

RESULT 47
DQ063199
LOCUS actinobacterium BAL218 411 bp DNA linear BCT 20-NOV-2004
DEFINITION Mycobacterium sp. 4BR14 16S ribosomal RNA gene, partial sequence.
ACCESSION AY792013
VERSION AY792013.1 GI:55740312
KEYWORDS
ORGANISM Mycobacterium sp. 4BR14
Mycobacterium sp. 4BR14
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 411)
AUTHORS Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.
TITLE Biorremediation of radioactive water with metallic materials
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 411)
AUTHORS Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.
TITLE Direct Submission
JOURNAL Submitted (25-OCT-2004) Dep Ingenieria Y Ciencia de los Materiales, Escuela Tecnica Superior de Ingenieros Industriales, Universidad Politecnica de Madrid, Jose Gutierrez Abascal, 2, Madrid, Madrid 28006, Spain
FEATURES
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            /organism="Mycobacterium sp. 4BR14"
            /mol_type="genomic DNA"
            /isolate="4BR14"
            /isolation_source="radioactive water"
            /db_xref="taxon:300864"
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            /product="16S ribosomal RNA"

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        Best Local Similarity 94.7%; Pred. No. 1.9e+03;
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Qy 1 GAACGGAAGGCGCTTCGG 19
Db 58 GAACGGAAGGCGCTTCGG 76

RESULT 48
AM085773
LOCUS Uncultured Mycobacterium sp. partial 16S rRNA gene, clone 16.
DEFINITION AM085773
ACCESSION AM085773.1 GI:75754596
VERSION AM085773.1 GI:75754596
KEYWORDS ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE uncultured Mycobacterium sp.
ORGANISM uncultured Mycobacterium sp.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental samples.
REFERENCE 1
AUTHORS Uytendaele,M., Vermeir,S., Wattiau,P., Ryngaert,A. and Springael,D.
TITLE Enrichment and characterization of a bacterial culture utilizing pyrene at pH 2 and dominated by a slow-growing Mycobacterium sp. from acidic polycyclic aromatic hydrocarbon contaminated soil
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VERSION DQ063154.1 GI:68139192
KEYWORDS
SOURCE actinobacterium BAL218
ORGANISM actinobacterium BAL218
Bacteria; Actinobacteria.
REFERENCE 1 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE Bacterial community composition in the central Baltic Sea analyzed by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences, University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES
    source
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            /db_xref="taxon:331796"
            /country="Sweden"
            /lat_lon="60.42.726N, 05.05.595E"
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            /product="16S ribosomal RNA"

    rRNA

    ORIGIN
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        Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTCGG 19
Db 17 GAACGGAAGGCGCTTCGG 35

RESULT 46
DQ063199
LOCUS actinobacterium BAL263 411 bp DNA linear BCT 27-JUN-2005
DEFINITION Actinobacterium BAL263 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ063199
VERSION DQ063199.1 GI:68139237
KEYWORDS
SOURCE actinobacterium BAL263
ORGANISM actinobacterium BAL263
Bacteria; Actinobacteria.
REFERENCE 1 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE Bacterial community composition in the central Baltic Sea analyzed by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences, University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
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            /strain="BAL263"
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            /country="Sweden"
            /lat_lon="60.42.726N, 05.05.595E"

    rRNA

    ORIGIN
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        Best Local Similarity 94.7%; Pred. No. 1.9e+03;
        Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTCGG 19
Db 17 GAACGGAAGGCGCTTCGG 35

RESULT 47
DQ063199
LOCUS actinobacterium BAL218 411 bp DNA linear BCT 20-NOV-2004
DEFINITION Mycobacterium sp. 4BR14 16S ribosomal RNA gene, partial sequence.
ACCESSION AY792013
VERSION AY792013.1 GI:55740312
KEYWORDS
ORGANISM Mycobacterium sp. 4BR14
Mycobacterium sp. 4BR14
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 411)
AUTHORS Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.
TITLE Biorremediation of radioactive water with metallic materials
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 411)
AUTHORS Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.
TITLE Direct Submission
JOURNAL Submitted (25-OCT-2004) Dep Ingenieria Y Ciencia de los Materiales, Escuela Tecnica Superior de Ingenieros Industriales, Universidad Politecnica de Madrid, Jose Gutierrez Abascal, 2, Madrid, Madrid 28006, Spain
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            /db_xref="taxon:300864"
            <1..>411
            /product="16S ribosomal RNA"

    rRNA

    ORIGIN
        Query Match          91.6%; Score 17.4; DB 15; Length 411;
        Best Local Similarity 94.7%; Pred. No. 1.9e+03;
        Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTCGG 19
Db 58 GAACGGAAGGCGCTTCGG 76

RESULT 48
AM085773
LOCUS Uncultured Mycobacterium sp. partial 16S rRNA gene, clone 16.
DEFINITION AM085773
ACCESSION AM085773.1 GI:75754596
VERSION AM085773.1 GI:75754596
KEYWORDS ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE uncultured Mycobacterium sp.
ORGANISM uncultured Mycobacterium sp.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental samples.
REFERENCE 1
AUTHORS Uytendaele,M., Vermeir,S., Wattiau,P., Ryngaert,A. and Springael,D.
TITLE Enrichment and characterization of a bacterial culture utilizing pyrene at pH 2 and dominated by a slow-growing Mycobacterium sp. from acidic polycyclic aromatic hydrocarbon contaminated soil
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JOURNAL Unpublished
REFERENCE 2 (bases 1 to 414)
AUTHORS Uyttebroek, M.
TITLE Direct Submission
JOURNAL Submitted (13-SEP-2005) Uyttebroek M., Division Soil and Water Management, Catholic University of Leuven, Kasteelpark Arenberg 20, B-3001 Leuven, BELGIUM
FEATURES Location/Qualifiers
source 1..414
/organism="uncultured Mycobacterium sp."
/mol_type="genomic DNA"
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/country="Belgium"
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/gene="16S rRNA"
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ORIGIN
Query Match 91.6%; Score 17.4; DB 1; Length 414;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCTTTCGG 19
|||||
Db 7 GAACGGAAAGGCTTTCGG 25

RESULT 49
LOCUS DQ223051 414 bp DNA linear ENV 22-OCT-2005
DEFINITION Uncultured bacterium clone HBO70 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ223051 GI:77744948
VERSION DQ223051.1
KEYWORDS ENV.
SOURCE uncultured bacterium
ORGANISM Bacteria; environmental samples.
REFERENCE 1 (bases 1 to 414)
AUTHORS Li, H. and Wu, B.
TITLE Phylogenetic diversity and community structure of bacteria in an oil-storage cavity as detected by 16S rRNA gene library
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 414)
AUTHORS Li, H. and Wu, B.
TITLE Direct Submission
JOURNAL Submitted (26-SEP-2005) Chemical and Pharmaceutical Institution, East China University of Science and Technology, Meilong Road, Shanghai 200237, China
FEATURES Location/Qualifiers
source 1..414
/organism="uncultured bacterium"
/mol_type="genomic DNA"
/isolation_source="oil-storage cavity"
/db_xref="taxon:77133"
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/environmental_sample
<1..>414
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 91.6%; Score 17.4; DB 1; Length 414;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCTTTCGG 19
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Db 57 GAACGGAAAGGCTTTCGG 75

RESULT 50
LOCUS DQ063108 415 bp DNA linear BCT 27-JUN-2005
DEFINITION Actinobacterium BAL168 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ063108
VERSION DQ063108.1 GI:68139141
KEYWORDS
SOURCE actinobacterium BAL168
ORGANISM actinobacterium BAL168
REFERENCE 1 (bases 1 to 415)
AUTHORS Bacteria; Actinobacteria.
Riemann, L., Leitet, C., Pommier, T., Simu, K., Holmfeldt, K. and Hagstrom, A.
TITLE Bacterial community composition in the central Baltic Sea analyzed by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 415)
AUTHORS Riemann, L., Leitet, C., Pommier, T., Simu, K., Holmfeldt, K. and Hagstrom, A.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences, University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES Location/Qualifiers
source 1..415
/organism="actinobacterium BAL168"
/mol_type="genomic DNA"
/strain="BAL168"
/isolation_source="Baltic Sea, 3m depth, Landsort deep St. BY31, Zobel1/R2A media"
/db_xref="taxon:331762"
/country="Sweden"
/lat_lon="60.42.726N, 05.05.595E"
/collection_date="8 October 2003"
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/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 91.6%; Score 17.4; DB 15; Length 415;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCTTTCGG 19
|||||
Db 7 GAACGGAAAGGCTTTCGG 25

RESULT 51
LOCUS AM085786 416 bp DNA linear ENV 21-SEP-2005
DEFINITION Uncultured Mycobacterium sp. partial 16S rRNA gene, clone K11.
ACCESSION AM085786
VERSION AM085786.1 GI:75754609
KEYWORDS ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE uncultured Mycobacterium sp.
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental samples.
REFERENCE 1
AUTHORS Uyttebroek, M., Breugelmans, P., Janssen, M., Wattiau, P., Joffe, B., Karlson, U., Ortega-Calvo, J.J., Bastiaens, L., Ryngaert, A. and Springael, D.
TITLE Distribution of the Mycobacterium sp. community and polycyclic aromatic hydrocarbons (PAHs) among different size fractions of a weathered PAH-contaminated soil
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 416)
AUTHORS Uyttebroek, M.
TITLE Direct Submission
JOURNAL Submitted (13-SEP-2005) Uyttebroek M., Division Soil and Water Management, Catholic University of Leuven, Kasteelpark Arenberg 20,

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FEATURES
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    Best Local Similarity 94.7%; Pred. No. 1.9e+03;
    Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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    Qy 1 GAACGGAAGGCGCTTTCGG 19
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    Db 10 GAACGGAAGGCGCTTTCGG 28
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RESULT 52
DQ063074          416 bp  DNA  linear  BCT 27-JUN-2005
LOCUS
DEFINITION
  Actinobacterium BAL134 16S ribosomal RNA gene, partial sequence.
ACCESSION
  DQ063074
VERSION
  DQ063074.1 GI:68139107
KEYWORDS
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SOURCE
  actinobacterium BAL134
  actinobacterium BAL134
  Bacteria; Actinobacteria.
REFERENCE
  1 (bases 1 to 416)
  Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
  Hagstrom,A.
  Bacterial community composition in the central Baltic Sea analyzed
  by cultivation and molecular-based methods
  Unpublished
  2 (bases 1 to 416)
  Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
  Hagstrom,A.
  Direct Submission
  Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
  University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
  Location/Qualifiers
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      /mol_type="genomic DNA"
      /strain="BAL134"
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      /db_xref="taxon:331785"
      /country="Sweden"
      /lat_lon="60.42.726N, 05.05.595E"
      /collection_date="8 October 2003"
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    Db 4 GAACGGAAGGCGCTTTCGG 22
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ORIGIN
  Query Match          91.6%; Score 17.4; DB 15; Length 417;
  Best Local Similarity 94.7%; Pred. No. 1.9e+03;
  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

  Qy 1 GAACGGAAGGCGCTTTCGG 19
      |||||
  Db 4 GAACGGAAGGCGCTTTCGG 22
      |||||

RESULT 54
AY673210
LOCUS
DEFINITION
  Mycobacteriaceae bacterium Ellin7044 16S ribosomal RNA gene,
  partial sequence.
ACCESSION
  AY673210
VERSION
  AY673210.1 GI:56683067
KEYWORDS
  .
SOURCE
  Mycobacteriaceae bacterium Ellin7044
  Mycobacteriaceae bacterium Ellin7044
  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
  Corynebacterineae; Mycobacteriaceae.
REFERENCE
  1 (bases 1 to 417)
  Davis,K.E., Joseph,S.J. and Janssen,P.H.
  Effects of growth medium, inoculum size, and incubation time on
  culturability and isolation of soil bacteria
  Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
  15691937
  2 (bases 1 to 417)
  Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
  Direct Submission
  Submitted (02-JUL-2004) Department of Microbiology and Immunology,
  University of Melbourne, Grattan Street, Parkville, Victoria 3010,
  Australia
  Location/Qualifiers
    1..417
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      /mol_type="genomic DNA"

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        |||||

ORIGIN
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  Best Local Similarity 94.7%; Pred. No. 1.9e+03;
  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

  Qy 1 GAACGGAAGGCGCTTTCGG 19
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    Db 3 GAACGGAAGGCGCTTTCGG 21
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RESULT 53

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DQ063073
LOCUS
DEFINITION
  Actinobacterium BAL133 16S ribosomal RNA gene, partial sequence.
ACCESSION
  DQ063073
VERSION
  DQ063073.1 GI:68139102
KEYWORDS
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SOURCE
  actinobacterium BAL133
  actinobacterium BAL133
  Bacteria; Actinobacteria.
REFERENCE
  1 (bases 1 to 417)
  Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
  Hagstrom,A.
  Bacterial community composition in the central Baltic Sea analyzed
  by cultivation and molecular-based methods
  Unpublished
  2 (bases 1 to 417)
  Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
  Hagstrom,A.
  Direct Submission
  Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
  University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
  Location/Qualifiers
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      /strain="BAL133"
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      /db_xref="taxon:331784"
      /country="Sweden"
      /lat_lon="60.42.726N, 05.05.595E"
      /collection_date="2 July 2003"
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        |||||

ORIGIN
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  Best Local Similarity 94.7%; Pred. No. 1.9e+03;
  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

  Qy 1 GAACGGAAGGCGCTTTCGG 19
      |||||
  Db 4 GAACGGAAGGCGCTTTCGG 22
      |||||

RESULT 54
AY673210
LOCUS
DEFINITION
  Mycobacteriaceae bacterium Ellin7044 16S ribosomal RNA gene,
  partial sequence.
ACCESSION
  AY673210
VERSION
  AY673210.1 GI:56683067
KEYWORDS
  .
SOURCE
  Mycobacteriaceae bacterium Ellin7044
  Mycobacteriaceae bacterium Ellin7044
  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
  Corynebacterineae; Mycobacteriaceae.
REFERENCE
  1 (bases 1 to 417)
  Davis,K.E., Joseph,S.J. and Janssen,P.H.
  Effects of growth medium, inoculum size, and incubation time on
  culturability and isolation of soil bacteria
  Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
  15691937
  2 (bases 1 to 417)
  Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
  Direct Submission
  Submitted (02-JUL-2004) Department of Microbiology and Immunology,
  University of Melbourne, Grattan Street, Parkville, Victoria 3010,
  Australia
  Location/Qualifiers
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      /mol_type="genomic DNA"

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    Db 3 GAACGGAAGGCGCTTTCGG 21
        |||||

ORIGIN
  Query Match          91.6%; Score 17.4; DB 15; Length 416;
  Best Local Similarity 94.7%; Pred. No. 1.9e+03;
  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

  Qy 1 GAACGGAAGGCGCTTTCGG 19
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RESULT 53

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ORIGIN
Query Match          91.6%; Score 17.4; DB 15; Length 417;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTCGG 19
|||||
Db 2 GAACGGAAGGCGCTTTCGG 20

RESULT 55
AM085788
LOCUS      418 bp      DNA      linear      ENV 21-SEP-2005
DEFINITION Uncultured Mycobacterium sp. partial 16S rRNA gene, clone K13.
ACCESSION  AM085788
VERSION     AM085788.1 GI:75754611
KEYWORDS    ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE      uncultured Mycobacterium sp.
ORGANISM    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental
samples.
REFERENCE   1
AUTHORS     Uytendaele, M., Breugelmans, P., Janssen, M., Wattiau, P., Joffe, B.,
            Karlsson, U., Ortega-Calvo, J.J., Bastiaens, L., Ryngaert, A. and
            Springael, D.
TITLE       Distribution of the Mycobacterium sp. community and polycyclic
            aromatic hydrocarbons (PAHs) among different size fractions of a
            weathered PAH-contaminated soil
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 418)
AUTHORS     Uytendaele, M.
TITLE       Direct Submission
JOURNAL     Submitted (13-SEP-2005) Uytendaele M., Division Soil and Water
            Management, Catholic University of Leuven, Kasteelpark Arenberg 20,
            B-3001 Leuven, BELGIUM
FEATURES    Location/Qualifiers
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               /product="16S ribosomal RNA"

gene
rRNA

ORIGIN
Query Match          91.6%; Score 17.4; DB 1; Length 418;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTCGG 19
|||||
Db 10 GAACGGAAGGCGCTTTCGG 28

RESULT 56
AY673261
LOCUS      418 bp      DNA      linear      BCT 20-MAY-2005
DEFINITION Mycobacteriaceae bacterium Ellin7095 16S ribosomal RNA gene,
            partial sequence.
ACCESSION  AY673261

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AY673261.1 GI:56683118
Mycobacteriaceae bacterium Ellin7095
Mycobacteriaceae bacterium Ellin7095
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
1 (bases 1 to 418)
Davis, K.E., Joseph, S.J. and Janssen, P.H.
Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
15691937
2 (bases 1 to 418)
Davis, K.E.R., Joseph, S.J. and Janssen, P.H.
Direct Submission
Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
Location/Qualifiers
1..418
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/isolate="Ellin7095"
/isolation_source="soil"
/db_xref="taxon:305281"
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/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          91.6%; Score 17.4; DB 15; Length 418;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTCGG 19
|||||
Db 37 GAACGGAAGGCGCTTTCGG 55

RESULT 57
AM085770
LOCUS      421 bp      DNA      linear      ENV 21-SEP-2005
DEFINITION Uncultured eubacterium partial 16S rRNA gene, clone T3.
ACCESSION  AM085770
VERSION     AM085770.1 GI:75754591
KEYWORDS    ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE      uncultured bacterium
ORGANISM    Bacteria; environmental samples.
REFERENCE   1
AUTHORS     Uytendaele, M., Vermeir, S., Wattiau, P., Ryngaert, A. and Springael, D.
TITLE       Enrichment and characterization of a bacterial culture utilizing
            pyrene at pH 2 and dominated by a slow-growing Mycobacterium sp.
            from acidic polycyclic aromatic hydrocarbon contaminated soil
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 421)
AUTHORS     Uytendaele, M.
TITLE       Direct Submission
JOURNAL     Submitted (13-SEP-2005) Uytendaele M., Division Soil and Water
            Management, Catholic University of Leuven, Kasteelpark Arenberg 20,
            B-3001 Leuven, BELGIUM
Location/Qualifiers
1..421
/organism="uncultured bacterium"
/mol_type="genomic DNA"
/isolation_source="PAH-contaminated soil"
/db_xref="taxon:77133"
/clone="T3"
/environmental_sample
/country="Belgium"
<1..>421
/gene="16S rRNA"
<1..>421
/gene="16S rRNA"

gene
rRNA

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ORIGIN
Query Match          91.6%; Score 17.4; DB 1; Length 421;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTCGG 19
    |||||
Db 16 GAACGGAAGGCTTCGG 34

/product="16S ribosomal RNA"

RESULT 58
AJ786807
LOCUS      422 bp      DNA      linear      BCT 29-OCT-2004
DEFINITION Mycobacterium sp. R-22838 partial 16S rRNA gene, isolate R-22838.
ACCESSION  AJ786807
VERSION     AJ786807.1 GI:54887545
KEYWORDS   16S ribosomal RNA; 16S rRNA gene.
SOURCE     Mycobacterium sp. R-22838
ORGANISM   Mycobacterium sp. R-22838
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE  1
AUTHORS    Vanparys,B., Heylen,K., Lebbe,L., Boon,N., Wittebolle,L.,
            Verstraete,W. and De Vos,P.
TITLE      The microbial community composition of a commercial nitrifying
            inoculum
JOURNAL
AUTHORS    Vanparys,B.
TITLE      Direct Submission
JOURNAL    Submitted (30-JUL-2004) Vanparys B., Laboratory of Microbiology,
            University of Gent, Ledeganckstraat 35, 9000 Gent, BELGIUM
FEATURES   Location/Qualifiers
            source          1..422
                        /organism="Mycobacterium sp. R-22838"
                        /mol_type="genomic DNA"
                        /isolate="R-22838"
                        /isolation_source="commercial nitrifying inoculum"
                        /db_xref="taxon:288999"
                        /country="Belgium"
            gene            1..422
                        /gene="16S rRNA"
            rRNA            <1..>422
                        /gene="16S rRNA"
                        /product="16S ribosomal RNA"

ORIGIN
Query Match          91.6%; Score 17.4; DB 15; Length 422;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTCGG 19
    |||||
Db 37 GAACGGAAGGCTTCGG 55

/product="16S ribosomal RNA"

RESULT 59
AY673284
LOCUS      422 bp      DNA      linear      BCT 20-MAY-2005
DEFINITION Micromonosporaceae bacterium Ellin7118 16S ribosomal RNA gene,
            partial sequence.
ACCESSION  AY673284
VERSION     AY673284.1 GI:56683141
KEYWORDS   Micromonosporaceae bacterium Ellin7118
            Micromonosporaceae bacterium Ellin7118
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Micromonosporineae; Micromonosporaceae.
            1 (bases 1 to 422)
            Davis,K.E., Joseph,S.J. and Janssen,P.H.
            Effects of growth medium, inoculum size, and incubation time on
            culturability and isolation of soil bacteria
            Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
            15691937
            2 (bases 1 to 423)
            Davis,K.E., Joseph,S.J. and Janssen,P.H.
            Effects of growth medium, inoculum size, and incubation time on
            culturability and isolation of soil bacteria
            Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
            15691937
            2 (bases 1 to 423)
            Davis,K.E., Joseph,S.J. and Janssen,P.H.
            Direct Submission
            Submitted (02-JUL-2004) Department of Microbiology and Immunology,
            University of Melbourne, Grattan Street, Parkville, Victoria 3010,
            Australia
FEATURES   Location/Qualifiers
            source          1..423
                        /organism="Mycobacteriaceae bacterium Ellin7039"
                        /mol_type="genomic DNA"
                        /isolate="Ellin7039"
                        /isolation_source="soil"
                        /db_xref="taxon:305258"
                        <1..>423
                        /product="16S ribosomal RNA"
            rRNA            <1..>423
                        /product="16S ribosomal RNA"

ORIGIN
Query Match          91.6%; Score 17.4; DB 15; Length 423;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTCGG 19
    |||||
Db 37 GAACGGAAGGCTTCGG 55

/product="16S ribosomal RNA"

culturability and isolation of soil bacteria
Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
15691937
2 (bases 1 to 422)
Davis,K.E., Joseph,S.J. and Janssen,P.H.
Direct Submission
Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES   Location/Qualifiers
            source          1..422
                        /organism="Micromonosporaceae bacterium Ellin7118"
                        /mol_type="genomic DNA"
                        /isolate="Ellin7118"
                        /isolation_source="soil"
                        /db_xref="taxon:305235"
                        <1..>422
                        /product="16S ribosomal RNA"
            rRNA            <1..>422
                        /product="16S ribosomal RNA"

ORIGIN
Query Match          91.6%; Score 17.4; DB 15; Length 422;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTCGG 19
    |||||
Db 36 GAGCGGAAGGCTTCGG 54

/product="16S ribosomal RNA"

RESULT 60
AY673205
LOCUS      423 bp      DNA      linear      BCT 20-MAY-2005
DEFINITION Mycobacteriaceae bacterium Ellin7039 16S ribosomal RNA gene,
            partial sequence.
ACCESSION  AY673205
VERSION     AY673205.1 GI:56683062
KEYWORDS   Mycobacteriaceae bacterium Ellin7039
            Mycobacteriaceae bacterium Ellin7039
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae.
            1 (bases 1 to 423)
            Davis,K.E., Joseph,S.J. and Janssen,P.H.
            Effects of growth medium, inoculum size, and incubation time on
            culturability and isolation of soil bacteria
            Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
            15691937
            2 (bases 1 to 423)
            Davis,K.E., Joseph,S.J. and Janssen,P.H.
            Direct Submission
            Submitted (02-JUL-2004) Department of Microbiology and Immunology,
            University of Melbourne, Grattan Street, Parkville, Victoria 3010,
            Australia
FEATURES   Location/Qualifiers
            source          1..423
                        /organism="Mycobacteriaceae bacterium Ellin7039"
                        /mol_type="genomic DNA"
                        /isolate="Ellin7039"
                        /isolation_source="soil"
                        /db_xref="taxon:305258"
                        <1..>423
                        /product="16S ribosomal RNA"
            rRNA            <1..>423
                        /product="16S ribosomal RNA"

ORIGIN
Query Match          91.6%; Score 17.4; DB 15; Length 423;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTCGG 19
    |||||
Db 37 GAACGGAAGGCTTCGG 55

/product="16S ribosomal RNA"

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REFERENCE 1 (bases 1 to 424)
AUTHORS Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
JOURNAL Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED 15891937
REFERENCE 2 (bases 1 to 424)
AUTHORS Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES
source Location/Qualifiers
1..424
/organism="Streptosporangiaceae bacterium Ellin7121"
/mol_type="genomic DNA"
/isolate="Ellin7121"
/isolation_source="soil"
/db_xref="taxon:305348"
<1..>424
/product="16S ribosomal RNA"

rRNA
<1..>424
/product="16S ribosomal RNA"

ORIGIN
Query Match 91.6%; Score 17.4; DB 15; Length 424;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCCTTCGG 19
Db 37 GAGCGGAAGGCCCTTCGG 55

RESULT 65
AV756031 424 bp DNA linear BCT 08-APR-2005
LOCUS Unidentified bacterium TMB805 16S ribosomal RNA gene, partial
DEFINITION sequence.
VERSION AV756031
KEYWORDS AV756031.1 GI:54299184
SOURCE Unidentified bacterium TMB805
ORGANISM Unidentified bacterium TMB805
Bacteria.
REFERENCE 1 (bases 1 to 424)
AUTHORS Chapon,V., Benzerara,K., Barakat,M., Achouak,W., Barras,F.,
Christen,R., Chevenet,F. and Heulin,T.
TITLE Diversity of Bacteria and Archae in the arid desert of Tataouine
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 424)
Chapon,V., Benzerara,K., Barakat,M., Achouak,W., Barras,F.,
Christen,R., Chevenet,F. and Heulin,T.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-2004) LEWIR-DEVN-DSV, CEA, Cadarache, Saint Paul
Lez Durance 13108, France
FEATURES
source Location/Qualifiers
1..424
/organism="Unidentified bacterium TMB805"
/mol_type="genomic DNA"
/strain="TMB805"
/isolation_source="arid soil"
/db_xref="taxon:297191"
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/product="16S ribosomal RNA"

rRNA
<1..>424
/product="16S ribosomal RNA"

ORIGIN
Query Match 91.6%; Score 17.4; DB 15; Length 424;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCCTTCGG 19
Db 7 GAACGGAAGGCCCTTCGG 25

RESULT 66
AV394635 425 bp DNA linear ENV 20-OCT-2003
LOCUS Uncultured Mycobacterium sp. clone W1-11 16S ribosomal RNA gene,
DEFINITION partial sequence.
VERSION AV394635
KEYWORDS AV394635.1 GI:37677560
SOURCE ENV.
ORGANISM uncultured Mycobacterium sp.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental
samples.
REFERENCE 1 (bases 1 to 425)
AUTHORS Benson,D.R., Benson,M.J., Gawronski,J.D. and Eveleigh,D.E.
TITLE Intracellular symbionts and other bacteria associated with deer
ticks (Ixodes scapularis) from Nantucket and Wellfleet, Cape Cod,
Massachusetts
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 425)
AUTHORS Benson,D.R., Benson,M.J., Gawronski,J.D. and Eveleigh,D.E.
TITLE Direct Submission
JOURNAL Submitted (19-SEP-2003) Molecular & Cell Biology, University of
Connecticut, U-3125, North Eagleville Rd., Storrs, CT 06279-3125,
USA
FEATURES
source Location/Qualifiers
1..425
/organism="uncultured Mycobacterium sp."
/mol_type="genomic DNA"
/specific_host="Ixodes scapularis"
/db_xref="taxon:171292"
/clone="W1-11"
/environmental sample
/country="USA; Massachusetts, Cape Cod, Nantucket,
Wellfleet"
<1..>425
/product="16S ribosomal RNA"

rRNA
<1..>425
/product="16S ribosomal RNA"

ORIGIN
Query Match 91.6%; Score 17.4; DB 1; Length 425;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCCTTCGG 19
Db 37 GAACGGAAGGCCCTTCGG 55

RESULT 67
AV673136 426 bp DNA linear BCT 22-DEC-2004
LOCUS Mycobacteriaceae bacterium Ellin5409 16S ribosomal RNA gene,
DEFINITION partial sequence.
VERSION AV673136
KEYWORDS AV673136.1 GI:56683290
SOURCE Mycobacteriaceae bacterium Ellin5409
ORGANISM Mycobacteriaceae bacterium Ellin5409
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
REFERENCE 1 (bases 1 to 426)
AUTHORS Osborne,C.A. and Janssen,P.H.
TITLE Direct Submission
JOURNAL Submitted (30-JUN-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES
source Location/Qualifiers
1..426
/organism="Mycobacteriaceae bacterium Ellin5409"
/mol_type="genomic DNA"
/isolate="Ellin5409"
/isolation_source="soil"

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/db_xref="taxon:305244"
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/product="16S ribosomal RNA"

ORIGIN
Query Match          91.6%; Score 17.4; DB 15; Length 426;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGCCCTTTCGG 19
|||||
Db 37 GAACGGAAAGCCCTTTCGG 55

RESULT 68
AB106918          428 bp  DNA  linear  BCT 09-SEP-2003
LOCUS             Gram-positive bacterium 1-6 for 16S ribosomal RNA, partial
DEFINITION
sequence.
AB106918
ACCESSION         AB106918.1 GI:29421132
VERSION
KEYWORDS
SOURCE            Gram-positive bacterium 1-6
ORGANISM          Gram-positive bacterium 1-6
Bacteria.
REFERENCE
1 Amachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
  Fujii,T. and Muramatsu,Y.
TITLE             Microbial participation in iodine volatilization from soils
JOURNAL           Environ. Sci. Technol. 37, 3885-3890 (2003)
REFERENCE
2 (bases 1 to 428)
AUTHORS           Amachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
  Fujii,T. and Muramatsu,Y.
TITLE             Direct Submission
JOURNAL           Submitted (27-MAR-2003) Seigo Amachi, Chiba University, Dept. of
  Bioreources Chem.; 648 Matsudo, Matsudo-shi, Chiba 271-8510, Japan
  (E-mail:amachi@faculty.chiba-u.jp, Tel:81-47-308-8868,
  Fax:81-47-308-8866)
FEATURES
source            Location/Qualifiers
1..428
/organism="Gram-positive bacterium 1-6"
/mol_type="genomic DNA"
/strain="1-6"
/db_xref="taxon:226200"
<1..>428
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          91.6%; Score 17.4; DB 15; Length 428;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGCCCTTTCGG 19
|||||
Db 37 GAACGGAAAGCCCTTTCGG 55

RESULT 69
DQ063058          428 bp  DNA  linear  BCT 27-JUN-2005
LOCUS             Actinobacterium BAL118 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION         DQ063058
VERSION           DQ063058.1 GI:68139087
KEYWORDS
SOURCE            actinobacterium BAL118
                  actinobacterium BAL118
                  Bacteria; Actinobacteria.
ORGANISM
REFERENCE
1 (bases 1 to 428)
AUTHORS           Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
  Hagstrom,A.
TITLE             Bacterial community composition in the central Baltic Sea analyzed
  by cultivation and molecular-based methods
JOURNAL           Unpublished

/db_xref="taxon:305244"
<1..>426
/product="16S ribosomal RNA"

ORIGIN
Query Match          91.6%; Score 17.4; DB 15; Length 426;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGCCCTTTCGG 19
|||||
Db 37 GAACGGAAAGCCCTTTCGG 55

RESULT 70
AJ786822          430 bp  DNA  linear  BCT 29-OCT-2004
LOCUS             Mycobacterium sp. R-23262 partial 16S rRNA gene, isolate R-23262.
DEFINITION
ACCESSION         AJ786822.1 GI:54887560
VERSION           AJ786822.1
KEYWORDS          16S ribosomal RNA; 16S rRNA gene.
SOURCE            Mycobacterium sp. R-23262
                  Mycobacterium sp. R-23262
                  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                  Corynebacterineae; Mycobacteriaceae; Mycobacterium.
ORGANISM
REFERENCE
1 Vanparrys,B., Heylen,K., Lebbe,L., Boon,N., Wittebolle,L.,
  Versaete,W. and De Vos,P.
TITLE             The microbial community composition of a commercial nitrifying
  inoculum
JOURNAL           Unpublished
REFERENCE
2 (bases 1 to 430)
AUTHORS           Vanparrys,B.
TITLE             Direct Submission
JOURNAL           Submitted (30-JUL-2004) Vanparrys B., Laboratory of Microbiology,
  University of Gent, Ledeganckstraat 35, 9000 Gent, BELGIUM
FEATURES
source            Location/Qualifiers
1..430
/organism="Mycobacterium sp. R-23262"
/mol_type="genomic DNA"
/isolate="R-23262"
/isolation_source="commercial nitrifying inoculum"
/db_xref="taxon:289008"
/country="Belgium"
1..430
/genes="16S rRNA"
<1..>430
/genes="16S rRNA"
/product="16S ribosomal RNA"

ORIGIN
Query Match          91.6%; Score 17.4; DB 15; Length 430;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGCCCTTTCGG 19
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Db 37 GAACGGAAAGCCCTTTCGG 19
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Db      37 GAACGGAAGGCCCTTCGG 55
RESULT 71
AY673202 LOCUS      430 bp      DNA      linear      BCT 20-MAY-2005
DEFINITION  Mycobacteriaceae bacterium Ellin7036 16S ribosomal RNA gene,
partial sequence.
ACCESSION  AY673202
VERSION    AY673202.1 GI:56683059
KEYWORDS
SOURCE     Mycobacteriaceae bacterium Ellin7036
ORGANISM   Mycobacteriaceae bacterium Ellin7036
REFERENCE  1 (bases 1 to 430)
AUTHORS    Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE      Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
JOURNAL    Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED     15691937
REFERENCE  2 (bases 1 to 430)
AUTHORS    Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE      Direct Submission
JOURNAL    Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES   Location/Qualifiers
            source
            1..430
            /organism="Mycobacteriaceae bacterium Ellin7036"
            /mol_type="genomic DNA"
            /isolate="Ellin7036"
            /isolation_source="soil"
            /db_xref="taxon:305257"
            <1_>430
            /product="16S ribosomal RNA"

rRNA
ORIGIN
Query Match      91.6%; Score 17.4; DB 15; Length 430;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GAACGGAAGGCCCTTCGG 19
|||||
Db      37 GAACGGAAGGCCCTTCGG 55

RESULT 72
AB106919 LOCUS      431 bp      DNA      linear      BCT 09-SEP-2003
DEFINITION  Gram-positive bacterium 2-1 for 16S ribosomal RNA, partial
sequence.
ACCESSION  AB106919
VERSION    AB106919.1 GI:29421133
KEYWORDS
SOURCE     Gram-positive bacterium 2-1
ORGANISM   Gram-positive bacterium 2-1
REFERENCE  1
AUTHORS    Anachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
Fuji,T. and Muramatsu,Y.
TITLE      Microbial participation in iodine volatilization from soils
JOURNAL    Environ. Sci. Technol. 37, 3885-3890 (2003)
REFERENCE  2 (bases 1 to 431)
AUTHORS    Anachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
Fuji,T. and Muramatsu,Y.
TITLE      Direct Submission
JOURNAL    Submitted (27-MAR-2003) Seigo Amachi, Chiba University, Dept. of
Bioresources Chem.; 648 Matsudo, Matsudo-shi, Chiba 271-8510, Japan
(E-mail:amachi@faculty.chiba-u.jp, Tel:81-47-308-8868,
Fax:81-47-308-8866)
FEATURES   Location/Qualifiers
            source
            1..431

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rRNA
ORIGIN
Query Match      91.6%; Score 17.4; DB 15; Length 431;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GAACGGAAGGCCCTTCGG 19
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Db      37 GAACGGAAGGCCCTTCGG 55

RESULT 73
AF078232 LOCUS      432 bp      DNA      linear      ENV 10-MAY-2004
DEFINITION  Grassland soil clone saf2_117 16S ribosomal RNA gene, partial
sequence.
ACCESSION  AF078232
VERSION    AF078232.1 GI:4590103
KEYWORDS
SOURCE     Grassland soil clone saf2_117
ORGANISM   grassland soil clone saf2_117
REFERENCE  1 (bases 1 to 432)
AUTHORS    McCaig,A.E., Glover,L.A. and Prosser,J.I.
TITLE      Molecular analysis of bacterial community structure and diversity
in unimproved and improved upland grass pastures
JOURNAL    Appl. Environ. Microbiol. 65 (4), 1721-1730 (1999)
PUBMED     10103273
REFERENCE  2 (bases 1 to 432)
AUTHORS    McCaig,A.E., Prosser,J.I. and Glover,L.A.
TITLE      Direct Submission
JOURNAL    Submitted (16-JUL-1998) Institute of Medical Sciences, Department
of Molecular and Cell Biology, University of Aberdeen,
Foresterhill, Aberdeen AB25 2ZD, Scotland, UK
FEATURES   Location/Qualifiers
            source
            1..432
            /organism="grassland soil clone saf2_117"
            /mol_type="genomic DNA"
            /db_xref="taxon:80202"
            /clone_lib="unimproved grassland soil SAF2"
            /environmental_sample
            <1_>432
            /product="16S ribosomal RNA"

rRNA
ORIGIN
Query Match      91.6%; Score 17.4; DB 1; Length 432;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GAACGGAAGGCCCTTCGG 19
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Db      15 GAACGGAAGGCCCTTCGG 33

RESULT 74
AY673198 LOCUS      433 bp      DNA      linear      BCT 20-MAY-2005
DEFINITION  Mycobacteriaceae bacterium Ellin7032 16S ribosomal RNA gene,
partial sequence.
ACCESSION  AY673198
VERSION    AY673198.1 GI:56683055
KEYWORDS
SOURCE     Mycobacteriaceae bacterium Ellin7032
ORGANISM   Mycobacteriaceae bacterium Ellin7032
REFERENCE  1 (bases 1 to 433)

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RESULT 76	
DO063195	
LOCUS	DO063195 435 bp DNA linear BCT 27-JUN-2005
DEFINITION	Actinobacterium BAL259 16S ribosomal RNA gene, partial sequence.
ACCESSION	DO063195
VERSION	DO063195.1 GI:68139233
KEYWORDS	
SOURCE	actinobacterium BAL259
ORGANISM	actinobacterium BAL259
REFERENCE	Bacteria; Actinobacteria.
AUTHORS	1 (bases 1 to 435)
TITLE	Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
JOURNAL	Bacterial community composition in the central Baltic Sea analyzed by cultivation and molecular-based methods
REFERENCE	Unpublished
AUTHORS	2 (bases 1 to 435)
TITLE	Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
JOURNAL	Direct Submission
FEATURES	Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences, University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden Location/Qualifiers
source	1..435
	/organism="actinobacterium BAL259"
	/mol_type="genomic DNA"
	/strain="BAL259"
	/isolation_source="Baltic Sea, 3m depth, Landsort deep St. BY31, Zobelii/R2A media"
	/db_xref="taxon:331808"
	/country="Sweden"
	/lat_lon="60.42.726N, 05.05.595E"
rRNA	/collection_date="17 May 2004"
	<1..>435
ORIGIN	/product="16S ribosomal RNA"
Query Match	91.6%; Score 17.4; DB 15; Length 435;
Best Local Similarity	94.7%; Pred.No. 1.9e+03;
Matches	18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 GAACGGAAAGGCGCTTCGG 19
Db	22 GAACGGAAAGGCGCTTCGG 40
RESULT 77	
AY234692	
LOCUS	AY234692 435 bp DNA linear BCT 08-DEC-2003
DEFINITION	Bacterium Elling6040 16S ribosomal RNA gene, partial sequence.
ACCESSION	AY234692
VERSION	AY234692.1 GI:37961849
KEYWORDS	
SOURCE	bacterium Elling6040
ORGANISM	bacterium Elling6040
REFERENCE	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae.
AUTHORS	1 (bases 1 to 435)
TITLE	Joseph,S.J., Hugenholtz,P., Sangwan,P., Osborne,C.A. and Jansen,P.H.
JOURNAL	Laboratory Cultivation of Widespread and Previously Uncultured Soil Bacteria
PUBMED	Appl. Environ. Microbiol. 69 (12), 7210-7215 (2003)
REFERENCE	14660368
AUTHORS	2 (bases 1 to 435)
TITLE	Joseph,S.J., Hugenholtz,P., Rana,P., Osborne,C.A., Sait,M. and Jansen,P.H.
JOURNAL	Direct Submission
FEATURES	Submitted (12-FEB-2003) Department of Microbiology and Immunology, University of Melbourne, Parkville, Victoria 3010, Australia Location/Qualifiers

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source
1. .435
/organism="bacterium Ellin7067"
/mol_type="genomic DNA"
/isolate="Ellin7067"
/db_xref="taxon:234122"
<1..>435
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 91.6%; Score 17.4; DB 15; Length 435;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCCTTCGG 19
Db 37 GAACGGAAGCCCTTCGG 55

RESULT 78
AY673233
LOCUS
DEFINITION Mycobacteriaceae bacterium Ellin7067 16S ribosomal RNA gene,
partial sequence.
ACCESSION AY673233
VERSION AY673233.1 GI:56683090
KEYWORDS
SOURCE
ORGANISM
Mycobacteriaceae bacterium Ellin7067
Mycobacteriaceae bacterium Ellin7067
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
REFERENCE
1 (bases 1 to 435)
Davis, K.E., Joseph, S.J. and Janssen, P.H.
Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
15691937
JOURNAL
PUBMED
REFERENCE
2 (bases 1 to 435)
Davis, K.E., Joseph, S.J. and Janssen, P.H.
Direct Submission
Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
AUSTRALIA
Location/Qualifiers
1. .435
/organism="Mycobacteriaceae bacterium Ellin7067"
/mol_type="genomic DNA"
/isolate="Ellin7067"
/isolation_source="soil"
/db_xref="taxon:305274"
<1..>435
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 91.6%; Score 17.4; DB 15; Length 435;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCCTTCGG 19
Db 37 GAACGGAAGCCCTTCGG 55

RESULT 79
DQ063046
LOCUS
DEFINITION Actinobacterium BAL106 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ063046
VERSION DQ063046.1 GI:68139075
KEYWORDS
SOURCE
actinobacterium BAL106
actinobacterium BAL106
Bacteria; Actinobacteria.
REFERENCE
1 (bases 1 to 436)

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AUTHORS
Riemann, L., Leitet, C., Pommier, T., Simu, K., Holmfeldt, K. and
Hagstrom, A.
TITLE
Bacterial community composition in the central Baltic Sea analyzed
by cultivation and molecular-based methods
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 436)
Riemann, L., Leitet, C., Pommier, T., Simu, K., Holmfeldt, K. and
Hagstrom, A.
TITLE
Direct Submission
Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
AUSTRALIA
Location/Qualifiers
1. .436
/organism="actinobacterium BAL106"
/mol_type="genomic DNA"
/strain="BAL106"
/isolation_source="Baltic Sea, 3m depth, Landsort deep St.
BY31, Zobel/R2A media"
/db_xref="taxon:331778"
/country="Sweden"
/lat_lon="60.42.726N, 05.05.595E"
/collection_date="2 July 2003"
<1..>436
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 91.6%; Score 17.4; DB 15; Length 436;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCCTTCGG 19
Db 26 GAACGGAAGCCCTTCGG 44

RESULT 80
AY673199
LOCUS
DEFINITION Mycobacteriaceae bacterium Ellin7033 16S ribosomal RNA gene,
partial sequence.
ACCESSION AY673199
VERSION AY673199.1 GI:56683056
KEYWORDS
SOURCE
Mycobacteriaceae bacterium Ellin7033
Mycobacteriaceae bacterium Ellin7033
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
REFERENCE
1 (bases 1 to 436)
Davis, K.E., Joseph, S.J. and Janssen, P.H.
Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
15691937
JOURNAL
PUBMED
REFERENCE
2 (bases 1 to 436)
Davis, K.E., Joseph, S.J. and Janssen, P.H.
Direct Submission
Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
AUSTRALIA
Location/Qualifiers
1. .436
/organism="Mycobacteriaceae bacterium Ellin7033"
/mol_type="genomic DNA"
/isolate="Ellin7033"
/isolation_source="soil"
/db_xref="taxon:305256"
<1..>436
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 91.6%; Score 17.4; DB 15; Length 436;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 GAACGGAAGGCGCTTCGG 19
    |||||
Db 37 GAACGGAAGGCGCTTCGG 55

RESULT 81
AY673304 436 bp DNA linear BCT 20-MAY-2005
LOCUS Mycobacteriaceae bacterium Ellin7138 16S ribosomal RNA gene,
DEFINITION Partial sequence.
ACCESSION AY673304
VERSION AY673304.1 GI:56683161
KEYWORDS
SOURCE Mycobacteriaceae bacterium Ellin7138
ORGANISM Mycobacteriaceae bacterium Ellin7138
          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Corynebacterineae; Mycobacteriaceae.
REFERENCE 1 (bases 1 to 436)
          Davis, K.E., Joseph, S.J. and Janssen, P.H.
          Effects of growth medium, inoculum size, and incubation time on
          TITLE culturability and isolation of soil bacteria
          JOURNAL Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
          PUBMED 15691937
          Davis, K.E.R., Joseph, S.J. and Janssen, P.H.
          Direct Submission.
          AUTHORS Submitted (02-JUL-2004) Department of Microbiology and Immunology,
          TITLE University of Melbourne, Grattan Street, Parkville, Victoria 3010,
          JOURNAL Australia
FEATURES             Location/Qualifiers
     source           1..436
                     /organism="Mycobacteriaceae bacterium Ellin7138"
                     /mol_type="genomic DNA"
                     /isolate="Ellin7138"
                     /isolation_source="soil"
                     /db_xref="taxon:305288"
     rRNA             <1..>436
                     /product="16S ribosomal RNA"

ORIGIN
Query Match          91.6%; Score 17.4; DB 15; Length 436;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTCGG 19
    |||||
Db 37 GAACGGAAGGCGCTTCGG 55

RESULT 82
AF078419 437 bp DNA linear ENV 10-MAY-2004
LOCUS Grassland soil clone sl3_612 16S ribosomal RNA gene, partial
DEFINITION sequence.
ACCESSION AF078419
VERSION AF078419.1 GI:4590290
KEYWORDS ENV.
SOURCE Grassland soil clone sl3_612
ORGANISM grassland soil clone sl3_612
          Bacteria; environmental samples.
REFERENCE 1 (bases 1 to 437)
          McCaig, A.E., Glover, L.A. and Prosser, J.I.
          TITLE Molecular analysis of bacterial community structure and diversity
          in unimproved and improved upland grass pastures
          JOURNAL Appl. Environ. Microbiol. 65 (4), 1721-1730 (1999)
          PUBMED 10103273
          McCaig, A.E., Prosser, J.I. and Glover, L.A.
          AUTHORS Direct Submission.
          TITLE Submitted (16-JUL-1998) Institute of Medical Sciences, Department
          JOURNAL of Molecular and Cell Biology, University of Aberdeen,
          Foresterhill, Aberdeen AB25 2ZD, Scotland, UK

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FEATURES             Location/Qualifiers
     source           1..437
                     /organism="grassland soil clone sl3_612"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:80115"
                     /clone_lib="improved grassland soil SL3"
                     /environmental_sample
     rRNA             <1..>437
                     /product="16S ribosomal RNA"

ORIGIN
Query Match          91.6%; Score 17.4; DB 1; Length 437;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTCGG 19
    |||||
Db 15 GAGCGGAAGGCGCTTCGG 33

RESULT 83
AB232370 441 bp DNA linear BCT 25-JAN-2006
LOCUS Mycobacterium kansasii gene for 16S rRNA, partial sequence,
DEFINITION strain:SA-10.
ACCESSION AB232370
VERSION AB232370.1 GI:73589607
KEYWORDS
SOURCE Mycobacterium kansasii
ORGANISM Mycobacterium kansasii
          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1
          Iwamoto, T. and Saito, H.
          TITLE Comparative study of two typing methods, hsp65 PRA and ITS
          sequencing, revealed a possible evolutionary link between
          JOURNAL Mycobacterium kansasii type I and II isolates
          REFERENCE FEMS Microbiol. Lett. 254, 129-133 (2006)
          AUTHORS 2 (bases 1 to 441)
          Iwamoto, T.
          TITLE Direct Submission
          JOURNAL Submitted (17-AUG-2005) Tomotada Iwamoto, Kobe Institute of Health,
          Department of Microbiology; Chuo-ku Minatojima-nakanishi 4-6, Kobe,
          Hyogo 6500046, Japan (E-mail: kx2t-iwmt@asahi-net.or.jp,
          URL:http://www.city.kobe.jp/cityoffice/18/menu03/h/kanken/kanken-
          top, Tel:81-78-302-6251, Fax:81-78-302-0894)
FEATURES             Location/Qualifiers
     source           1..441
                     /organism="Mycobacterium kansasii"
                     /mol_type="genomic DNA"
                     /strain="SA-10"
                     /db_xref="taxon:1768"
                     /note="type II"
     rRNA             <1..>441
                     /product="16S ribosomal RNA"

ORIGIN
Query Match          91.6%; Score 17.4; DB 15; Length 441;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTCGG 19
    |||||
Db 11 GAACGGAAGGCGCTTCGG 29

RESULT 84
AY306201 442 bp DNA linear BCT 25-JUN-2003
LOCUS Mycobacterium sp. 1351 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION AY306201
VERSION AY306201.1 GI:32250950
KEYWORDS

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SOURCE
ORGANISM  Mycobacterium sp. 1351
           Mycobacterium sp. 1351
           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
           Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS   Pauls,R.J., Turenne,C.Y., Wolfe,J.N. and Kabani,A.
TITLE     A High Proportion of Novel Mycobacteria Species Identified by 16S
           rDNA Analysis Among Slowly Growing AccuProbe Negative Strains in a
           Clinical Setting
JOURNAL   Unpublished
REFERENCE
AUTHORS   2 (bases 1 to 442)
TITLE     Direct Submission
JOURNAL   Submitted (26-MAY-2003) National Reference Centre for
           Microbiology, National Microbiology Laboratory, Health Canada,
           1015 Arlington Street, Winnipeg, MB R3E 3R2, Canada
FEATURES
source    Location/Qualifiers
           1..442
           /organism="Mycobacterium sp. 1351"
           /mol_type="genomic DNA"
           /strain="1351"
           /isolation_source="mouth ulcer"
           /specific_host="Homo sapiens"
           /db_xref="taxon:235254"
           <1..>442
           /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      91.6%; Score 17.4; DB 15; Length 442;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1  GAACGGAAGGCTTCGG 19
    |||||
Db  11 GAACGGAAGGCTTCGG 29

RESULT 85
AY306205
LOCUS      444 bp      DNA      linear      BCT 25-JUN-2003
DEFINITION Mycobacterium sp. HSC507 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY306205
VERSION     AY306205.1 GI:32250954
KEYWORDS
SOURCE      Mycobacterium sp. HSC507
ORGANISM    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
           Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS     Pauls,R.J., Turenne,C.Y., Wolfe,J.N. and Kabani,A.
TITLE       A High Proportion of Novel Mycobacteria Species Identified by 16S
           rDNA Analysis Among Slowly Growing AccuProbe Negative Strains in a
           Clinical Setting
JOURNAL     Unpublished
REFERENCE
AUTHORS     2 (bases 1 to 444)
TITLE       Direct Submission
JOURNAL     Submitted (26-MAY-2003) National Reference Centre for
           Microbiology, National Microbiology Laboratory, Health Canada,
           1015 Arlington Street, Winnipeg, MB R3E 3R2, Canada
FEATURES
source      Location/Qualifiers
           1..444
           /organism="Mycobacterium sp. HSC507"
           /mol_type="genomic DNA"
           /strain="HSC507"
           /isolation_source="sputum"
           /specific_host="Homo sapiens"
           /db_xref="taxon:235258"
           <1..>444
           /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      91.6%; Score 17.4; DB 15; Length 444;

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SOURCE
ORGANISM  Mycobacterium sp. 1351
           Mycobacterium sp. 1351
           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
           Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS   Pauls,R.J., Turenne,C.Y., Wolfe,J.N. and Kabani,A.
TITLE     A High Proportion of Novel Mycobacteria Species Identified by 16S
           rDNA Analysis Among Slowly Growing AccuProbe Negative Strains in a
           Clinical Setting
JOURNAL   Unpublished
REFERENCE
AUTHORS   2 (bases 1 to 442)
TITLE     Direct Submission
JOURNAL   Submitted (26-MAY-2003) National Reference Centre for
           Microbiology, National Microbiology Laboratory, Health Canada,
           1015 Arlington Street, Winnipeg, MB R3E 3R2, Canada
FEATURES
source    Location/Qualifiers
           1..442
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           /mol_type="genomic DNA"
           /strain="1351"
           /isolation_source="mouth ulcer"
           /specific_host="Homo sapiens"
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           /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      91.6%; Score 17.4; DB 15; Length 442;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1  GAACGGAAGGCTTCGG 19
    |||||
Db  11 GAACGGAAGGCTTCGG 29

RESULT 86
AB106917
LOCUS      445 bp      DNA      linear      BCT 09-SEP-2003
DEFINITION Gram-positive bacterium 1-3 for 16S ribosomal RNA, partial
           sequence.
ACCESSION  AB106917
VERSION     AB106917.1 GI:29421131
KEYWORDS
SOURCE      Gram-positive bacterium 1-3
           Gram-positive bacterium 1-3
           Bacteria.
REFERENCE
AUTHORS     Amachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
           Fujii,T. and Muramatsu,Y.
TITLE       Microbial participation in iodine volatilization from soils
JOURNAL     Environ. Sci. Technol. 37, 3885-3890 (2003)
REFERENCE
AUTHORS     Amachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
           Fujii,T. and Muramatsu,Y.
TITLE       Direct Submission
JOURNAL     Submitted (27-MAR-2003) Seigo Amachi, Chiba University, Dept. of
           Bioresources Chem.; 648 Matsudo, Matsudo-shi, Chiba 271-8510, Japan
           (E-mail:amachi@faculty.chiba-u.jp, Tel:81-47-308-8868,
           Fax:81-47-308-8866)
FEATURES
source      Location/Qualifiers
           1..445
           /organism="Gram-positive bacterium 1-3"
           /mol_type="genomic DNA"
           /strain="1-3"
           /db_xref="taxon:226199"
           <1..>445
           /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      91.6%; Score 17.4; DB 15; Length 445;
Best Local Similarity 94.7%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1  GAACGGAAGGCTTCGG 19
    |||||
Db  37 GAACGGAAGGCTTCGG 55

RESULT 87
DQ067466
LOCUS      445 bp      DNA      linear      BCT 18-JUL-2005
DEFINITION Mycobacterium sp. FI05167 16S ribosomal RNA gene, partial sequence.
ACCESSION  DQ067466
VERSION     DQ067466.1 GI:67528039
KEYWORDS
SOURCE      Mycobacterium sp. FI05167
           Mycobacterium sp. FI05167
           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
           Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS     Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE       Unusual mycobacteria isolated from clinical samples
JOURNAL     Unpublished
REFERENCE
AUTHORS     2 (bases 1 to 445)
TITLE       Direct Submission
JOURNAL     Submitted (17-MAY-2005) Reg. Reference Center for Mycobacteria,
           Careggi Hospital, Piastra dei Servizi, Ospedale Careggi, v.le
           Morgagni 85, Firenze, FI 50134, Italy
           Location/Qualifiers

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source 1. .445
/organism="Mycobacterium sp. FI05167"
/mol_type="genomic DNA"
/strain="FI05167"
/db_xref="taxon:332013"
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/product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match 91.6%; Score 17.4; DB 15; Length 445;
Best Local Similarity 94.7%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCCTTCGG 19
|||||
Db 15 GAACGGAAGGCCCTTCGG 33

RESULT 88
AY957708
LOCUS AY957708 447 bp DNA linear ENV 16-SEP-2005
DEFINITION Uncultured bacterium clone P3DKE08 16S small subunit ribosomal RNA
gene, partial sequence.
ACCESSION AY957708
VERSION AY957708.1 GI:62005486
KEYWORDS ENV.
SOURCE uncultured bacterium
ORGANISM uncultured bacterium
Bacteria; environmental samples.
REFERENCE 1 (bases 1 to 447)
McManus,C.J. and Kelley,S.T.
TITLE Molecular survey of aeroplane bacterial contamination
JOURNAL J. Appl. Microbiol. 99 (3), 502-508 (2005)
PUBMED 16108791
REFERENCE 2 (bases 1 to 447)
McManus,C.J. and Kelley,S.T.
AUTHORS Direct Submission
TITLE Submitted (09-WAR-2005) Biology, San Diego State University, 5500
JOURNAL Campanile Dr., San Diego, CA 92182, USA
FEATURES Location/Qualifiers
source 1. .447
/organism="uncultured bacterium"
/mol_type="genomic DNA"
/isolation_source="airplane"
/db_xref="taxon:77133"
/clone="P3DKE08"
/environmental_sample
<1. .5447
/product="16S small subunit ribosomal RNA"

rRNA

ORIGIN

Query Match 91.6%; Score 17.4; DB 1; Length 447;
Best Local Similarity 94.7%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCCTTCGG 19
|||||
Db 5 GAACGGAAGGCCCTTCGG 23

RESULT 89
MS91016SR
LOCUS MS91016SR 450 bp DNA linear BCT 01-AUG-1997
DEFINITION Mycobacterium sp.16S rRNA gene, isolate BN910, partial.
Y08205
ACCESSION Y08205.1 GI:2292948
VERSION Y08205.1
KEYWORDS 16S ribosomal RNA; 16S rRNA.
SOURCE Mycobacterium sp.
ORGANISM Mycobacterium sp.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
1
Hagenau,C., Behringer,K., Naumann,L., Kaiser,R. and

JOURNAL Schulze-Roebecke,R.
REFERENCE Unpublished
AUTHORS 2 (bases 1 to 450)
Hagenau,C.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-1996) C. Hagenau, Hygiene-Institute, University
of Bonn, Sigmund-Freud-Strasse 25, D-53105 Bonn, FRG
COMMENT Related sequence M95469
FEATURES Location/Qualifiers
source 1. .450
/organism="Mycobacterium sp."
/mol_type="genomic DNA"
/isolate="BN910"
/db_xref="taxon:1785"
/map="E.coli position 38-503"
1. .450
/gene="16S rRNA"
<1. .>450
/genes="16S rRNA"
/product="16S ribosomal RNA"

gene

rRNA

ORIGIN

Query Match 91.6%; Score 17.4; DB 15; Length 450;
Best Local Similarity 94.7%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCCTTCGG 19
|||||
Db 27 GAACGGAAGGCCCTTCGG 45

RESULT 90
MS916SR
LOCUS MS916SR 450 bp DNA linear BCT 01-AUG-1997
DEFINITION Mycobacterium sp. 16S rRNA gene.
Y07954
ACCESSION Y07954.1 GI:2292951
VERSION Y07954.1
KEYWORDS 16S ribosomal RNA; 16S rRNA gene.
SOURCE Mycobacterium sp.
ORGANISM Mycobacterium sp.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
1
Hagenau,C., Behringer,K., Naumann,L., Kaiser,R. and
Schulze-Roebecke,R.
AUTHORS Unpublished
JOURNAL 2 (bases 1 to 450)
Hagenau,C.
TITLE Direct Submission
JOURNAL Submitted (12-SEP-1996) C. Hagenau, Hygiene-Institute, University
of Bonn, Sigmund-Freud-Strasse 25, D-53105 Bonn, FRG
COMMENT Related sequence: M95469.
FEATURES Location/Qualifiers
source 1. .450
/organism="Mycobacterium sp."
/mol_type="genomic DNA"
/isolate="BN737"
/db_xref="taxon:1785"
/map="E.coli 38-503"
1. .450
/gene="16S rRNA"
<1. .>450
/genes="16S rRNA"
/product="16S ribosomal RNA"

gene

rRNA

ORIGIN

Query Match 91.6%; Score 17.4; DB 15; Length 450;
Best Local Similarity 94.7%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCCTTCGG 19
|||||
Db 27 GAACGGAAGGCCCTTCGG 45

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RESULT 91
LOCUS      AY358002               450 bp    DNA        linear    BCT 19-AUG-2005
DEFINITION Actinobacterium irIII7 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY358002
VERSION     AY358002.1 GI:34500643
KEYWORDS
SOURCE      .
ORGANISM    actinobacterium irIII7
            actinobacterium irIII7
            Bacteria; Actinobacteria.
REFERENCE   1 (bases 1 to 450)
AUTHORS     Idris,R., Trifonova,R., Puschenreiter,M., Wenzel,W.W. and
            Sessitsch,A.
TITLE       Bacterial Communities Associated with Flowering Plants of the Ni
            Hyperaccumulator Thlaspi goesingense
JOURNAL     Appl. Environ. Microbiol. 70 (5), 2667-2677 (2004)
PUBMED     15128517
REFERENCE   2 (bases 1 to 450)
AUTHORS     Idris,R. and Sessitsch,A.
TITLE       Direct Submission
JOURNAL     Submitted (01-AUG-2003) Environmental and Life Sciences, ARC
            Seibersdorf Research GmbH, Seibersdorf A-2444, Austria
FEATURES
            Location/Qualifiers
            source
            1..450
               /organism="actinobacterium irIII7"
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               /strain="irIII7"
               /db_xref="taxon:244182"
               <1..>450
               /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      91.6%; Score 17.4; DB 15; Length 450;
Best Local Similarity 94.7%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCTTCGG 19
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Db 59 GAACGGAAGGCCTTCGG 77

RESULT 92
LOCUS      AJ746062               454 bp    DNA        linear    BCT 11-MAR-2005
DEFINITION Mycobacterium sp. MG5 partial 16S rRNA gene, isolate MG5.
ACCESSION  AJ746062
VERSION     AJ746062.1 GI:61097518
KEYWORDS    16S ribosomal RNA; 16S rRNA gene.
SOURCE      Mycobacterium sp. MG5
ORGANISM    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE   1
AUTHORS     Gomila,M., Gasco,J., Busquets,A., Gil,J., Bernabeu,R., Buades,J.M.
            and Lalucat,J.
TITLE       Identification of culturable bacteria present in haemodialysis
            water and fluid
JOURNAL     FEMS Microbiol. Ecol. 52 (1), 101-114 (2005)
REFERENCE   2 (bases 1 to 454)
AUTHORS     Gomila,M.
TITLE       Direct Submission
JOURNAL     Submitted (07-JUN-2004) Gomila M., Biologia-IMEDEA. Microbiologia,
            Universitat de les Illes Balears, Ctra. Valldemossa, km. 7.5, 07122
            Palma de Mallorca, SPAIN
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Qy 1 GAACGGAAGGCCTTCGG 19
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Db 30 GAACGGAAGGCCTTCGG 48

RESULT 93
LOCUS      AY358001               456 bp    DNA        linear    BCT 19-AUG-2005
DEFINITION Actinobacterium irIII6 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY358001
VERSION     AY358001.1 GI:34500642
KEYWORDS    .
SOURCE      actinobacterium irIII6
            actinobacterium irIII6
            Bacteria; Actinobacteria.
REFERENCE   1 (bases 1 to 456)
AUTHORS     Idris,R., Trifonova,R., Puschenreiter,M., Wenzel,W.W. and
            Sessitsch,A.
TITLE       Bacterial Communities Associated with Flowering Plants of the Ni
            Hyperaccumulator Thlaspi goesingense
JOURNAL     Appl. Environ. Microbiol. 70 (5), 2667-2677 (2004)
PUBMED     15128517
REFERENCE   2 (bases 1 to 456)
AUTHORS     Idris,R. and Sessitsch,A.
TITLE       Direct Submission
JOURNAL     Submitted (01-AUG-2003) Environmental and Life Sciences, ARC
            Seibersdorf Research GmbH, Seibersdorf A-2444, Austria
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Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCTTCGG 19
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Db 59 GAACGGAAGGCCTTCGG 77

RESULT 94
LOCUS      AJ609008               459 bp    DNA        linear    ENV 20-JAN-2004
DEFINITION Uncultured bacterium partial 16S rRNA gene, clone 24-9.
ACCESSION  AJ609008
VERSION     AJ609008.1 GI:41033549
KEYWORDS    ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE      uncultured bacterium
            uncultured bacterium
            Bacteria; environmental samples.
REFERENCE   1
AUTHORS     Schneider,B.A., Huettli,R.F. and Schneider,B.U.
TITLE       Evidence for a diverse bacterial consortium specialized to the
            degradation of aliphatic and aromatic hydrocarbons in lignite

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matter of a forest reclamation site
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 459)
 AUTHORS Schneider,B.A.
 TITLE Direct Submission
 JOURNAL Submitted (20-NOV-2003) Schneider B.A., Soil Protection and
 Recultivation, Brandenburg Technical University,
 Theodor-Neubauer-Str. 6, D-03046 Cottbus, GERMANY
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 Db 15 GAACGGTAAGCGCTTTCGG 33
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 DEFINITION sequence.
 ACCESSION AY754884
 VERSION AY754884.1 GI:54065968
 KEYWORDS
 SOURCE
 ORGANISM
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 Mycobacterium vaccae
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 REFERENCE 1 (bases 1 to 459)
 AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
 TITLE Unusual mycobacteria isolated from clinical samples
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 459)
 AUTHORS Tortoli,E.
 TITLE Direct Submission
 JOURNAL Submitted (16-SEP-2004) Microbiology, Careggi Hospital, viale
 Morgagni 85, Firenze, FI 50134, Italy
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 Db 31 GAACGGAAAGGCGCTTTCGG 49

RESULT 96
 AY754885 459 bp DNA linear BCT 17-OCT-2004
 LOCUS Mycobacterium sp. FI02139 16S ribosomal RNA gene, partial sequence.
 DEFINITION
 ACCESSION AY754885
 VERSION AY754885.1 GI:54065976
 KEYWORDS
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 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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 REFERENCE 1 (bases 1 to 459)
 AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
 TITLE Unusual mycobacteria isolated from clinical samples
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 459)
 AUTHORS Tortoli,E.
 TITLE Direct Submission
 JOURNAL Submitted (16-SEP-2004) Microbiology, Careggi Hospital, viale
 Morgagni 85, Firenze, FI 50134, Italy
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 Db 30 GAACGGAAAGGCGCTTTCGG 48
 RESULT 97
 AB118817 464 bp DNA linear BCT 01-JUN-2005
 LOCUS Denitrifying bacterium W67a gene for 16S ribosomal RNA, partial
 DEFINITION sequence.
 ACCESSION AB118817
 VERSION AB118817.1 GI:66841148
 KEYWORDS
 SOURCE
 ORGANISM
 denitrifying bacterium W67a
 denitrifying bacterium W67a
 Bacteria; Actinobacteria.
 REFERENCE 1
 HASHIMOTO,T., Whang,K.S. and Nagaoka,K.
 AUTHORS A Quantitative Evaluation and Phylogenetic Characterization of
 TITLE Oligotrophic Denitrifying Bacteria Harbored in Subsurface Upland
 JOURNAL Soil Using Improved Culturability
 REFERENCE 2 (bases 1 to 464)
 AUTHORS Hashimoto,T. and Whang,K.
 TITLE Direct Submission
 JOURNAL Submitted (29-AUG-2003) Tomoyoshi Hashimoto, National Agricultural
 Research Center for Kyushu Okinawa Region, Department of
 Agro-Environmental Research, Nishigoushi-cho Suva 2421,
 Kikuchi-gun, Kumamoto, 861-1192, Japan
 (E-mail:hashimoto@affrc.go.jp, Tel:0962427765, Fax:0962491002)
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DEFINITION Mycobacterium sp. FI03023 16S ribosomal RNA gene, partial sequence.
ACCESSION  DQ142669
VERSION    DQ142669.1 GI:71912648
KEYWORDS
SOURCE     Mycobacterium sp. FI03023
ORGANISM   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE  Tortoli,E., Mariottini,A. and Mazzarelli,G.
            Unusual mycobacteria isolated from clinical specimens
            Unpublished
JOURNAL
AUTHORS   Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE     Direct Submission
JOURNAL   Submitted (18-JUL-2005) Microbiology, Careggi Hospital, Viale
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Qy 1 GAACGGAAGGCCCTTCGG 19
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Db 30 GAACGGAAGGCCCTTCGG 48

RESULT 99
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LOCUS      DQ142672          464 bp      DNA      linear      BCT 13-AUG-2005
DEFINITION Mycobacterium sp. FI05244 16S ribosomal RNA gene, partial sequence.
ACCESSION  DQ142672
VERSION    DQ142672.1 GI:71912651
KEYWORDS
SOURCE     Mycobacterium sp. FI05244
ORGANISM   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE  Tortoli,E., Mariottini,A. and Mazzarelli,G.
            Unusual mycobacteria isolated from clinical specimens
            Unpublished
JOURNAL
AUTHORS   Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE     Direct Submission
JOURNAL   Submitted (25-JUL-2005) Microbiology, Careggi Hospital, Viale
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Db 30 GAACGGAAGGCCCTTCGG 48

RESULT 100
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DEFINITION Mycobacterium sp. FI05038 16S ribosomal RNA gene, partial sequence.
ACCESSION  DQ067465
VERSION    DQ067465.1 GI:67528030
KEYWORDS
SOURCE     Mycobacterium sp. FI05038
ORGANISM   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE  Tortoli,E., Mantella,A., Mariottini,A., Mazzarelli,G., Pecile,P.,
            Rogasi,P.G., Sterrantino,G., Fantoni,E. and Leoncini,F.
            Successfully treated spondylodiscitis due to a previously
            unreported mycobacterium
JOURNAL   J. Med. Microbiol. 55 (PT 1), 119-121 (2006)
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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 02:22:49 ; Search time 294.729 Seconds
(without alignments)
591.412 Million cell updates/sec

Title: US-10-665-708-21

Perfect score: 25

Sequence: 1 gcaagtcgaacggaaggccttgcg 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 524920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 104899840

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Listing first 300 summaries

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- 15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	25	100.0	25	10	ADG88352 Mycobacte
3	25	100.0	25	14	AEA08227 Mycobacte
4	24	96.0	24	4	AAD11272 Mycobacte
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6	24	96.0	24	14	AEA08228 Mycobacte
7	23.4	93.6	500	13	ADZ20587 Formaldeh
8	23.4	93.6	1449	14	AEA22405 Mycobacte
9	23.4	93.6	1455	14	AEA22412 Mycobacte
10	23.4	93.6	1482	14	AEA22404 Mycobacte
11	21.8	87.2	50	12	ADF94057 Microorga
12	21.8	87.2	166	2	AAX32481 Preferred
13	21.8	87.2	460	8	ABZ76674 Microtetr
14	21.8	87.2	497	14	ABZ72673 Streptosp
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18	21.8	87.2	1403	12	ADJ38609 Micromono

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22	21.8	87.2	1483	14	AED35651
23	21.8	87.2	1511	13	ADR90327
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AED41084	coralli
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ADW11024	Probe #4
ADW11017	PCR prime
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AAX99196	M. fortui
ADF94050	Microorga
AEF98762	Mycobacte
ABT23571	Stabilisi
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AEF98771	Mycobacte
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ACF64469	Propionib
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AAX99201	M. simium
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ADY86147	Saccharot
ADC61232	Baeyer-Vi
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ADY86148	Saccharot
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ADW12667	Rhodococc
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AEA22410	Mycobacte
AD085868	Gordonia
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ADW11823	DNA of RN
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AEA08220	Mycobacte
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AAX99194	M. bovis
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ADF94047	Microorga
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98	19.8	79.2	1524	4	AA530719	Aae30719 Mycobacte	171	17	58.0	981	8	ACA27357	ACA27357 Prokaryot
99	19.8	79.2	1536	10	ADB61681	Adb61681 16S rRNA	172	17	58.0	1420	14	ADM16254	Adm16254 DNA copy
100	19.8	79.2	1536	10	ADB61682	Adb61682 16S rRNA	173	17	58.0	1468	14	AED50856	Aed50856 M. haemof
101	19.8	79.2	1537	10	ADB74385	Adf1649 Mycobacte	174	17	58.0	1476	14	AEE94382	Aee94382 Streptomy
c 102	19.8	79.2	36241	10	ADBF74385	Adbf74385 Mycobacte	c 175	17	58.0	1476	14	AEE94381	Aee94381 Streptomy
c 103	19.8	79.2	36470	10	ADB74374	Adb74374 Mycobacte	176	17	58.0	2106	11	ABD08113	Abd08113 Pseudomon
104	19.8	79.2	110000	4	AAI99682_14	Continuation (15 o	c 177	17	58.0	2199	8	ACA43833	ACA43833 Prokaryot
105	19.8	79.2	110000	4	AAI99683_14	Continuation (15 o	c 178	17	58.0	2325	4	RA551444	RA551444 Pseudomon
106	19.4	77.6	39	14	ADU69984	Adue9984 LAMP reac	c 179	17	58.0	2325	8	ACA19423	ACA19423 Prokaryot
107	19.4	77.6	39	14	ADU69983	Adue9983 LAMP reac	c 180	17	58.0	2427	11	ABD04295	Abd04295 Pseudomon
108	19.4	77.6	39	14	ADU69985	Adue9985 LAMP reac	181	17	58.0	2556	11	ABD04470	Abd04470 Pseudomon
109	19.4	77.6	39	14	AEb98765	Aeb98765 Mycobacte	182	17	58.0	4839	4	ABL14642	ABL14642 Drosophil
110	19.4	77.6	39	14	AEb98779	Aeb98779 Mycobacte	183	17	58.0	35058	4	ABL05556	ABL05556 Drosophil
111	19.4	77.6	39	15	AEF95350	Aef95350 Nucleic a	c 184	17	58.0	110000	6	ABA03041_07	Continuation (8 of
112	19.4	77.6	41	14	ADU69960	Adue9960 LAMP reac	c 185	16.8	67.2	36538	10	ABV75558	ABv75558 Saccharop
113	19.4	77.6	41	14	ADU69958	Adue9958 LAMP reac	c 186	16.6	66.4	338	6	ABQ99174	Abq99174 Human ORF
114	19.4	77.6	42	14	ADU69959	Adue9959 LAMP reac	c 187	16.6	66.4	381	5	RA577874	RA577874 DNA encod
115	19.4	77.6	42	14	ADU69957	Adue9957 LAMP reac	c 188	16.6	66.4	479	4	AAK79949	AAk79949 Human imm
116	19.2	76.8	1158	14	ADM16249	Adm16249 DNA copy	c 189	16.6	66.4	479	4	AAK79948	AAk79948 Human imm
117	19	76.0	23	4	AD11277	Ad11277 Mycobacte	c 190	16.6	66.4	508	5	RA534274	RA534274 Human cDN
118	19	76.0	23	10	ADG88358	Adg88358 Mycobacte	191	16.6	66.4	580	13	ADQ51208	Adq51208 Novel can
119	19	76.0	23	14	AEA08233	Aea08233 Mycobacte	c 192	16.6	66.4	671	13	ADQ79174	Adq79174 Novel can
120	19	76.0	50	2	AX99197	Aax99197 M. sorofu	c 193	16.6	66.4	780	6	ABQ90469	Abq90469 M. capsul
121	18.8	75.2	1418	8	ABZ25595	Abz25595 Rhodococc	c 194	16.6	66.4	906	13	ADS61681	Ads61681 Bacterial
122	18.4	73.6	36	14	ADU69991	Adue9991 LAMP reac	c 195	16.6	66.4	1020	6	ABN74681	Abn74681 Bovine em
123	18.4	73.6	37	14	ADU69989	Adue9989 LAMP reac	c 196	16.6	66.4	1392	8	ACA23504	ACA23504 Prokaryot
124	18.4	73.6	1452	14	AEA22408	Aea22408 Mycobacte	197	16.6	66.4	1522	6	ABN89870	ABn89870 Clostridi
125	18	72.0	19	4	AD11274	Ad11274 Mycobacte	c 198	16.6	66.4	2077	4	ABL04789	ABl04789 Drosophil
126	18	72.0	19	10	ADG88355	Adg88355 Mycobacte	c 199	16.6	66.4	3216	13	ADV97351	Adv97351 N. tabacum
127	18	72.0	19	14	AEA08230	Aea08230 Mycobacte	c 200	16.6	66.4	4456	4	ABL04788	ABl04788 Drosophil
128	18	72.0	23	2	AAV59060	Aav59060 Primer KY	c 201	16.6	66.4	9591	14	AEC36640	Aec36640 Zucchini
129	18	72.0	23	10	ADF41650	Adf41650 Mycobacte	c 202	16.6	66.4	18900	13	ADW00484	Adw00484 Escherich
130	18	72.0	23	13	ADR90575	Adr90575 Mycobacte	c 203	16.6	66.4	41723	4	ABL23684	ABl23684 Drosophil
c 131	18	72.0	50	2	AX99200	Aax99200 M. intrac	c 204	16.6	66.4	43572	12	ADQ97861	Adq97861 Mouse can
132	18	72.0	1137	9	AD57239	Ad57239 Human CGD	c 205	16.4	65.6	18	8	ACC59438	Acc59438 T. dentico
133	18	72.0	1452	13	ADR90573	Adr90573 M. intrace	c 206	16.4	65.6	18	10	ADD10217	Add10217 Probe #3
134	17.8	71.2	1366	13	ADX59584	Adx59584 Plant ful	c 207	16.4	65.6	23	2	AAQ36781	AAq36781 Mycobacte
135	17.8	71.2	4540	6	ABK63777	Abk63777 Rat sequ	c 208	16.4	65.6	25	2	AAV24418	AAv24418 Target se
c 136	17.8	71.2	4540	10	ADB58396	Adb58396 Toxicity-	c 209	16.4	65.6	25	2	AAV13026	AAv13026 Mycobacte
137	17.6	70.4	465	10	AB57680	Ab57680 Toxicity-	c 210	16.4	65.6	25	4	AA530718	AA530718 Mycobacte
138	17.6	70.4	960	11	ACN44517	Acn44517 Mouse mRN	c 211	16.4	65.6	25	4	AA530718	AA530718 Mycobacte
139	17.6	70.4	1436	14	ADM16288	Adm16288 DNA copy	c 212	16.4	65.6	549	3	ABLI5533	ABl15533 Drosophil
140	17.6	70.4	1561	13	ADR07240	Adr07240 Full leng	c 213	16.4	65.6	1405	3	AAA15482	AAa15482 16S rRNA
141	17.6	70.4	1763	15	AE88040	Aee88040 Human cDN	c 214	16.4	65.6	1413	3	AAA15478	AAa15478 16S rRNA
142	17.6	70.4	1787	4	AAH14162	Aah14162 Human cDN	c 215	16.4	65.6	1432	12	ADK72438	Adk72438 Cyclocias
143	17.6	70.4	1792	12	ADQ84493	Adq84493 Human tum	c 216	16.4	65.6	1460	12	ADK72439	Adk72439 Cyclocias
144	17.6	70.4	1792	12	ADQ85308	Adq85308 Human tum	c 217	16.4	65.6	1462	3	AAA15480	AAa15480 16S rRNA
145	17.6	70.4	43800	11	ACN44516	Acn44516 Mouse gen	c 218	16.4	65.6	1526	5	AAAF76237	AAf76237 Cyclocias
146	17.4	69.6	36	14	ADU69990	Adue69990 LAMP reac	c 219	16.4	65.6	1528	5	AAAF76235	AAf76235 Cyclocias
147	17.4	69.6	1456	15	AE807725	Aeg07725 Nocardioid	c 220	16.4	65.6	1529	5	AAAF76236	AAf76236 Cyclocias
148	17.2	68.8	1417	12	ADJ87468	Adj87468 Tomato Le	c 221	16.4	65.6	2274	13	ADX62498	Adx62498 Plant ful
149	17.2	68.8	1735	13	AAV53856	AAv53856 Plant ful	c 222	16.4	65.6	5503	4	ABL15532	ABl15532 Drosophil
150	17.2	68.8	1776	2	AAV59559	AAv59559 Human sec	c 223	16.2	64.8	587	8	ABZ53802	ABz53802 Aspergill
151	17.2	68.8	1776	6	AB573546	Ab573546 Human cDN	c 224	16.2	64.8	590	8	AQB83792	Aqb83792 Normal co
152	17.2	68.8	1776	9	ACD82689	Ac82689 cDNA sequ	c 225	16.2	64.8	637	3	AAF14590	AAf14590 Aspergill
153	17.2	68.8	1776	10	ADI22774	Adi22774 cDNA enco	c 226	16.2	64.8	637	13	ADU58631	Adu58631 Aspergill
154	17.2	68.8	1776	12	ADH73776	Adh73776 Human sec	c 227	16.2	64.8	637	14	ADZ96634	Adz96634 Aspergill
155	17.2	68.8	1791	2	AAV59723	AAv59723 Human sec	c 228	16.2	64.8	665	14	AEb88183	Aeb88183 Human cDN
156	17.2	68.8	1791	6	AB573713	Ab573713 Human cDN	c 229	16.2	64.8	755	14	AEb88269	Aeb88269 Human DNA
157	17.2	68.8	1791	9	ACD82856	Ac82856 cDNA sequ	c 230	16.2	64.8	788	3	AAC33114	Aac33114 Arabidops
158	17.2	68.8	1791	10	ADI22941	Adi22941 cDNA enco	c 231	16.2	64.8	790	14	AEb88271	Aeb88271 Human DNA
159	17.2	68.8	1791	12	ADH73943	Adh73943 Human sec	c 232	16.2	64.8	813	14	AEb88267	Aeb88267 Human DNA
c 160	17.2	68.8	2919	13	ADS59960	Ad559960 Bacterial	c 233	16.2	64.8	972	6	ABK77386	ABk77386 Bacillus
161	17.2	68.8	3757	4	ABL14492	ABl14492 Drosophil	c 234	16.2	64.8	1049	13	ADS95257	Ad95257 Murine th
162	17.2	68.8	5656	4	ABL14490	ABl14490 Drosophil	c 235	16.2	64.8	1049	13	ADV68114	Adv68114 Biologica
163	17.2	68.8	13206	4	ABL14494	ABl14494 Drosophil	c 236	16.2	64.8	1393	3	AAC41244	Aac41244 Arabidops
164	17	68.0	60	6	AA42509	Ala42509 Self-asse	c 237	16.2	64.8	1447	13	ADT15563	Adt15563 Plant cDN

c 238 16.2 64.8 1498 4 AAF63387
 c 239 16.2 64.8 1588 4 AAF63423
 c 240 16.2 64.8 1902 13 ADT48449
 c 241 16.2 64.8 2226 13 ACN43714
 c 242 16.2 64.8 2239 4 ABL02095
 c 243 16.2 64.8 2294 4 AAF63419
 c 244 16.2 64.8 2340 8 ACA04767
 c 245 16.2 64.8 2371 4 AAF63416
 c 246 16.2 64.8 2497 4 AAF63421
 c 247 16.2 64.8 2597 13 ACN43713
 c 248 16.2 64.8 2648 6 ABT05471
 c 249 16.2 64.8 2693 4 AAF63418
 c 250 16.2 64.8 2693 6 ABT05470
 c 251 16.2 64.8 2729 12 ADQ87074
 c 252 16.2 64.8 2736 6 ABL39778
 c 253 16.2 64.8 2762 3 AA96066
 c 254 16.2 64.8 2762 4 AAF63422
 c 255 16.2 64.8 2762 4 AAF63386
 c 256 16.2 64.8 2762 6 AAD31693
 c 257 16.2 64.8 2762 12 ADQ99441
 c 258 16.2 64.8 2762 13 ADR69170
 c 259 16.2 64.8 2762 13 ADR69004
 c 260 16.2 64.8 2762 13 ACN40734
 c 261 16.2 64.8 2762 13 ADR17884
 c 262 16.2 64.8 2762 13 ADR87780
 c 263 16.2 64.8 2762 13 ADR65838
 c 264 16.2 64.8 2762 13 ADR65522
 c 265 16.2 64.8 2762 13 ADS09773
 c 266 16.2 64.8 2762 14 ADV16894
 c 267 16.2 64.8 2762 14 ADZ66963
 c 268 16.2 64.8 2762 14 ADZ74432
 c 269 16.2 64.8 2805 4 AAF63420
 c 270 16.2 64.8 2837 5 AAS87012
 c 271 16.2 64.8 2882 4 AAF63424
 c 272 16.2 64.8 2888 10 ADC14273
 c 273 16.2 64.8 3200 4 ABL25350
 c 274 16.2 64.8 3417 4 ABL02094
 c 275 16.2 64.8 5498 4 ABL08702
 c 276 16.2 64.8 110000 14 AEB35724_2
 c 277 16.2 64.8 110000 14 AEB35724_3
 c 278 16.2 64.8 110000 14 AEB39175_23
 c 279 16.2 64.8 110000 14 AEB39175_24
 c 280 16.2 64.8 110000 14 AEB42401_23
 c 281 16 64.0 17 14 ADU70004
 c 282 16 64.0 20 2 AAQ94743
 c 283 16 64.0 24 2 AAV59061
 c 284 16 64.0 24 12 ADP04297
 c 285 16 64.0 24 14 AEA89585
 c 286 16 64.0 26 4 AAD11278
 c 287 16 64.0 26 10 ADG88359
 c 288 16 64.0 26 14 AEA08234
 c 289 16 64.0 121 12 ADK91427
 c 290 16 64.0 161 6 ABK79321
 c 291 16 64.0 171 12 ACH86554
 c 292 16 64.0 330 4 AAS27929
 c 293 16 64.0 330 10 ADG40833
 c 294 16 64.0 330 11 ADI96607
 c 295 16 64.0 360 6 ABO92667
 c 296 16 64.0 455 3 AAC55929
 c 297 16 64.0 455 3 AAC57218
 c 298 16 64.0 465 11 ABD15057
 c 299 16 64.0 496 5 AAS87009
 c 300 16 64.0 506 12 ACH77915

ALIGNMENTS

RESULT 1
 ID AAD11271
 XX AAD11271 standard; DNA; 25 BP.
 AC AAD11271;

XX 24-SEP-2001 (first entry)
 DT Mycobacterium 16S rRNA amplifying primer #15.
 DE Mycobacterium 16S rRNA; 16S ribosomal RNA; amplification;
 KW Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
 XX Mycobacterium sp.
 OS WO200144510-A2.
 PN 21-JUN-2001.
 XX 17-DEC-1999; 99WO-US030346.
 PF 17-DEC-1999; 99WO-US030346.
 PR (GENP-) GEN-PROBE INC.
 XX (INNR) BIOMERIEUX SA.
 PA Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodriguez M;
 XX WPI; 2001-398170/42.
 DR Detecting Mycobacterium species, involves in vitro amplification of 16S
 PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using
 PT specific primers, and detecting the amplified nucleic acid.
 XX Claim 1; Page 36; 44pp; English.
 XX The invention relates to a method of detecting Mycobacterium species,
 CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
 CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture
 CC comprising a polymerase, and at least two primers, and then detecting the
 CC amplified nucleic acid. The method is relatively simple and useful for
 CC detecting the presence of various Mycobacterium species in a biological
 CC sample, and thus important for diagnosis of infections resulting from
 CC them. The method is especially important for screening opportunistic
 CC infections caused by M. tuberculosis or a Mycobacterium other than
 CC tuberculosis (MOTT). The present sequence is a PCR primer used for
 CC amplifying Mycobacterium 16S rRNA
 SQ Sequence 25 BP; 7 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
 Query Match 100.0%; Score 25; DB 4; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.057; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0;
 QY 1 GCAAGTCGACGAAAGGCGCTTTTCG 25
 ||||||||||||||||||||||||||||
 Db 1 GCAAGTCGACGAAAGGCGCTTTTCG 25
 RESULT 2
 ADG88352
 ID ADG88352 standard; DNA; 25 BP.
 XX
 AC ADG88352;
 XX
 DT 11-MAR-2004 (first entry)
 DE Mycobacterium amplifying PCR primer #21.
 XX
 KW In vitro amplification; PCR; primer; ss.
 XX Mycobacterium celatum.
 OS US2003165824-A1.
 PN 04-SEP-2003.
 PD 15-DEC-2000; 2000US-00738274.
 PF

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XX 17-DEC-1999; 99US-0172190P.
XX (BREN/) BRENTANO S T.
XX (JUCK/) JUCKER M T.
XX (DELG/) DELGADO F D.
XX (CLEU/) CLEUZIAT P.
XX (RODR/) RODRIGUE M.
XX
XX Pi Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
XX WPI; 2003-898044/82.
XX
XX PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX PT in a biological sample comprises performing in vitro nucleic acid
XX PT amplification and detection of amplified products.
XX
XX PS Claim 1; SEQ ID NO 21; 20pp; English.
XX
XX CC The present invention relates to a method of detecting Mycobacterium
XX CC species present in a biological sample comprises performing an in vitro
XX CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
XX CC detecting the amplified Mycobacterium nucleic acid. The present sequence
XX CC is Mycobacterium amplifying PCR primer.
XX
XX SQ Sequence 25 BP; 7 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 25; DB 10; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 0.057;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
XX Db 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
XX
XX RESULT 4
XX AAD11272
XX ID AAD11272 standard; DNA; 24 BP.
XX
XX AC AAD11272;
XX
XX XX 24-SEP-2001 (first entry)
XX DT
XX XX Mycobacterium 16S rRNA amplifying primer #16.
XX DE
XX XX Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
XX KW Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
XX KW
XX OS Mycobacterium sp.
XX OS
XX PN WO200144510-A2.
XX XX
XX PD 21-JUN-2001.
XX
XX XX 17-DEC-1999; 99WO-US030346.
XX PF
XX XX 17-DEC-1999; 99WO-US030346.
XX PR
XX XX (GENP-) GEN-PROBE INC.
XX PA (INMR ) BIOMERIEUX SA.
XX PA
XX PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
XX DR WPI; 2001-398170/42.
XX
XX PT Detecting Mycobacterium species, involves in vitro amplification of 16S
XX PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using
XX PT specific primers, and detecting the amplified nucleic acid.
XX
XX PS Claim 1; Page 36; 44pp; English.
XX
XX CC The invention relates to a method of detecting Mycobacterium species,
XX CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
XX CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture
XX CC comprising a polymerase, and at least two primers, and then detecting the
XX CC amplified nucleic acid. The method is relatively simple and useful for
XX CC detecting the presence of various Mycobacterium species in a biological
XX CC sample, and thus important for diagnosis of infections resulting from
XX CC them. The method is especially important for screening opportunistic
XX CC infections caused by M. tuberculosis or a Mycobacterium other than
XX CC tuberculosis (MOTT). The present sequence is a PCR primer used for
XX CC amplifying Mycobacterium 16S rRNA
XX
XX SQ Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 96.0%; Score 24; DB 4; Length 24;

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Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCGCTTTTCG 25
Db 1 CAAGTCGAACGGAAGGCGCTTTTCG 24

RESULT 5
ADG88353
ID ADG88353 standard; DNA; 24 BP.
XX
AC ADG88353;
XX
DT 11-MAR-2004 (first entry)
DE Mycobacterium amplifying PCR primer #22.
XX
KW In vitro amplification; PCR; primer; ss.
XX
OS Mycobacterium celatum.
XX
PN US2003165824-A1.
XX
PD 04-SEP-2003.
XX
PF 15-DEC-2000; 2000US-00738274.
XX
PR 17-DEC-1999; 99US-0172190P.
XX
PA (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAT P.
PA (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
DR WPI; 2003-898044/82.
XX
PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample comprises performing in vitro nucleic acid
PT amplification and detection of amplified products.
XX
PS Claim 1; SEQ ID NO 22; 20pp; English.
XX
CC The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample comprises performing an in vitro
CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
CC detecting the amplified Mycobacterium nucleic acid. The present sequence
CC is Mycobacterium amplifying PCR primer.
XX
SQ Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 96.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCGCTTTTCG 25
Db 1 CAAGTCGAACGGAAGGCGCTTTTCG 24

RESULT 6
AEA08228
ID AEA08228 standard; DNA; 24 BP.
XX
AC AEA08228;
XX
DT 14-JUL-2005 (first entry)
DE Mycobacterium celatum 16SrRNA amplifying non-T7 primer, SEQ ID NO: 22.
XX

Microorganism detection; DNA amplification; 16s ribosomal RNA; 16s rRNA;
PCR; primer; ss.
OS Mycobacterium celatum.
XX
PN US2005100915-A1.
XX
PD 12-MAY-2005.
XX
PF 18-SEP-2003; 2003US-00665708.
XX
PR 17-DEC-1999; 99US-0172190P.
PR 15-DEC-2000; 2000US-00738274.
XX
PA (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAT P.
PA (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
DR WPI; 2005-345392/35.
XX
PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample, comprises using in vitro nucleic acid
PT amplification and detection of amplified products.
XX
PS Claim 8; SEQ ID NO 22; 21pp; English.
XX
CC The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample. The method involves using in
CC vitro nucleic acid amplification and detection of amplified products. The
CC invention is useful for diagnostic detection of pathogenic bacteria such
CC as Mycobacterium species. The present sequence is the Mycobacterium
CC celatum (ATCC 51130 and ATCC 51131) 16S ribosomal RNA (16SrRNA)
CC amplifying non-T7 PCR primer.
XX
SQ Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 96.0%; Score 24; DB 14; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCGCTTTTCG 25
Db 1 CAAGTCGAACGGAAGGCGCTTTTCG 24

RESULT 7
ADZ20587
ID ADZ20587 standard; DNA; 500 BP.
XX
AC ADZ20587;
XX
DT 16-JUN-2005 (first entry)
DE Formaldehyde decomposition related Mycobacterium sp. DNA.
XX
KW decomposition; formaldehyde; ds.
XX
OS Mycobacterium sp.
XX
PN JP2003284548-A.
XX
PD 07-OCT-2003.
XX
PF 27-MAR-2002; 2002JP-00089307.
XX
PR 27-MAR-2002; 2002JP-00089307.
XX
PA (KUNO-) KUNOMOTO KEN PREFECTURE.
PA (MITS-) MITSUWA CORP YG.
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PA (MITS-) MITSUWA BIPRO KK.
 XX
 DR WPI; 2004-172963/17.
 XX
 PT Decomposing formaldehyde by Mycobacterium and/or growth medium of the
 PT cells.
 XX
 PS Example 1; SEQ ID NO 1; 20pp; Japanese.
 XX
 CC The invention relates to a novel method for decomposing formaldehyde by
 CC using microbial cells that belong to Mycobacterium sp. or Fusarium
 CC oxysporum, and/or the growth medium of the microbial cells. The invention
 CC further comprises: microbial cells which belong to Mycobacterium sp.
 CC having the ability to decompose formaldehyde; a formaldehyde
 CC decomposition agent comprising Mycobacterium sp. and/or the growth medium
 CC of the microbial cells; and a formaldehyde decomposition agent comprising
 CC F. oxysporum and/or its growth medium. The method is useful for
 CC decomposing formaldehyde in sea water by Mycobacterium sp. or F.
 CC oxysporum that is deposited under FERM P-S18690 or FERM P-18483,
 CC respectively. This polynucleotide sequence represents the Mycobacterium
 CC sp. DNA of the invention.
 XX
 SQ Sequence 500 BP; 108 A; 119 C; 178 G; 95 T; 0 U; 0 Other;
 XX
 Query Match 93.6%; Score 23.4; DB 13; Length 500;
 Best Local Similarity 96.0%; Pred. No. 0.45; Mismatches 0; Gaps 0;
 Matches 24; Conservative 0; Indels 1; Indels 0; Gaps 0;
 Qy 1 GCAAGTCGACGGAAGGCGCTTCG 25
 Db 53 GCAAGTCGACGGAAGGCGCTTCG 77
 RESULT 8
 AEA22405
 ID AEA22405 standard; DNA; 1449 BP.
 AC AEA22405;
 XX
 DT 25-AUG-2005 (first entry)
 XX
 DE Mycobacterium fortuitum 16S rRNA sequence SEQ ID NO:6.
 XX
 KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
 XX
 OS Mycobacterium fortuitum.
 XX
 PN US2005130168-A1.
 XX
 PD 16-JUN-2005.
 XX
 PF 31-OCT-2003; 2003US-00697802.
 XX
 PR 31-OCT-2003; 2003US-00697802.
 XX
 PA (HANX/) HAN X.
 PA (PHAM/) PHAM A S.
 XX
 PI Han X, Pham AS;
 XX
 DR WPI; 2005-424597/43.
 XX
 PT Determining a bacterium species comprises providing oligonucleotide
 PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
 XX
 PS Disclosure; SEQ ID NO 6; 74pp; English.
 XX
 CC The invention relates to a method (M1) for determining a bacterium
 CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
 CC extracting a genomic nucleotide from the bacterium to provide a
 CC nucleotide template; (c) annealing a region of a nucleotide template to a
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
 CC complimentary fashion, the primer set designed to provide a product

CC having a predetermined size dictated by a complimentary primer set; (d)
 CC amplifying the region of the nucleotide template to produce the product;
 CC and (e) determining a species of a bacterium in a nucleotide sequence of
 CC the product. Also described is an alternative method (M2) for determining
 CC a bacterium species comprising: (a) providing a specimen or a sample
 CC having a template; (b) providing a pair of primers selected from: (i) a
 CC first forward primer having consecutive bases of an AFB-f comprising any
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
 CC or variations and a first reverse primer having consecutive bases of an
 CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
 CC or their fragments or variations; (ii) a second forward primer having
 CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
 CC bp (AEA22489-AEA22516) or their fragments or variations and a second
 CC reverse primer having consecutive bases of an UB-r comprising any of the
 CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
 CC variations; or (iii) a first forward primer having consecutive bases of
 CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
 CC second reverse primer having consecutive bases of an UB-r of AEA22517-
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)
 CC comparing the product from the specimen with a nucleotide sequence from a
 CC database to determine the bacterium species present in the specimen. The
 CC methods are useful for determining a bacterium species. The present
 CC sequence represents a Mycobacterium fortuitum 16S rRNA nucleotide
 CC sequence, which is used in the exemplification of the present invention.
 XX
 SQ Sequence 1449 BP; 322 A; 342 C; 495 G; 290 T; 0 U; 0 Other;
 XX
 Query Match 93.6%; Score 23.4; DB 14; Length 1449;
 Best Local Similarity 96.0%; Pred. No. 0.51;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GCAAGTCGACGGAAGGCGCTTCG 25
 Db 20 GCAAGTCGACGGAAGGCGCTTCG 44
 RESULT 9
 AEA22412
 ID AEA22412 standard; DNA; 1455 BP.
 AC AEA22412;
 XX
 DT 25-AUG-2005 (first entry)
 XX
 DE Mycobacterium mucogenicum 16S rRNA sequence SEQ ID NO:13.
 XX
 KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
 XX
 OS Mycobacterium mucogenicum.
 XX
 PN US2005130168-A1.
 XX
 PD 16-JUN-2005.
 XX
 PF 31-OCT-2003; 2003US-00697802.
 XX
 PR 31-OCT-2003; 2003US-00697802.
 XX
 PA (HANX/) HAN X.
 PA (PHAM/) PHAM A S.
 XX
 PI Han X, Pham AS;
 XX
 DR WPI; 2005-424597/43.
 XX
 PT Determining a bacterium species comprises providing oligonucleotide
 PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
 XX
 PS Disclosure; SEQ ID NO 13; 74pp; English.
 XX
 CC The invention relates to a method (M1) for determining a bacterium
 CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
 CC extracting a genomic nucleotide from the bacterium to provide a
 CC nucleotide template; (c) annealing a region of a nucleotide template to a
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
 CC complimentary fashion, the primer set designed to provide a product

CC nucleotide template; (c) annealing a region of a nucleotide template to a
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
 CC complementary fashion, the primer set designed to provide a product
 CC having a predetermined size dictated by a complementary primer set; (d)
 CC amplifying the region of the nucleotide template to produce the product;
 CC and (e) determining a species of a bacterium in a nucleotide sequence of
 CC the product. Also described is an alternative method (M2) for determining
 CC a bacterium species comprising: (a) providing a specimen or a sample
 CC having a template; (b) providing a pair of primers selected from: (i) a
 CC first forward primer having consecutive bases of an AFB-f comprising any
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
 CC or variations, and a first reverse primer having consecutive bases of an
 CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
 CC bp (AEA22489-AEA22516) or their fragments or variations, (ii) a second forward primer having
 CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
 CC reverse primer having consecutive bases of an UB-r comprising any of the
 CC variations, or (iii) a first forward primer having consecutive bases of
 CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a second
 CC second reverse primer having consecutive bases of an UB-r of AEA22517-
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)
 CC comparing the product from the specimen with a nucleotide sequence from a
 CC database to determine the bacterium species present in the specimen. The
 CC methods are useful for determining a bacterium species. The present
 CC sequence represents a Mycobacterium mucogenicum 16S rRNA nucleotide
 CC sequence, which is used in the exemplification of the present invention.

XX Sequence 1455 BP; 321 A; 347 C; 500 G; 287 T; 0 U; 0 Other;

Query Match 93.6%; Score 23.4; DB 14; Length 1455;
 Best Local Similarity 96.0%; Pred. No. 0.51;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAGTCGACGGAAGGCCCTTCG 25
 Db 30 GCAAGTCGACGGAAGGCCCTTCG 54

RESULT 10
 AEA22404
 ID AEA22404 standard; DNA; 1482 BP.
 XX AEA22404;
 AC AEA22404;
 XX 25-AUG-2005 (first entry)
 XX Mycobacterium farcinogenes 16S rRNA sequence SEQ ID NO:5.
 DE microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
 KW Mycobacterium farcinogenes.
 OS Mycobacterium farcinogenes.
 XX US2005130168-A1.
 PN 16-JUN-2005.
 PD 31-OCT-2003; 2003US-00697802.
 PF 31-OCT-2003; 2003US-00697802.
 XX (HANK/) HAN X.
 PA (PHAM/) PHAM A S.
 XX Han X, Pham AS;
 PI WPI; 2005-424597/43.
 XX Determining a bacterium species comprises providing oligonucleotide
 PT primer set comprising SEQ-FOR and SEQ-REV in a complementary fashion.
 XX Disclosure; SEQ ID NO 5; 74pp; English.

CC The invention relates to a method (M1) for determining a bacterium
 CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
 CC extracting a genomic nucleotide from the bacterium to provide a
 CC nucleotide template; (c) annealing a region of a nucleotide template to a
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
 CC complementary fashion, the primer set designed to provide a product
 CC having a predetermined size dictated by a complementary primer set; (d)
 CC amplifying the region of the nucleotide template to produce the product;
 CC and (e) determining a species of a bacterium in a nucleotide sequence of
 CC the product. Also described is an alternative method (M2) for determining
 CC a bacterium species comprising: (a) providing a specimen or a sample
 CC having a template; (b) providing a pair of primers selected from: (i) a
 CC first forward primer having consecutive bases of an AFB-f comprising any
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
 CC or variations, and a first reverse primer having consecutive bases of an
 CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
 CC bp (AEA22489-AEA22516) or their fragments or variations, (ii) a second forward primer having
 CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
 CC reverse primer having consecutive bases of an UB-r comprising any of the
 CC variations, or (iii) a first forward primer having consecutive bases of
 CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
 CC second reverse primer having consecutive bases of an UB-r of AEA22517-
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)
 CC comparing the product from the specimen with a nucleotide sequence from a
 CC database to determine the bacterium species present in the specimen. The
 CC methods are useful for determining a bacterium species. The present
 CC sequence represents a Mycobacterium farcinogenes 16S rRNA nucleotide
 CC sequence, which is used in the exemplification of the present invention.

XX Sequence 1482 BP; 327 A; 353 C; 507 G; 295 T; 0 U; 0 Other;

Query Match 93.6%; Score 23.4; DB 14; Length 1482;
 Best Local Similarity 96.0%; Pred. No. 0.51;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCCTTCG 25
 Db 28 GCAAGTCGACGGAAGGCCCTTCG 52

RESULT 11
 ADF94057
 ID ADF94057 standard; DNA; 50 BP.
 XX ADF94057;
 AC ADF94057;
 XX 11-MAR-2004 (first entry)
 DE Microorganism detection probe, SEQ ID 150.
 KW Probe; detection; identification; microorganism; food; drug;
 KW 16S rRNA VI region; 16S rRNA V2 region; 16S rRNA V3 region; ss.
 XX Mycobacterium gordonae.
 OS WO2003106676-A1.
 PN 24-DEC-2003.
 PD 16-JUN-2003; 2003WO-JP007620.
 PF 14-JUN-2002; 2002JP-00174564.
 PR (HISF) HITACHI SOFTWARE ENG CO LTD.
 PA (MITS-) MITSUBISHI KAGAKU BIO-CLINICAL LAB INC.
 XX Hashida J, Ueno S, Muto I, Naruse K, Tamura M, Matsuda K;
 PI Shimadzu M, Kobayashi I, Ishiko H;
 XX WPI; 2004-071565/07.

PT 20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a
 PT microorganism for specific detection and identification of the
 PT microorganism in foods and drug compositions.

XX Claim 2; SEQ ID NO 150; 150pp; Japanese.

XX The present invention relates to probes (ADF93908-ADF94059) for the
 CC specific detection and identification of harmful microorganisms in
 CC samples of foods and drug compositions. The probe sequences are derived
 CC from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism,
 CC or its complementary sequence. Detection and identification of the
 CC microorganism is by amplification of the complete 16S rRNA gene using
 CC primers ADF94060 and ADF94061, labelling the amplification product (a
 CC fluorescence label is preferred) and hybridising to the probe or probes
 CC of the invention. The probes may be immobilised on a DNA chip. The
 CC microorganism is selected from *Actinobacillus actinomycetemcomitans*,
 CC *Acinetobacter calcoaceticus*, *Haemophilus influenzae*, *Stenotrophomonas*
 CC *malophilia*, *Proteus mirabilis*, *Streptococcus pneumoniae*, *Pseudomonas*
 CC *aeruginosa*, *Citrobacter freundii*, *Veillonella parvula*, *Providencia*
 CC *stuartii*, *Neisseria gonorrhoeae*, *Streptococcus agalactiae*, *Morganella*
 CC *morganii*, *Bacteroides fragilis*, *Staphylococcus hominis*, *Staphylococcus*
 CC *warneri*, *Staphylococcus haemolyticus*, *Enterobacter cloacae*, *Enterobacter*
 CC *Serratia marcescens*, *Streptococcus arginosus*, *Escherichia coli*,
 CC *Klebsiella pneumoniae*, *Enterococcus faecalis*, *Streptococcus faecium*,
 CC *Streptococcus sanguinis*, *Streptococcus mitis*, *Streptococcus intermedius*,
 CC *Listeria monocytogenes*, *Clostridium perfringens*, *Corynebacterium*
 CC *aquaticum*, *Streptococcus oralis*, *Staphylococcus aureus*, *Neisseria*
 CC *meningitidis*, *Campylobacter fetus*, *Enterococcus gallinarum*, *Enterococcus*
 CC *caseliflavus*, *Aeromonas hydrophila*, *Salmonella paratyphi*, *Salmonella*
 CC *typhi*, *Streptococcus equisimilis*, *Streptococcus canis*, *Klebsiella*
 CC *oxytoca*, *Staphylococcus saprophyticus*, *Pasteurella multocida*, *Legionella*
 CC *corrodens*, *Streptococcus pyogenes*, *Moraxella catarrhalis*, *Legionella*
 CC *pneumophila*, *Mycobacterium tuberculosis*, *Mycobacterium avium*,
 CC *Mycobacterium intracellulare*, *Mycobacterium kansasii* or *Mycobacterium*
 CC *gordonae*.

SQ Sequence 50 BP; 12 A; 11 C; 19 G; 8 T; 0 U; 0 Other;

Query Match 87.2%; Score 21.8; DB 12; Length 50;
 Best Local Similarity 92.0%; Pred. No. 2.1;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GCAAGTCGACGGAAGGCGCTTCG 25
 Db 3 GCAAGTCGACGGAAGGCGCTTCG 27

RESULT 12

AAX32481
 ID AAX32481 standard; DNA; 166 BP.

XX AAX32481;

DT 22-JUN-1999 (first entry)

DE Preferred probe of the invention.

KW 16S rRNA; maduromycetes; hybridisation; streptomycetes; probe; ss.

XX Synthetic.

OS Streptomyces ambofaciens.

XX WO9914361-A1.

XX 25-MAR-1999.

XX 16-SEP-1998; 98WO-EP06038.

XX 18-SEP-1997; 97US-0059295P.

XX 16-DEC-1997; 97US-0069748P.

XX (MERI) MERCK SHARP & DOHME ESPANA SAE.

XX Genilloud O, Mellado RP, Parro V, Rodriguez V;
 XX WPI; 1999-229548/19.

PT New probes used for detection of maduromycetes bacteria and to
 PT differentiate between maduromycetes and streptomycetes.

PS Disclosure; Fig 1; 22pp; English.

XX The invention relates to a novel nucleic acid probe hybridises to a
 CC nucleic acid encoding a portion of 16S rRNA of maduromycetes bacteria
 CC under hybridisation conditions, and does not hybridise to nucleic acids
 CC encoding a portion of 16S rRNA of streptomycetes under identical
 CC hybridisation conditions. The probes can be used for detecting the
 CC presence of maduromycetes bacteria in a sample and for differentiating
 CC between maduromycetes and streptomycetes bacteria in a sample. The
 CC present sequence represents a preferred probe of the invention

SQ Sequence 166 BP; 39 A; 43 C; 55 G; 29 T; 0 U; 0 Other;

Query Match 87.2%; Score 21.8; DB 2; Length 166;
 Best Local Similarity 92.0%; Pred. No. 2.3;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GCAAGTCGACGGAAGGCGCTTCG 25
 Db 56 GCAAGTCGACGGAAGGCGCTTCG 80

RESULT 13

ABZ76674

ID ABZ76674 standard; DNA; 460 BP.

XX ABZ76674;

DT 30-APR-2003 (first entry)

DE Microtetraspora recticatena IFO14525 DNA sequence SEQ ID NO:5.

KW Streptomyces sp. TM-7; pravastatin; compactin; hyperlipidaemia;
 KW antilipase; microorganism; gene; ds.

OS Nonomuraea recticatena.

XX WO200299109-A1.

XX 12-DEC-2002.

XX 30-MAY-2002; 2002WO-JP005252.

XX 01-JUN-2001; 2001JP-00166412.

XX (SAOC) MERCIAN CORP.

PI Fujii T, Hirose S, Aritoku Y, Morimiya T, Johdo O, Isshiki K;

XX WPI; 2003-149672/14.

XX Novel Streptomyces sp. produced polypeptide for hydroxylation of
 PT compactin at 6beta-position and its encoded DNA, applicable in
 PT constructing transformant microbes to synthesize pravastatin for treating
 PT hyperlipidemia.

PS Disclosure; Page 50-51; 67pp; Japanese.

XX The present invention describes a DNA sequence which contains a base
 CC sequence from bases 544-1758 in the sequence of (I) with 1992 base pairs,
 CC or a DNA hybridisable with the DNA under stringent conditions and
 CC encoding a polypeptide with the hydroxylase activity on compactin at 6beta-
 CC position. Also described: (1) DNA containing base sequences from bases
 CC 544-1758 and from bases 1782-1970 in the sequence of (I) or a DNA
 CC hybridisable with the DNA under stringent conditions and encoding a

CC polypeptide with hydroxylase activity on compactin at the 6beta-position;
CC (2) a polypeptide encoded by any of the DNA or containing an amino acid
CC sequence based on the polypeptide but with some amino acids deleted,
CC substituted or added and having hydroxylase activity on compactin at the
CC 6beta-position; (3) a recombinant DNA obtained by integrating with any of
CC the DNA; (4) a microorganism transferred with the recombinant DNA; (5) a
CC process for producing pravastatin by culturing the transformant
CC microorganism before isolating the culture liquor or cells, and addition
CC of compactin for reaction to give pravastatin for recovery; and (6)
CC Streptomyces sp. TM-6 (FERM BP-8002) or TM-7 (FERM BP-8003). (I) has
CC antilipaeamic activity. The polypeptide and its encoded DNA are applicable
CC in constructing transformant microorganisms to synthesise pravastatin for
CC treating hyperlipidaemia. With the recombinant microorganisms,
CC pravastatin can be produced efficiently, with much less 6alpha
CC hydroxylated epimer formed. The present sequence represents a
CC Microtetraspora recticatenata IF014525 nucleotide sequence, which is given
CC in the exemplification of the present invention
XX
SQ Sequence 460 BP; 97 A; 119 C; 166 G; 78 T; 0 U; 0 Other;
Query Match 87.2%; Score 21.8; DB 8; Length 460;
Best Local Similarity 92.0%; Pred. No. 2.6;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCAAGTCGAACGGAAGGCGCTTTTCG 25
||||||| ||||||| ||||||| |||||
Db 30 GCAAGTCGAGCGGAAGGCGCTTCG 54
RESULT 14
AEB72673
ID AEB72673 standard; DNA; 497 BP.
AC AEB72673;
XX
XX 06-OCT-2005 (first entry)
DT
DE Streptosporangium sp. AF935 16S rDNA, SEQ ID 2.
XX
KW cyclosporin; cyclosporin A; ds.
XX
OS Streptosporangium sp.
XX
XX JP2005198543-A.
XX
XX 28-JUL-2005.
XX
PF 15-JAN-2004; 2004JP-00007488.
XX
PR 15-JAN-2004; 2004JP-00007488.
XX
XX (SAOC) MERCIAN CORP.
XX
XX Ota K, Uematsu H, Kaneko K, Tsuchida T;
PI
DR WPI; 2005-537020/55.
XX
XX Producing cyclosporin derivative useful as reference standard for
PT quantitative measurement of cyclosporin A in blood, by incubating
PT cyclosporin A in presence of Dactylosporangium and extracting cyclosporin
PT derivative.
XX
XX Disclosure; SEQ ID NO 2; 12pp; Japanese.
XX
XX The invention relates to a novel method for producing a cyclosporin
CC derivative. The method involves incubating cyclosporin A in the presence
CC of a strain belonging to Dactylosporangium, Streptomyces, Nocardia,
CC Pseudonocardia or Streptosporangium or its cultured microbial cells and
CC extracting the cyclosporin derivative from the incubated liquid. The
CC cyclosporin derivative is used as a reference standard for quantitative
CC measurement of cyclosporin A and its metabolite in blood and urine. This
CC polynucleotide represents a Streptosporangium 16S rDNA sequence used in
CC the cyclosporin production method of the invention.

XX
SQ Sequence 497 BP; 105 A; 121 C; 178 G; 93 T; 0 U; 0 Other;
Query Match 87.2%; Score 21.8; DB 14; Length 497;
Best Local Similarity 92.0%; Pred. No. 2.6;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCAAGTCGAACGGAAGGCGCTTTTCG 25
||||||| ||||||| ||||||| |||||
Db 53 GCAAGTCGAGCGGAAGGCGCTTCG 77
RESULT 15
AED64356
ID AED64356 standard; DNA; 500 BP.
XX
XX AED64356;
AC
XX
XX 12-JAN-2006 (first entry)
DT
XX Rhodococcus sp. 16S rDNA, SEQ ID 1.
DE
XX 16S ribosomal RNA; 16S rRNA; ds.
KW
XX Rhodococcus sp.; Z-35-1 strain.
OS
XX JP2005304498-A.
PN
XX 04-NOV-2005.
PD
XX 22-MAR-2005; 2005JP-00081977.
PF
XX 23-MAR-2004; 2004JP-00083956.
PR
XX (SANY-) SANYO FINE KK.
PA
XX Isobe K, Matsura A, Sakaguchi T;
PI
XX WPI; 2005-762911/78.
DR
XX Producing alpha-L- or -D-amino adipic acid semialdehyde derivative or its
PT salt, involves oxidatively deaminating aminomethyl group of alpha-amino
PT protecting group of L- or D-lysine, by utilizing oxidase derived from
PT Rhodococcus.
XX
XX Disclosure; SEQ ID NO 1; 30pp; Japanese.
XX
XX The present invention relates to a method (M1) for producing alpha-L- or
CC -D-amino adipic acid semialdehyde derivatives. The method involves
CC oxidatively deaminating the aminomethyl group of the alpha-amino
CC protecting group of L- or D-lysine into an aldehyde group, by utilizing
CC an oxidase derived from Rhodococcus. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 500 BP; 113 A; 120 C; 173 G; 88 T; 0 U; 6 Other;
Query Match 87.2%; Score 21.8; DB 14; Length 500;
Best Local Similarity 92.0%; Pred. No. 2.6;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCAAGTCGAACGGAAGGCGCTTTTCG 25
||||||| ||||||| ||||||| |||||
Db 53 GCAAGTCGAGCGGTAAGGCGCTTCG 77
RESULT 16
ADO80217/c
ID ADO80217 standard; DNA; 1343 BP.
XX
XX ADO80217;
AC
XX 29-JUL-2004 (first entry)
DT
XX

```

DE Rhodococcus sp. GR-002 strain 16S rDNA.
XX
KW cyclic hydrocarbon degrading agent; Rhodococcus; gram positive bacillus;
KW catalase test positive; nitrate-reduction ability positive;
KW pyrazinamidase negative; pyrrolidonyl allyl amidase negative;
KW alkali phosphatase positive; beta-glucuronidase negative;
KW beta-galactosidase negative; alpha-glucosidase positive;
KW N-acetyl-beta-glucosaminidase negative; urease positive; GR-002 strain;
KW FERM P-18804; waste engine oil; aromatic hydrocarbon;
KW cycloaliphatic hydrocarbon; polycyclic aromatic hydrocarbon; ds.
XX
OS Rhodococcus sp.
XX
PN JP2004113197-A.
XX
PD 15-APR-2004.
XX
XX
XX 27-SEP-2002; 2002JP-00284521.
XX
XX 27-SEP-2002; 2002JP-00284521.
XX
XX (GEIT-) GEITO KK.
XX
XX WPI; 2004-322544/30.
XX
XX Novel cyclic hydrocarbon degrading Rhodococcus species GR-002 strain
XX having biochemical properties e.g. gram positive bacillus, catalase test
XX positive, pyrazinamidase negative, useful for degrading waste engine oil.
XX
XX Claim 2; SEQ ID NO 1; 13pp; Japanese.
XX
XX The invention relates to a novel cyclic hydrocarbon degrading agent from
XX the Rhodococcus genus. The cyclic hydrocarbon degrading agent having
XX biochemical properties such as: gram positive bacillus, catalase test
XX positive, nitrate-reduction ability positive, pyrazinamidase negative,
XX pyrrolidonyl allyl amidase negative, alkali phosphatase positive, beta-
XX glucuronidase negative, beta-galactosidase negative, alpha-glucosidase
XX positive, N-acetyl-beta-glucosaminidase negative, urease positive. The
XX novel Rhodococcus microorganism is Rhodococcus sp. GR-002 strain having
XX the accession number FERM P-18804. The cyclic hydrocarbon degrading agent
XX is useful for processing a cyclic hydrocarbon-containing substance, such
XX as a waste engine oil. The novel Rhodococcus microorganism is useful for
XX degrading cyclic hydrocarbons containing aromatic hydrocarbons,
XX cycloaliphatic hydrocarbons, and/or polycyclic aromatic hydrocarbons.
XX This polynucleotide represents the novel Rhodococcus microorganism 16S
XX rDNA sequence of the invention.
XX
SQ Sequence 1343 BP; 263 A; 452 C; 320 G; 308 T; 0 U; 0 Other;

Query Match 87.2%; Score 21.8; DB 12; Length 1343;
Best Local Similarity 92.0%; Pred. No. 2.9;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGCGGTAAGGCCTTCG 25
Db 1294 GCAAGTCGACGCGGTAAGGCCTTCG 1270

RESULT 17
ADW16264
ID ADW16264 standard; DNA; 1390 BP.
XX
XX AC ADW16264;
XX
XX 07-APR-2005 (first entry)
XX
XX DNA copy of the N_albus 16S ribosomal RNA EN46 isolate Seq 16.
XX
XX 16S ribosomal RNA; ds; 16S rRNA; medicinal plant; plant breeding;
KW disease resistance; insect resistance; crop improvement;
KW plant growth factor; antibacterial; antimicrobial; fungicide;
KW insecticide; nematocide.
XX
XX

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```

OS Nocardioides albus.
XX
PN WO2005003328-A1.
XX
PD 13-JAN-2005.
XX
XX 07-JUL-2004; 2004WO-AU0000914.
XX
XX 07-JUL-2003; 2003US-0485241P.
XX
XX 22-SEP-2003; 2003US-0504703P.
XX
XX (FLIN-) FLINDERS TECHNOLOGIES PTY LTD.
XX
XX Franco CMW, Coombs JT;
XX
XX WPI; 2005-091806/10.
XX
XX Improving plant productivity comprises introducing into the plant or
XX propagation material an endophytic actinomycete that facilitates
XX induction of at least one characteristic related to improved
XX productivity.
XX
XX Claim 1; SEQ ID NO 16; 235pp; English.
XX
XX This invention relates to a novel method for improving plant
XX productivity. Specifically, it refers to introducing into the plant or
XX propagation material an endophytic actinomycetes or variant thereof,
XX where the actinomycetes facilitate induction of a characteristic related
XX to improved productivity. The present invention further describes
XX metabolites of the actinomycetes microorganism such as auxin, gibberellin
XX or cytokinin that are able to induce disease resistance in plants i.e.
XX provide disease bio-control capabilities against pathogen infection.
XX Accordingly, the method facilitates the improvement of cereal crop
XX productivity including increasing germination by up-regulating plant
XX growth promoting activities, as well as improving plant vigor or flower
XX and fruit yield. Furthermore, the new actinomycete or metabolite is
XX useful in the manufacture of a medicament for the therapeutic and/or
XX prophylactic treatment of a mammalian or non-mammalian subject i.e.
XX plant. As such, this method provides plant protectants and plant growth
XX stimulants that exhibit antibacterial, antimicrobial, fungicide,
XX insecticide and nematocide activities. This polynucleotide is the DNA
XX sequence of an actinomycetes 16S ribosomal RNA sequence of the invention.
XX
SQ Sequence 1390 BP; 324 A; 348 C; 443 G; 266 T; 0 U; 9 Other;

Query Match 87.2%; Score 21.8; DB 14; Length 1390;
Best Local Similarity 92.0%; Pred. No. 2.9;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGCGGTAAGGCCTTCG 25
Db 3 GCAAGTCGACGCGGTAAGGCCTTCG 27

RESULT 18
ADJ38609
ID ADJ38609 standard; DNA; 1403 BP.
XX
XX AC ADJ38609;
XX
XX 06-MAY-2004 (first entry)
XX
XX Micromonospora sp. M42 16S rRNA, SEQ ID 1.
XX
XX Protozoacide; Tuberculoostatic; Antitubercular; Antimalarial;
KW Cerebroprotective; Actinomycete; manzamine; 16S rRNA; antibiotic; ds.
XX
XX Micromonospora sp. M42.
XX
XX WO2004013297-A2.
XX
XX 12-FEB-2004.
XX
XX

```

PF 01-AUG-2003; 2003WO-US024238.
 XX
 PR 01-AUG-2002; 2002US-0400330P.
 XX
 PA (UYNA-) UNIV MARYLAND BIOTECHNOLOGY.
 PA (UMIS) UNIV MISSISSIPPI.
 PI Hill RT, Hamann MT, Peraud O, Kasanah N;
 XX WPI; 2004-169330/16.
 DR
 XX New isolated actinomycete useful for producing antibiotics produces
 PT manzamine having antituberculosis and antimalarial activity.
 PT
 XX Claim 19; SEQ ID NO 1; 46pp; English.
 PS
 XX The present invention relates to an isolated actinomycete (A1) producing
 CC manzamine, which comprises a 16S rRNA (ADJ38609). (A1) is useful for
 CC producing manzamine by fermentation, which involves culturing (A1) having
 CC manzamine producing ability in a culture medium suitable for the growth
 CC of manzamine compounds and production of manzamine and separating the
 CC manzamine from the culturing medium. (A1) is useful for producing
 CC antibiotics.
 CC
 XX Sequence 1403 BP; 304 A; 361 C; 484 G; 254 T; 0 U; 0 Other;
 SQ
 Query Match 87.2%; Score 21.8; DB 12; Length 1403;
 Best Local Similarity 92.0%; Pred. No. 2.9;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GCAAGTCGACGGAAGGCTTCG 25
 DB 25 GCAAGTCGACGGAAGGCTTCG 49
 RESULT 19
 ADW16290
 ID ADW16290 standard; DNA; 1427 BP.
 XX
 AC ADW16290;
 XX
 DT 07-APR-2005 (first entry)
 XX
 DE DNA copy of the Actinomycete 16S ribosomal RNA EN47 isolate.
 XX
 KW 16S ribosomal RNA; ds; 16S rRNA; medicinal plant; plant breeding;
 KW disease resistance; insect resistance; crop improvement;
 KW plant growth factor; antibacterial; antimicrobial; fungicide;
 KW insecticide; nematocide.
 XX
 OS Actinomycetales.
 XX
 PN WO2005003328-A1.
 XX
 PD 13-JAN-2005.
 XX
 PF 07-JUL-2004; 2004WO-AU000914.
 XX
 PR 07-JUL-2003; 2003US-0485241P.
 PR 22-SEP-2003; 2003US-0504703P.
 XX
 PA (FLIN-) FLINDERS TECHNOLOGIES PTY LTD.
 XX
 PI Franco CMM, Coombs JT;
 XX WPI; 2005-091806/10.
 DR
 XX Improving plant productivity comprises introducing into the plant or
 PT propagation material an endophytic actinomycete that facilitates
 PT induction of at least one characteristic related to improved
 PT productivity.
 PT
 XX Example 18; Fig 19; 235pp; English.

XX This invention relates to a novel method for improving plant
 CC productivity. Specifically, it refers to introducing into the plant or
 CC propagation material an endophytic actinomycetes or variant thereof,
 CC where the actinomycetes facilitate induction of a characteristic related
 CC to improved productivity. The present invention further describes
 CC metabolites of the actinomycetes microorganism such as auxin, gibberellin
 CC or cytokinin that are able to induce disease resistance in plants i.e.
 CC provide disease bio-control capabilities against pathogen infection.
 CC Accordingly, the method facilitates the improvement of cereal crop
 CC productivity including increasing germination by up-regulating plant
 CC growth promoting activities, as well as improving plant vigor or flower
 CC and fruit yield. Furthermore, the new actinomycete or metabolite is
 CC useful in the manufacture of a medicament for the therapeutic and/or
 CC prophylactic treatment of a mammalian or non-mammalian subject i.e.
 CC plant. As such, this method provides plant protectants and plant growth
 CC stimulants that exhibit antibacterial, antimicrobial, fungicide,
 CC insecticide and nematocide activities. This polynucleotide is the DNA
 CC sequence of an actinomycetes 16S ribosomal RNA sequence of the invention.
 XX
 SQ Sequence 1427 BP; 326 A; 351 C; 471 G; 277 T; 0 U; 2 Other;
 Query Match 87.2%; Score 21.8; DB 14; Length 1427;
 Best Local Similarity 92.0%; Pred. No. 2.9;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GCAAGTCGACGGAAGGCTTCG 25
 DB 24 GCAAGTCGACGGAAGGCTTCG 48
 RESULT 20
 ADX38843
 ID ADX38843 standard; DNA; 1443 BP.
 XX
 AC ADX38843;
 XX
 DT 05-MAY-2005 (first entry)
 XX
 DE Microbispora 16S rDNA.
 XX
 KW antibiotic; bacterial infection; animal growth; 16S rDNA; ds;
 KW antibacterial; anabolic.
 XX
 OS Microbispora sp. ATCC PTA-5024.
 XX
 PN WO2005014628-A1.
 XX
 PD 17-FEB-2005.
 XX
 PF 12-JUL-2004; 2004WO-EP007658.
 XX
 PR 18-JUL-2003; 2003EP-00016306.
 XX
 PA (VICU-) VICURON PHARM INC.
 XX
 PI Lazzarini A, Gastaldo L, Candiani G, Ciciliato I, Losi D;
 PI Marinelli F, Selva E, Parenti F;
 XX WPI; 2005-173079/18.
 DR
 XX New antibiotic 107891 complex comprising Factor A1 and Factor A2 and
 PT having specified physico-chemical characteristics, used to form
 PT medicament for the treatment or prevention of bacterial infections, or
 PT used as animal growth promoter.
 XX
 PS Disclosure; SEQ ID NO 1; 85pp; English.
 XX
 CC The invention relates to an antibiotic 107891 complex comprising Factor
 CC A1 and Factor A2. The antibiotic is used to form a pharmaceutical
 CC composition used as medicament for the treatment or prevention of
 CC bacterial infections, or as animal growth promoter. The present sequence
 CC represents the Microbispora 16S rDNA.

XX
SQ Sequence 1443 BP; 308 A; 352 C; 504 G; 279 T; 0 U; 0 Other;
Query Match 87.2%; Score 21.8; DB 14; Length 1443;
Best Local Similarity 92.0%; Pred. No. 2.9;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1 GCAAGTCGAACGGAAGGCTTCG 25
Db 30 GCAAGTCGAGCGGAAGGCTTCG 54
RESULT 21
ID AEA22406
XX AEA22406 standard; DNA; 1461 BP.
AC AEA22406;
DT 25-AUG-2005 (first entry)
XX
DE Mycobacterium gordonae 16S rRNA sequence SEQ ID NO:7.
XX
KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
XX
OS Mycobacterium gordonae.
XX
PN US2005130168-A1.
XX
PD 16-JUN-2005.
XX
PF 31-OCT-2003; 2003US-00697802.
XX
PR 31-OCT-2003; 2003US-00697802.
XX
PA (HANX/) HAN X.
XX (PHAM/) PHAM A S.
XX
PI Han X, Pham AS;
XX
DR WPI; 2005-424597/43.
XX
PT Determining a bacterium species comprises providing oligonucleotide
primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
XX
PS Disclosure; SEQ ID NO 7; 74pp; English.
XX
CC The invention relates to a method (M1) for determining a bacterium
species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
extracting a genomic nucleotide from the bacterium to provide a
nucleotide template; (c) annealing a region of a nucleotide template to a
specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
complimentary fashion, the primer set designed to provide a product
having a predetermined size dictated by a complimentary primer set; (d)
amplifying the region of the nucleotide template to produce the product;
and (e) determining a species of a bacterium in a nucleotide sequence of
the product. Also described is an alternative method (M2) for determining
a bacterium species comprising: (a) providing a specimen or a sample
having a template; (b) providing a pair of primers selected from: (i) a
first forward primer having consecutive bases of an APB-f comprising any
of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
or variations and a first reverse primer having consecutive bases of an
APB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
or their fragments or variations, (ii) a second forward primer having
consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
bp (AEA22489-AEA22516) or their fragments or variations and a second
reverse primer having consecutive bases of an UB-r comprising any of the
28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
variations, or (iii) a first forward primer having consecutive bases of
an APB-f of AEA22417-AEA22452 or their fragments or variations and a
second reverse primer having consecutive bases of an UB-r of AEA22517-
AEA22544 or their fragments or variations; (c) the specimen; and (d)
comparing the product from the specimen with a nucleotide sequence from a
database to determine the bacterium species present in the specimen. The

CC methods are useful for determining a bacterium species. The present
sequence represents a Mycobacterium gordonae 16S rRNA nucleotide
sequence, which is used in the exemplification of the present invention.
SQ Sequence 1461 BP; 319 A; 350 C; 500 G; 292 T; 0 U; 0 Other;
Query Match 87.2%; Score 21.8; DB 14; Length 1461;
Best Local Similarity 92.0%; Pred. No. 2.9;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1 GCAAGTCGAACGGAAGGCTTCG 25
Db 20 GCAAGTCGAACGGAAGGCTTCG 44
RESULT 22
ID AED35651
XX AED35651 standard; DNA; 1483 BP.
AC AED35651;
DT 15-DEC-2005 (first entry)
XX
DE Pseudonocardia sp. 727713 melanocortin receptor modulator WS727713.
XX
KW ds; melanocortin receptor; cosmetics; brain injury; cerebroprotective;
inflammation; renal disease; nephrotropic; ischemia;
cardiovascular disease; Vasotropic; reperfusion injury; inflammation;
hepatitis; Hepatotropic; Virucide; sepsis; septic shock; Antibacterial;
Immunosuppressive; respiratory distress syndrome; Respiratory-Gen.;
respiratory disease; rheumatoid arthritis; arthritis; Antirheumatic;
Antiarthritic; immune disorder; gout; Antigout; osteoarthritis;
osteopathic; nephritis; genitourinary disease; nephrotropic;
hypersensitivity; Antiallergic; gastrointestinal disease; Endocrine-Gen.;
Gastrointestinal-Gen.; gastrointestinal inflammatory bowel disease;
genitourinary disease; female sexual dysfunction;
male sexual dysfunction; Gynecological; transplant rejection; Analgesic;
pain; neurological disease; HIV infection; Anti-HIV; hypopigmentation;
Dermatological; dermatological disease; tinea; Fungicide;
diabetes mellitus; Antidiabetic; metabolic disorder; anorexia nervosa;
Eating-Disorder-General.; Cardiovascular-Gen.; Anorectic;
nutritional disorder; psychiatric disorder; fever; Antipyretic;
temperature disorder; functional bowel disorder; obesity; pancreatitis;
fibroid; scar tissue; keloid; scleroderma; graft versus host disease;
liver cirrhosis; pulmonary fibrosis; nephropathy; Ophthalmological;
uveitis; Bence's disease; hematological disease; sarcoidosis; vasculitis;
infection; antimicrobial; celiac disease; melanoma; neoplasm; Cytostatic;
Anabolic.
XX
OS Pseudonocardia sp. 727713.
XX
FN WO2005097973-A1.
XX
PD 20-OCT-2005.
XX
PF 22-MAR-2005; 2005WO-JP005653.
XX
PR 08-APR-2004; 2004AU-00901919.
XX
PA (FUJI) FUJISAWA PHARM CO LTD.
XX
PI Otsuka T, Ueda H, Fujie K, Muramatsu H, Hashimoto M, Takase S;
XX
DR WPI; 2005-703551/72.
XX
PT New pure WS727713 compound which is a melanocortin receptor modulator
useful as antiinflammatory and for treating e.g. hypoxic shock, acute
respiratory distress syndrome, rheumatic arthritis and melanoma invasion.
XX
PS Disclosure; SEQ ID NO 1; 41pp; English.
XX
CC This invention describes a novel compound WS727713 isolated from
Pseudonocardia sp. 727713 in a leaf litter sample. The compound is

CC capable of modulating the melanocortin receptor and has a potent anti-inflammatory effect. The compound can be used as a medicament or a cosmetic for treating or preventing ischemic or reperfusion injury, brain and renal inflammatory diseases, hepatitis, sepsis/septic shock, hypoxic shock, acute respiratory distress syndrome (ARDS), rheumatic arthritis, gouty arthritis, aortic regurgitation, juvenile chronic arthritis, osteoarthritis, nephritis, induction of tolerance, contact hypersensitivity, inflammatory bowel disease, sexual dysfunction, transplantation, pain, disease progression of HIV, post inflammatory hypopigmentation, tinea versicolor, idiopathic guttate hypomelanosis, fever, functional bowel disease, obesity, satiety effect, diabetes mellitus, modulation of dermal exocrine function, canities (canities circumscripta), gray hair, pancreatitis, fibrotic disorders (hypertrophic scars, keloids, localized scleroderma, systemic sclerosis, sclerodermic graft versus host disease of the skin, cirrhosis of the liver, idiopathic and bleomycin induced lung fibrosis, cyclosporin induced nephropathy), uveitis (especially in Behcet's syndrome and sarcoidosis), vasculitis, microbial infections, celiac disease, vulvar vestibulitis syndrome, melanoma invasion or anorexia in human or an animal.

XX
SQ Sequence 1483 BP; 320 A; 360 C; 509 G; 289 T; 0 U; 5 Other;

Query Match 87.2%; Score 21.8; DB 14; Length 1483;
Best Local Similarity 92.0%; Pred. No. 2.9;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGCGTAAGGCCTTTTCG 25
||||||| ||| |||||||||
Db 31 GCAAGTCGACGCGTAAGGCCTTTTCG 55

RESULT 23
ADR90327
ID ADR90327 standard; DNA; 1511 BP.
XX
AC ADR90327;
XX
DT 16-DEC-2004 (first entry)
XX
DE Rhodococcus sp. M-15 bioremediation-related 16S rDNA.
XX
KW alkane; petroleum; bioremediation; 16S ribosomal RNA; 16S rRNA; ds.
XX
OS Rhodococcus sp.
XX
PN JP2004261126-A.
XX
PD 24-SEP-2004.
XX
PF 03-MAR-2003; 2003JP-00056155.
XX
PR 03-MAR-2003; 2003JP-00056155.
XX
PA (EBAR) EBARA CORP.
XX
DR WPI; 2004-665486/65.
XX
PT Evaluating the ability of an environmental sample to degrade alkanes for providing alkane degrading bacteria, comprises measuring alkane degrading bacteria having high resolving power of alkane present in petroleum.

XX
PS Claim 1; SEQ ID NO 3; 33pp; Japanese.

CC The invention relates to a novel method for evaluating the ability of an environmental sample to degrade alkanes. The method comprises measuring the number of alkane-degrading bacteria present in the sample, where the bacteria have high resolving power of a type of alkane present in petroleum and gyrB (gyrase beta subunit) DNA and 16S rDNA. The method of the invention may be useful for evaluating the ability of an environmental sample to degrade alkanes and thus, for providing alkane-degrading bacteria to be utilized in bioremediation of an environment contaminated with petroleum. The method is rapid and simple. The current sequence is that of the Rhodococcus sp. M-15 bioremediation-related 16S

CC ribosomal RNA gene (rDNA) of the invention.
XX
SQ Sequence 1511 BP; 342 A; 362 C; 510 G; 297 T; 0 U; 0 Other;

Query Match 87.2%; Score 21.8; DB 13; Length 1511;
Best Local Similarity 92.0%; Pred. No. 2.9;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGCGTAAGGCCTTTTCG 25
||||||| ||| |||||||||
Db 50 GCAAGTCGACGCGTAAGGCCTTTTCG 74

RESULT 24
ADR90325
ID ADR90325 standard; DNA; 1511 BP.
XX
AC ADR90325;
XX
DT 16-DEC-2004 (first entry)
XX
DE Rhodococcus sp. M-13 bioremediation-related 16S rDNA.
XX
KW alkane; petroleum; bioremediation; 16S ribosomal RNA; 16S rRNA; ds.
XX
OS Rhodococcus sp.
XX
PN JP2004261126-A.
XX
PD 24-SEP-2004.
XX
PF 03-MAR-2003; 2003JP-00056155.
XX
PR 03-MAR-2003; 2003JP-00056155.
XX
PA (EBAR) EBARA CORP.
XX
DR WPI; 2004-665486/65.
XX

PT Evaluating the ability of an environmental sample to degrade alkanes for providing alkane degrading bacteria, comprises measuring alkane degrading bacteria having high resolving power of alkane present in petroleum.

XX Claim 1; SEQ ID NO 1; 33pp; Japanese.

CC The invention relates to a novel method for evaluating the ability of an environmental sample to degrade alkanes. The method comprises measuring the number of alkane-degrading bacteria present in the sample, where the bacteria have high resolving power of a type of alkane present in petroleum and gyrB (gyrase beta subunit) DNA and 16S rDNA. The method of the invention may be useful for evaluating the ability of an environmental sample to degrade alkanes and thus, for providing alkane-degrading bacteria to be utilized in bioremediation of an environment contaminated with petroleum. The method is rapid and simple. The current sequence is that of the Rhodococcus sp. M-13 bioremediation-related 16S ribosomal RNA gene (rDNA) of the invention.

XX
SQ Sequence 1511 BP; 343 A; 367 C; 507 G; 294 T; 0 U; 0 Other;

Query Match 87.2%; Score 21.8; DB 13; Length 1511;
Best Local Similarity 92.0%; Pred. No. 2.9;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGCGTAAGGCCTTTTCG 25
||||||| ||| |||||||||
Db 50 GCAAGTCGACGCGTAAGGCCTTTTCG 74

RESULT 25
AED11327
ID AED11327 standard; DNA; 1511 BP.
XX
AC AED11327;

XX 01-DEC-2005 (first entry)
 DT Aliphatic hydrocarbon degrading R. erythropolis strain 16S rRNA gene.
 DE degradation; aliphatic hydrocarbon; bioremediation; oil degradation;
 XX pollutant; degradation; groundwater decontamination; 16S rRNA;
 KW 16S ribosomal RNA; gene; ds.
 XX Rhodococcus erythropolis.
 OS JP2005261218-A.
 XX 29-SEP-2005.
 PD
 XX 16-MAR-2004; 2004JP-00074370.
 PF 16-MAR-2004; 2004JP-00074370.
 XX (EBAR) EBARA CORP.
 XX Karube M, Tamatsubo K, Miya A;
 XX WPI; 2005-678804/70.
 DR Novel Rhodococcus erythropolis M-13 strain capable of degrading aliphatic
 PT hydrocarbon, useful for bioremediation of oil-polluted environment such
 PT as river water, underground water, ocean, sea cost.
 XX Claim 1; SEQ ID NO 1; 14pp; Japanese.
 XX The invention relates to a novel Rhodococcus erythropolis M-13 strain
 CC capable of degrading aliphatic hydrocarbons. The invention further
 CC provides the 16S rRNA gene of the novel strain showing 98% or more
 CC homology with a nucleotide sequence of a fully defined 1511 nucleotide
 CC (AED11327) sequence given in specification. The novel strain is useful
 CC for the bioremediation of an oil-polluted environment, such as river
 CC water, underground water, ocean, sea cost, etc. The novel strain degrades
 CC linear or branched aliphatic hydrocarbons efficiently. This
 CC polynucleotide sequence represents the DNA of the novel Rhodococcus
 CC erythropolis M-13 strain 16S rRNA gene of the invention.
 XX Sequence 1511 BP; 343 A; 367 C; 507 G; 294 T; 0 U; 0 Other;
 SQ
 Query Match 87.2%; Score 21.8; DB 14; Length 1511;
 Best Local Similarity 92.0%; Pred. No. 2.9;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 GCAAGTCGACGGAAGGCGCTTCG 25
 DB 50 GCAAGTCGACGGAAGGCGCTTCG 74
 RESULT 26
 ID ADE41084
 DE ADE41084 standard; rRNA; 1584 BP.
 XX
 AC ADE41084;
 XX
 DT 29-JAN-2004 (first entry)
 DE . corallina partial 16S rRNA sequence.
 XX Antibiotic; ss; 16S rRNA; MF-BA-1768alpal; MF-BA-1768betal;
 KW Staphylococcus; Enterococcus; Streptococcus; Haemophilus; Escherichia;
 KW bacterial infection.
 XX Microbispora corallina; strain NRRL 30420.
 OS
 XX US5551591-B1.
 FN
 XX 22-APR-2003.
 PD
 . XX

PF 07-SEP-2001; 2001US-00949230.
 XX 07-SEP-2001; 2001US-00949230.
 PR (ESSE-) ESSENTIAL THERAPEUTICS INC.
 PA Lee MD;
 XX WPI; 2003-895156/82.
 DR Novel antibiotics isolated from fermentation broth of novel strain of
 XX Microbispora corallina, useful for treating a wide range of bacterial
 PT infections.
 PT Disclosure; SEQ ID NO 1; 20pp; English.
 PS
 XX The invention relates to antibiotic MF-BA-1768alpal or MF-BA-1768-betal
 CC or its pharmaceutically acceptable salt, having physicochemical
 CC characteristics in the non-salt form as detailed in the specification.
 CC The antibiotics are isolated from a novel strain of Microbispora
 CC corallina designated NRRL 30420. Also included are producing the above
 CC antibiotic (by cultivating Microbispora corallina NRRL 30420, or an
 CC antibiotic MF- BA-1768alpal or MF-BA-1768betal -producing mutant,
 CC variant or its recombinant form, in a culture medium containing
 CC assimilable sources of carbon, nitrogen and inorganic salts under aerobic
 CC fermentation conditions until the antibiotic is produced and then
 CC recovering the antibiotic) and a composition comprising the above
 CC antibiotic or its salt. The antibiotics are useful for treating a
 CC bacterial infection caused by Staphylococcus (e.g. S.aureus , S.epidermis
 CC , S.haemolyticus), Enterococcus (e.g. E.faecalis , E.faecium),
 CC Streptococcus (e.g. S.pneumoniae , S.pyrogenes), Haemophilus (e.g.
 CC H.influenzae) or Escherichia (e.g. E.coli) in a patient. The present
 CC sequence is partial 16S rRNA sequence from M. corallina NRRL 30420, which
 CC identifies the strain.
 XX Sequence 1584 BP; 339 A; 384 C; 525 G; 320 T; 0 U; 16 Other;
 SQ
 Query Match 87.2%; Score 21.8; DB 10; Length 1584;
 Best Local Similarity 92.0%; Pred. No. 3;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 GCAAGTCGACGGAAGGCGCTTCG 25
 DB 124 GCAAGTCGACGGAAGGCGCTTCG 148
 RESULT 27
 ID AED48445/c
 DE AED48445 standard; DNA; 84222 BP.
 XX
 AC AED48445;
 XX
 DT 15-DEC-2005 (first entry)
 DE M. echinospora gentamycin biosynthetic gene cluster DNA.
 XX ds; gene; antibiotic; virucide; aminoglycoside; bacterial infection;
 KW viral infection; gentamycin; genP; gmrB; genB1; genQ; genD3; genM1; gmrA;
 KW genS1; genC; genD2; genM2; genD1; genS2; genW; genB4; genB3; genK;
 KW genB2; genX; genU; genT; genE; genY; genA; genF; genG; genH; genI; genJ;
 KW genL; genN; DNA polymerase beta chain; integral membrane protein;
 KW agglutinin; esterase; Trp-trNA ligase;
 KW guanine/archaeosine tRNA-ribosyltransferase; ribosomal methyltransferase;
 KW gentamicin (hexosamyl-6-)aminotransferase I; gentamicin oxidoreductase;
 KW (N-acetyl-) hexosamyltransferase; ribosomal methyltransferase;
 KW L-glutamine:ketcyclitol; 2-deoxy-scyllol-inosose synthase;
 KW gentamicin glycosyltransferase II; gentamicin aminotransferase II;
 KW gentamicin production protein; gentamicin aminotransferase IV;
 KW aminoglycoside 3'-phosphotransferase; gentamicin aminotransferase III;
 KW gentamicin C-methyltransferase; gentamicin aminotransferase II;
 KW gentamicin exporter; aminocyclitol 1-dehydrogenase; cation transporter;
 KW gentamicin methyltransferase; two-component system histidine kinase;
 KW two-component system response regulator; serine protease;

KW DNA polymerase III epsilon subunit; RNA polymerase sigma factor;
 KW subtilase; transcriptional regulator; acetyltransferase;
 XX ATP-binding protein; ABC-transporter, permease component.
 OS Micromonospora echinospora.

XX Key Location/Qualifiers
 FH 191..1264
 CDS /tag= a
 FT /product= "putative DNA polymerase beta chain"
 FT /note= "ORF MecP21.15"
 FT complement(1347..2321)
 FT /tag= b
 FT /product= "putative integral membrane protein"
 FT /note= "ORF MecP21.16c"
 CDS 2374..2847
 FT /tag= c
 FT /product= "hypothetical protein"
 FT /note= "ORF MecP21.17"
 CDS 2847..4517
 FT /tag= d
 FT /product= "hypothetical protein"
 FT /note= "ORF MecP21.18"
 CDS complement(4571..5590)
 FT /tag= e
 FT /product= "putative plus agglutinin"
 FT /note= "ORF MecP21.19c"
 CDS complement(5628..6206)
 FT /tag= f
 FT /product= "hypothetical protein"
 FT /note= "ORF MecP21.20c"
 CDS complement(6297..6899)
 FT /tag= g
 FT /product= "putative esterase"
 FT /note= "ORF MecP21.21c"
 CDS 7683..9389
 FT /tag= h
 FT /product= "hypothetical protein"
 FT /note= "ORF MecP21.22"
 CDS complement(9518..10144)
 FT /tag= i
 FT /product= "hypothetical protein"
 FT /note= "ORF MecP21.23c"
 CDS 16081..16620
 FT /tag= j
 FT /product= "hypothetical protein"
 FT /note= "ORF MecE04.1"
 CDS 16711..17790
 FT /tag= k
 FT /product= "putative Trp-tRNA ligase"
 FT /note= "ORF MecE04.2"
 CDS 17857..19014
 FT /tag= l
 FT /product= "guanine/archaeosine tRNA-ribosyltransferase"
 FT /gene= "genP"
 CDS 19121..19939
 FT /tag= m
 FT /gene= "gmrB"
 FT /product= "putative ribosomal methyltransferase"
 FT complement(19953..21206)
 CDS /tag= n
 FT /product= "gentamicin (hexosaminyl-6-)aminotransferase I"
 FT /gene= "genB1"
 CDS complement(21238..22761)
 FT /tag= o
 FT /gene= "genQ"
 FT /product= "gentamicin (hexosaminyl-6-)aminotransferase I"
 CDS complement(22934..23743)
 FT /tag= p
 FT /product= "putative gentamicin oxidoreductase"
 FT /gene= "genB3"
 CDS complement(23758..25005)
 FT /tag= q

FT /gene= "genM1"
 FT /product= "putative (N-acetyl-) hexosaminyltransferase"
 FT complement(25042..25866)
 FT /tag= r
 FT /product= "putative ribosomal methyltransferase"
 FT /gene= "gmrA"
 CDS 26161..27423
 FT /tag= s
 FT /gene= "genS1"
 FT /product= "putative L-glutamine:ketocyclitol"
 CDS 27558..28751
 FT /tag= t
 FT /product= "2-deoxy-scylo-inosose synthase"
 FT /gene= "genC"
 CDS 28744..29769
 FT /tag= u
 FT /gene= "genD2"
 FT /product= "putative gentamicin oxidoreductase"
 CDS 29858..31030
 FT /tag= v
 FT /product= "putative gentamicin glycosyltransferase II"
 FT /gene= "genM2"
 CDS 31032..33011
 FT /tag= w
 FT /gene= "genD1"
 FT /product= "putative gentamicin oxidoreductase"
 CDS 33011..34267
 FT /tag= x
 FT /product= "putative gentamicin aminotransferase II"
 FT /gene= "genS2"
 CDS 34275..34646
 FT /tag= y
 FT /gene= "genW"
 FT /product= "putative gentamicin production protein"
 CDS complement(34741..36078)
 FT /tag= z
 FT /product= "putative gentamicin aminotransferase IV"
 FT /gene= "genB4"
 CDS complement(36137..36943)
 FT /tag= aa
 FT /gene= "genJ"
 FT /product= "biosynthetic aminoglycoside 3'-
 FT phosphotransferase"
 CDS complement(36981..38453)
 FT /tag= ab
 FT /product= "putative gentamicin aminotransferase III"
 CDS /gene= "genB3"
 FT complement(38969..40885)
 FT /tag= ac
 FT /gene= "genK"
 FT /product= "putative gentamicin C-methyltransferase"
 CDS 41135..42379
 FT /tag= ad
 FT /product= "putative gentamicin aminotransferase II"
 FT /gene= "genB2"
 CDS complement(42465..42977)
 FT /tag= ae
 FT /gene= "genX"
 FT /product= "putative gentamicin production protein"
 CDS complement(43032..43967)
 FT /tag= af
 FT /product= "putative gentamicin production protein"
 CDS complement(44162..45568)
 FT /tag= ag
 FT /gene= "genT"
 FT /product= "putative gentamicin exporter"
 CDS complement(45861..46883)
 FT /tag= ah
 FT /product= "putative aminocyclitol 1-dehydrogenase"
 FT /gene= "genE"
 CDS 47364..48878
 FT /tag= ai


```

FT FT /gene= "genY"
FT FT /product= "putative cation antiporter"
FT FT 49000. .49737
FT FT /*tag= aj
FT FT /product= "putative gentamicin production protein"
FT FT /gene= "genA"
FT FT 49734. .50381
FT FT /*tag= ak
FT FT /gene= "genF"
FT FT /product= "putative gentamicin production protein"
FT FT 50381. .50734
FT FT /*tag= al
FT FT /product= "putative gentamicin production protein"
FT FT /gene= "genG"
FT FT complement(50813. .54229)
FT FT /*tag= am
FT FT /product= "putative gentamicin exporter "
FT FT /gene= "genH"
FT FT complement(54226. .56163)
FT FT /*tag= an
FT FT /gene= "genI"
FT FT /product= "putative gentamicin exporter "
FT FT complement(56689. .57627)
FT FT /*tag= ao
FT FT /gene= "genJ"
FT FT /product= "putative gentamicin production protein"
FT FT 58121. .58741
FT FT /*tag= ap
FT FT /product= "putative gentamicin production protein"

Query Match 87.2%; Score 21.8; DB 14; Length 84222;
Best Local Similarity 92.0%; Pred. No. 4.5;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCTTCG 25
Db 15396 GCAAGTCGACGGAAGGCCTTCG 15372

RESULT 29
AAD11024/c
ID AAD11024 standard; DNA; 32 BP.
AC AAD11024;
XX
XX
DT 24-SEP-2001 (first entry)
XX
XX
DE Probe #4 to detect amplified MAC 16S rRNA or DNA encoding 16S rRNA.
XX
XX Mycobacterium avium complex; MAC; 16S ribosomal RNA; pathogenic bacteria;
XX in vitro amplification; MAC infection; probe; ss.
XX Mycobacterium sp.
XX
XX WO200144511-A2.
XX
XX 21-JUN-2001.
XX
XX 15-DEC-2000; 2000WO-US033872.
XX
XX 15-DEC-1999; 99US-0171202P.
XX
XX (GENP-) GEN-PROBE INC.
XX (BREN/) BRENTANO S T.
XX (LANK/) LANKFORD R L.
XX
XX Brentano ST, Lankford RL;
XX
XX WPI; 2001-398171/42.
XX
XX Detecting Mycobacterium avium complex organisms, comprises using in vitro
XX nucleic acid amplification with amplification oligonucleotides specific
XX for 16S ribosomal RNA or DNA encoding 16S rRNA from the bacterial

```

```

PT species.
XX Claim 11; Page 27; 27pp; English.
XX
CC The present invention relates to a method for detecting Mycobacterium
CC avium complex (MAC) organisms (eg. M. avium, M. intracellulare, M.
CC tuberculosis, M. paratuberculosis) present in a biological sample. The
CC method comprises amplifying a 16S ribosomal RNA (rRNA) or DNA encoding
CC 16S rRNA obtained from a biological sample containing nucleic acid from a
CC MAC species in an in vitro nucleic acid amplification mixture comprising
CC a polymerase activity and a pair of primers to produce an amplified
CC nucleic acid and detecting amplified nucleic acid. The method is useful
CC for in vitro diagnostic detection of pathogenic bacteria, particularly
CC detecting infections caused by MAC organisms, distinguished from other
CC closely-related Mycobacterium species. The present sequence is a probe
CC used to detect amplified MAC 16S rRNA sequence or DNA encoding 16S rRNA
XX
SQ Sequence 32 BP; 5 A; 11 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 85.6%; Score 21.4; DB 4; Length 32;
Best Local Similarity 95.7%; Pred. No. 3;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCTTT 23
Db 32 GCAAGTCGACGGAAGGCCTCT 10

RESULT 29
AAD11017
ID AAD11017 standard; DNA; 32 BP.
XX
XX AAD11017;
AC
XX
XX 24-SEP-2001 (first entry)
DT
XX
XX PCR primer #4 used for in vitro amplification of MAC rRNA.
DE
XX Mycobacterium avium complex; MAC; 16S ribosomal RNA; pathogenic bacteria;
XX in vitro amplification; MAC infection; PCR primer; ss.
XX Mycobacterium sp.
XX
XX WO200144511-A2.
XX
XX 21-JUN-2001.
XX
XX 15-DEC-2000; 2000WO-US033872.
XX
XX 15-DEC-1999; 99US-0171202P.
XX
XX (GENP-) GEN-PROBE INC.
XX (BREN/) BRENTANO S T.
XX (LANK/) LANKFORD R L.
XX
XX Brentano ST, Lankford RL;
XX
XX WPI; 2001-398171/42.
XX
XX Detecting Mycobacterium avium complex organisms, comprises using in vitro
XX nucleic acid amplification with amplification oligonucleotides specific
XX for 16S ribosomal RNA or DNA encoding 16S rRNA from the bacterial
XX species.
XX
XX Claim 1; Page 12; 27pp; English.
XX
XX The present invention relates to a method for detecting Mycobacterium
XX avium complex (MAC) organisms (eg. M. avium, M. intracellulare, M.
XX tuberculosis, M. paratuberculosis) present in a biological sample. The
XX method comprises amplifying a 16S ribosomal RNA (rRNA) or DNA encoding
XX 16S rRNA obtained from a biological sample containing nucleic acid from a
XX MAC species in an in vitro nucleic acid amplification mixture comprising
XX a polymerase activity and a pair of primers to produce an amplified

```

CC nucleic acid and detecting amplified nucleic acid. The method is useful
CC for in vitro diagnostic detection of pathogenic bacteria, particularly
CC detecting infections caused by MAC organisms, distinguished from other
CC closely-related Mycobacterium species. The present sequence is a PCR
CC primer used for in vitro amplification of MAC rRNA
XX
SQ Sequence 32 BP; 9 A; 7 C; 11 G; 5 T; 0 U; 0 Other;

Query Match 85.6%; Score 21.4; DB 4; Length 32;
Best Local Similarity 95.7%; Pred. No. 3;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCTTT 23
|||||
Db 1 GCAAGTCGACGGAAGGCCTCT 23

RESULT 30

AAX99195

ID AAX99195 standard; DNA; 50 BP.

XX

AC AAX99195;

XX

XX 28-SEP-1999 (first entry)

XX

DE M. avium 16S rRNA gene fragment.

XX

KW Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA;

XX shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.

XX

OS Mycobacterium avium.

XX

XX WO9935284-A1.

XX

XX 15-JUL-1999.

XX

XX 30-DEC-1997; 97WO-BR000087.

XX

XX 30-DEC-1997; 97WO-BR000087.

XX

XX (UYMI-) UNIV FEDERAL MINAS GERAIS.

XX

XX Peregrino Ferreira PC, Geessien Kroon E;

XX Bernardes Margutti Pinto ME, Aleixo AW;

XX

XX WPI; 1999-444201/37.

XX

XX Detection of mycobacteria by shift mobility assay.

XX

XX Disclosure; Fig 7; 20pp; English.

XX

XX The invention describes a new method for diagnosis, identification and

XX characterisation of Mycobacterium tuberculosis or any other mycobacteria

XX by using polymerase chain reaction (PCR) and shift mobility assay (SMA)

XX in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,

XX DNA amplification and shift mobility assay. The method is based on

XX divergence in sequences found in 16S rRNA to identify mycobacteria

XX species, since a remarkable shift of heteroduplex bands are obtained

XX between single stranded and homoduplex bands in UPAGE. The method is

XX fast, simple and can produce information not easily obtained when

XX compared with other detection methods. The sensitivity of other assays

XX suffer due to the tendency of the denatured PCR product strands to

XX reassociate and exclude oligonucleotide probes, and steric interference

XX between the bound oligonucleotides and the solid support which impede

XX hybridization to nucleic acids in solution. Sequences AAX99193-237

XX represent 16S rRNA gene regions of some mycobacterial species

XX

SQ Sequence 50 BP; 15 A; 12 C; 14 G; 9 T; 0 U; 0 Other;

Query Match

Best Local Similarity 85.6%; Score 21.4; DB 2; Length 50;

Matches 22; Conservative

0; Mismatches

1; Indels

0; Gaps

0;

Qy 1 GCAAGTCGACGGAAGGCCTTT 23
|||||
Db 9 GCAAGTCGACGGAAGGCCTCT 31

RESULT 31

AAX99196

ID AAX99196 standard; DNA; 50 BP.

XX

AC AAX99196;

XX

XX 28-SEP-1999 (first entry)

XX

DE M. fortuitum 16S rRNA gene fragment.

XX

KW Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA;

XX shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.

XX

OS Mycobacterium fortuitum.

XX

XX WO9935284-A1.

XX

XX 15-JUL-1999.

XX

XX 30-DEC-1997; 97WO-BR000087.

XX

XX 30-DEC-1997; 97WO-BR000087.

XX

XX (UYMI-) UNIV FEDERAL MINAS GERAIS.

XX

XX Peregrino Ferreira PC, Geessien Kroon E;

XX Bernardes Margutti Pinto ME, Aleixo AW;

XX

XX WPI; 1999-444201/37.

XX

XX Detection of mycobacteria by shift mobility assay.

XX

XX Disclosure; Fig 7; 20pp; English.

XX

XX The invention describes a new method for diagnosis, identification and

XX characterisation of Mycobacterium tuberculosis or any other mycobacteria

XX by using polymerase chain reaction (PCR) and shift mobility assay (SMA)

XX in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,

XX DNA amplification and shift mobility assay. The method is based on

XX divergence in sequences found in 16S rRNA to identify mycobacteria

XX species, since a remarkable shift of heteroduplex bands are obtained

XX between single stranded and homoduplex bands in UPAGE. The method is

XX fast, simple and can produce information not easily obtained when

XX compared with other detection methods. The sensitivity of other assays

XX suffer due to the tendency of the denatured PCR product strands to

XX reassociate and exclude oligonucleotide probes, and steric interference

XX between the bound oligonucleotides and the solid support which impede

XX hybridization to nucleic acids in solution. Sequences AAX99193-237

XX represent 16S rRNA gene regions of some mycobacterial species

XX

SQ Sequence 50 BP; 14 A; 12 C; 14 G; 9 T; 0 U; 1 Other;

Query Match

Best Local Similarity 85.6%; Score 21.4; DB 2; Length 50;

Matches 22; Conservative

0; Mismatches

1; Indels

0; Gaps

0;

Qy 1 GCAAGTCGACGGAAGGCCTTT 23
|||||
Db 9 GCAAGTCGACGGAAGGCCTCT 31

RESULT 32

ADF94050

ID ADF94050 standard; DNA; 50 BP.

XX

AC ADF94050;

XX

XX 11-MAR-2004 (first entry)

XX

XX (HENK) HENKEL KGAA.
PA (VERM-) VERMICON AG.
XX
PI Saettler A, Jassoy C, Scholtyssek R, Maisenschein V, Nieveler S;
PI Weiss A, Trebesius K, Beimfohr C, Ludwig W, Bamberg RR, Schleifer K;
PI Mueller S, Adomat C, Bergmaier I;
XX
DR WPI; 2004-123402/12.
XX
XX New oligonucleotides for specific detection of microorganisms, useful
PT e.g. for detecting or quantifying microbes on the skin, in foods,
PT clinical samples or water, by in situ hybridization.
XX
XX Disclosure; Page 66-67; 67pp; German.
XX
XX The present invention provides a number of oligonucleotides for the
CC specific detection of microorganisms. The oligonucleotides are used to
CC detect and/or quantify microorganisms, especially on the skin, in foods
CC or the environment (water, soil and air), from waste waters or biofilms,
CC in clinical samples (body fluids or tissues), and in pharmaceutical or
CC cosmetic compositions. The present sequence is a *Corynebacterium* 16S rRNA
CC sequence.
XX
XX Sequence 1431 BP; 308 A; 327 C; 488 G; 0 T; 307 U; 1 Other;
SQ

Query Match 85.6%; Score 21.4; DB 12; Length 1431;
Best Local Similarity 82.6%; Pred. No. 4.5;
Matches 19; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
||||:|||||: :
Db 30 GCAAGUCGAACGGAAGGCCUCU 52

RESULT 37
ADK66445
ID ADK66445 standard; RNA; 1431 BP.
AC ADK66445;
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX *Corynebacterium* 16S rRNA sequence.
DE
XX ss; 16S rRNA; microorganism detection; skin; acne.
XX
XX *Corynebacterium* sp.
OS
XX WO2004009843-A2.
XX
XX 29-JAN-2004.
PD
XX
XX 16-JUL-2003; 2003WO-EP007718.
PF
XX
XX 18-JUL-2002; 2002DE-01032775.
PR
XX 14-FEB-2003; 2003DE-01006616.
PR
XX (HENK) HENKEL KGAA.
PA
XX Saettler A, Jassoy C, Scholtyssek R, Maisenschein V, Nieveler S;
PI Weiss A, Trebesius K, Beimfohr C, Ludwig W, Bamberg RR, Schleifer K;
PI Mueller S, Adomat C, Bergmaier I;
XX
XX WPI; 2004-123405/12.
DR
XX
XX Kit for detection of microorganisms on skin, useful e.g. for diagnosis of
PT infection, comprises specific oligonucleotides for in situ hybridization.
PT
XX
XX Disclosure; Page 62-63; 63pp; German.
PS
XX
XX The present invention relates to a kit for detecting microorganisms that
CC contains at least one oligonucleotide specific for at least one species,

CC or group of species, that is present on the skin. The kit is used to
CC detect and/or quantify microorganisms that are present on the skin; e.g.
CC for early diagnosis of secondary infection in cases of acne. The present
CC sequence is a *Corynebacterium* 16S rRNA sequence.
XX
XX Sequence 1431 BP; 308 A; 327 C; 488 G; 0 T; 307 U; 1 Other;
SQ

Query Match 85.6%; Score 21.4; DB 12; Length 1431;
Best Local Similarity 82.6%; Pred. No. 4.5;
Matches 19; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
||||:|||||: :
Db 30 GCAAGUCGAACGGAAGGCCUCU 52

RESULT 38
AAQ37639
ID AAQ37639 standard; rRNA; 1449 BP.
XX
XX AAQ37639;
AC
XX
XX 25-MAR-2003 (revised)
DT
XX 18-JUN-1993 (first entry)
DT
XX
XX *Mycobacterium* *genavense* 16S rRNA.
DE
XX
XX Detection; rapid; immunosuppressed patients; AIDS; ss.
KW
XX
XX *Mycobacterium* *genavense*.
OS
XX
XX EP529985-A1.
PN
XX
XX 03-MAR-1993.
PD
XX
XX 21-AUG-1992; 92EP-00307690.
PF
XX
XX 23-AUG-1991; 91GB-00018262.
PR
XX 09-JUL-1992; 92GB-00014601.
PR
XX (PINA/) CHANG PINARES H R.
PA (BOET/) BOETTGER E C.
PA (HIRS/) HIRSCHHEL B J.
XX
XX Chang Pinares HR, Boettger EC, Hirschhel BJ;
PI
XX WPI; 1993-068993/09.
DR
XX
XX New 16S ribosomal RNA sequence of new *Mycobacterium* *genavense* - also
PT probes and primers specific for the sequence, for detecting *M. genavense*
PT infections in AIDS patients.
XX
XX Claim 1; Page 17; 21pp; English.
PS
XX
XX The sequence is that of the 16S rRNA of *Mycobacterium* *genavense* sp. nov.
CC from which nucleic acid sequences can be obtd. for use in a method for
CC the reliable and rapid detection and identification of *M. genavense*,
CC partic. opportunistic *M. genavense* infections in highly immunosuppressed
CC patients suffering from AIDS. It was isolated by PCR amplification of DNA
CC from liver, spleen, lymph nodes and polymorphonuclear leukocytes (PMNs,
CC buffy coats) from AIDS patients. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX Sequence 1449 BP; 316 A; 345 C; 495 G; 289 T; 0 U; 4 Other;
SQ

Query Match 85.6%; Score 21.4; DB 2; Length 1449;
Best Local Similarity 95.7%; Pred. No. 4.5;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
||||:|||||: :
Db 47 GCAAGTCGAACGGAAGGCCTTCT 69

```

RESULT 39
AEA22401
ID AEA22401 standard; DNA; 1454 BP.
XX
AC AEA22401;
XX
DT 25-AUG-2005 (first entry)
XX
DE Mycobacterium avium 16S rRNA sequence SEQ ID NO:2.
XX
KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
XX
OS Mycobacterium avium.
XX
PN US2005130168-A1.
XX
PD 16-JUN-2005.
XX
PF 31-OCT-2003; 2003US-00697802.
XX
PR 31-OCT-2003; 2003US-00697802.
XX
PA (HANK/) HAN X.
PA (PHAM/) PHAM A S.
XX
PI Han X, Pham AS;
XX
DR WPI; 2005-424597/43.
XX
CC Determining a bacterium species comprises providing oligonucleotide
CC primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
CC
CC Disclosure; SEQ ID NO 2; 74pp; English.
XX
CC The invention relates to a method (M1) for determining a bacterium
CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
CC extracting a genomic nucleotide from the bacterium to provide a
CC nucleotide template; (c) annealing a region of a nucleotide template to a
CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
CC complimentary fashion, the primer set designed to provide a product
CC having a predetermined size dictated by a complimentary primer set; (d)
CC amplifying the region of the nucleotide template to produce the product;
CC and (e) determining a species of a bacterium in a nucleotide sequence of
CC the product. Also described is an alternative method (M2) for determining
CC a bacterium species comprising: (a) providing a specimen or a sample
CC having a template; (b) providing a pair of primers selected from: (i) a
CC first forward primer having consecutive bases of an AFB-f comprising any
CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
CC or variations and a first reverse primer having consecutive bases of an
CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
CC or their fragments or variations, (ii) a second forward primer having
CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
CC bp (AEA22489-AEA22516) or their fragments or variations and a second
CC reverse primer having consecutive bases of an UB-r comprising any of the
CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
CC variations, or (iii) a first forward primer having consecutive bases of
CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
CC second reverse primer having consecutive bases of an UB-r of AEA22517-
CC AEA22544 or their fragments or variations; (c) the specimen; and (d)
CC comparing the product from the specimen with a nucleotide sequence from a
CC database to determine the bacterium species present in the specimen. The
CC methods are useful for determining a bacterium species. The present
CC sequence represents a Mycobacterium avium 16S rRNA nucleotide sequence,
CC which is used in the exemplification of the present invention.
XX
SQ Sequence 1454 BP; 316 A; 348 C; 494 G; 296 T; 0 U; 0 Other;
XX
Query Match 85.6%; Score 21.4; DB 14; Length 1454;
Best Local Similarity 95.7%; Pred. No. 4.5;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCAAGTCGAACGGAAGGCGCTTT 23

```

```

Db 30 GCAAAGTCGAACGGAAGGCGCTCT 52
|||||
RESULT 40
ADB61680
ID ADB61680 standard; DNA; 1465 BP.
XX
AC ADB61680;
XX
DT 04-DEC-2003 (first entry)
XX
DE 16S rRNA of Mycobacterium avium DNA sequence.
XX
KW enriching mRNA; high quality bacterial mRNA; bacterial gene expression;
KW poly-A tail; mRNA purification; oligo-dT capture;
KW prokaryote mRNA purification; bridging oligonucleotide; targeting region;
KW capture oligonucleotide; prokaryotic 16S rRNA; prokaryotic 23S rRNA;
KW eukaryotic 17S rRNA; eukaryotic 18S rRNA; eukaryotic 28S rRNA;
KW 28S eukaryotic rRNA bridging oligonucleotide; ds.
XX
OS Mycobacterium avium.
XX
PN WO2003054162-A2.
XX
PD 03-JUL-2003.
XX
PF 19-DEC-2002; 2002WO-US041014.
XX
PR 20-DEC-2001; 2001US-00029997.
XX
PA (AMBI-) AMBION INC.
XX
PI Murphy GL, Whitley JP;
XX
DR WPI; 2003-663255/62.
XX
CC Depleting or isolating targeted nucleic acids e.g. rRNA, involves using a
CC bridging oligonucleotide comprising bridging region and a targeting
CC region complementary to a targeted nucleic acid, and a capture
CC oligonucleotide.
XX
CC Claim 4; Page 168; 208pp; English.
XX
CC This invention relates to a novel method for isolating, depleting or
CC separating a targeted nucleic acid, such as rRNA, from a sample
CC comprising targeted and non-targeted nucleic acids. It effects a way of
CC enriching for non-targeted nucleic acids such as mRNAs. Isolating
CC sufficient quantities of high quality bacterial mRNA is a demanding
CC process which impedes analysis of bacterial gene expression in the
CC presence of host cells. A small percentage of bacterial mRNAs may be poly
CC -A tailed, but these are targeted for degradation and tend to be
CC unstable. As a result, the commonly employed method for mRNA purification
CC with eukaryotic cells, oligo-dT capture, is ineffective. The present
CC invention provides an alternative, more suitable method for mRNA
CC purification from prokaryotes. The method of the invention comprises the
CC incubation of a sample with a bridging oligonucleotide (containing a
CC targeting region) and subsequently incubating with a capture
CC oligonucleotide allowing the isolation of the target from the sample. The
CC method is useful for depleting or isolating targeted nucleic acid, for
CC example rRNA such as prokaryotic 16S or prokaryotic 23S, eukaryotic 17S
CC or 18S or eukaryotic 28S rRNA, from a sample. The rRNA sequence may
CC comprise any one of 64 fully defined sequences as given in the
CC specification. The present sequence is that of a DNA sequence which
CC represents the sequence of 16S rRNA of Mycobacterium avium related to the
CC invention.
XX
SQ Sequence 1465 BP; 321 A; 345 C; 496 G; 298 T; 0 U; 5 Other;
XX
Query Match 85.6%; Score 21.4; DB 10; Length 1465;
Best Local Similarity 95.7%; Pred. No. 4.5;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Oy 1 GCAAGTCGACGGAAGGCCTTT 23
Db 20 GCAAGTCGACGGAAGGCCTCT 42

RESULT 41
ADR90572
ID ADR90572 standard; DNA; 1472 BP.
XX
AC ADR90572;
XX
XX 02-DEC-2004 (first entry)
XX
DE M avium 16S rRNA gene sequence SeqID1.
XX
KW acid-fast bacterium; differentiation; 16S rRNA; M avium complex; MAC;
KW taxonomic-tree analysis; atypical-mycobacteria; gene; ds.
XX
OS Mycobacterium avium.
XX
XX Key Location/Qualifiers
FH variation 893
FT /*tag= a
FT variation 1312
FT /*tag= b
FT variation 1393
FT /*tag= c
XX
PN JP2004254591-A.
XX
XX 16-SEP-2004.
XX
XX 26-FEB-2003; 2003JP-00048654.
XX
XX 26-FEB-2003; 2003JP-00048654.
XX
XX (M1TP ) MITSUBISHI YUKA BCL KK.
XX
XX WPI; 2004-664464/65.
XX
XX Differentiating acid-fast bacterium e.g., Mycobacterium avium complex,
XX useful for detecting mutant of M.avium complex, and for grouping strains
XX of M.kansasii, involves detecting mutation in 16S rRNA gene of acid-fast
XX bacterium.
XX
XX Claim 3; SEQ ID NO 1; 23pp; Japanese.
XX
XX This invention relates to a novel method of differentiating acid-fast
XX bacterium, which involves detecting a mutation in the 16S rRNA gene of
XX the acid-fast bacterium. The method is useful for differentiating acid-
XX fast bacterium such as M avium complex (MAC) or M kansasii, in particular
XX for detecting mutants of MAC, and for grouping strains of M kansasii. The
XX method is also useful for carrying out taxonomic-tree analysis of
XX atypical-mycobacteria and enables detection of MAC accurately and
XX reliably. The present sequence is that of a Mycobacterium 16S rRNA gene
XX which may be used in the method of the invention.
XX
XX Sequence 1472 BP; 323 A; 348 C; 500 G; 298 T; 0 U; 3 Other;

Query Match 85.6%; Score 21.4; DB 13; Length 1472;
Best Local Similarity 95.7%; Pred. No. 4.6;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GCAAGTCGACGGAAGGCCTTT 23
Db 30 GCAAGTCGACGGAAGGCCTCT 52

RESULT 42
AAD11273
ID AAD11273 standard; DNA; 22 BP.
XX
XX AAD11273;

```

```

XX 24-SEP-2001 (first entry)
DT XX
XX Mycobacterium 16S rRNA amplifying primer #17.
DE XX
XX Mycobacterium 16S rRNA; 16S ribosomal RNA; amplification;
KW XX
KW Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
XX
XX Mycobacterium sp.
OS XX
PN WO200144510-A2.
XX
PD 21-JUN-2001.
XX
XX 17-DEC-1999; 99WO-US030346.
PF XX
XX 17-DEC-1999; 99WO-US030346.
PR XX
XX (GENP-) GEN-PROBE INC.
XX (INMR ) BIOMERIEUX SA.
PA
XX Brentano ST, Jucker MT, Deigado FD, Cleuziat P, Rodrigue M;
XX WPI; 2001-398170/42.
XX
XX Detecting Mycobacterium species, involves in vitro amplification of 16S
XX rRNA or DNA encoding RNA in nucleic acid amplification mixture using
XX specific primers, and detecting the amplified nucleic acid.
XX
XX Claim 1; Page 36; 44pp; English.
XX
XX The invention relates to a method of detecting Mycobacterium species,
XX that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
XX encoding 16S rRNA in an in vitro nucleic acid amplification mixture
XX comprising a polymerase, and at least two primers, and then detecting the
XX amplified nucleic acid. The method is relatively simple and useful for
XX detecting the presence of various Mycobacterium species in a biological
XX sample, and thus important for diagnosis of infections resulting from
XX them. The method is especially important for screening opportunistic
XX infections caused by M. tuberculosis or a Mycobacterium other than
XX tuberculosis (MOTT). The present sequence is a PCR primer used for
XX amplifying Mycobacterium 16S rRNA
XX
XX Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 84.0%; Score 21; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 GTCGAACGGAAGGCCTTTCG 25
Db 1 GTCGAACGGAAGGCCTTTCG 21

RESULT 43
ADG88354
ID ADG88354 standard; DNA; 22 BP.
XX
AC ADG88354;
XX
XX 11-MAR-2004 (first entry)
DT XX
XX Mycobacterium amplifying PCR primer #23.
DE XX
XX In vitro amplification; PCR; primer; ss.
KW XX
XX Mycobacterium celatum.
OS XX
XX US2003165824-A1.
PN XX
PD 04-SEP-2003.
XX
XX 15-DEC-2000; 2000US-00738274.

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XX 17-DEC-1999; 99US-0172190P.
XX (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZAT P.
PA (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
XX WPI; 2003-898044/82.
XX
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample comprises performing in vitro nucleic acid
PT amplification and detection of amplified products.
XX
PS Claim 1; SEQ ID NO 23; 20pp; English.
XX
XX The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample comprises performing an in vitro
CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
CC detecting the amplified Mycobacterium nucleic acid. The present sequence
CC is Mycobacterium amplifying PCR primer.
XX
XX Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;
SQ
Query Match 84.0%; Score 21; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GTCGAACGGAAGGCTTTTCG 25
Db 1 GTCGAACGGAAGGCTTTTCG 21
RESULT 44
ID AEA08229 standard; DNA; 22 BP.
XX
XX AEA08229;
XX
XX 14-JUL-2005 (first entry)
XX
XX Mycobacterium celatum 16SrRNA amplifying non-T7 primer, SEQ ID NO: 23.
XX
XX Microorganism detection; DNA amplification; 16s ribosomal RNA; 16s rRNA;
KW PCR; primer; ss.
XX
XX Mycobacterium celatum.
XX
XX US2005100915-A1.
XX
XX 12-MAY-2005.
XX
XX 18-SEP-2003; 2003US-00665708.
XX
XX 17-DEC-1999; 99US-0172190P.
XX
XX 15-DEC-2000; 2000US-00738274.
XX
XX (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZAT P.
PA (RODR/) RODRIGUE M.
XX
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
PI
XX
XX WPI; 2005-345392/35.
XX
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample, comprises using in vitro nucleic acid
PT amplification and detection of amplified products.
XX
Claim 8; SEQ ID NO 23; 21pp; English.
XX
XX The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample. The method involves using in
CC vitro nucleic acid amplification and detection of amplified products. The
CC invention is useful for diagnostic detection of pathogenic bacteria such
CC as Mycobacterium species. The present sequence is the Mycobacterium
CC celatum (ATCC 51130 and ATCC 51131) 16S ribosomal RNA (16SrRNA)
CC amplifying non-T7 PCR primer.
XX
XX Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;
SQ
Query Match 84.0%; Score 21; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GTCGAACGGAAGGCTTTTCG 25
Db 1 GTCGAACGGAAGGCTTTTCG 21
RESULT 45
ID AEB98771 standard; DNA; 39 BP.
XX
XX AEB98771;
XX
XX 06-OCT-2005 (first entry)
XX
XX Mycobacterium avium identification LAMP primer, SEQ ID 13.
XX
XX microorganism detection; mycobacterium infection; antibacterial; primer;
KW PCR; ss; LAMP.
XX
XX Mycobacterium avium.
OS Synthetic.
XX
XX JP2005204582-A.
XX
XX 04-AUG-2005.
XX
XX 23-JAN-2004; 2004JP-00015195.
XX
XX 23-JAN-2004; 2004JP-00015195.
XX
XX (ASAH ) ASahi KASEI KK.
PA
XX Oda N;
PI
XX
XX WPI; 2005-526965/54.
XX
XX New single-stranded oligonucleotide, useful for amplifying the nucleic
PT acid of Mycobacterium avium, Mycobacterium intracellulare, and
PT Mycobacterium kansasii.
XX
XX Claim 1; SEQ ID NO 13; 14pp; Japanese.
XX
XX The invention relates to a novel single-stranded oligonucleotide used in
CC a detection method of an atypical mycobacteria group. The invention
CC further includes: amplifying the nucleic acid of Mycobacterium avium by a
CC loop-mediated isothermal amplification (LAMP) method; amplifying the
CC nucleic acid of M. intracellulare by a LAMP method; amplifying the
CC nucleic acid of M. kansasii by a LAMP method; and a kit for detecting the
CC nucleic acid of M. avium by a LAMP method; detecting the nucleic acid of
CC M. intracellulare by a LAMP method; or detecting the nucleic acid of M.
CC kansasii by a LAMP method. The single-stranded oligonucleotide is useful
CC in medical applications. This oligo sequence represents a loop-mediated
CC isothermal amplification (LAMP) primer used in the exemplification of the
CC invention.
XX
XX Sequence 39 BP; 10 A; 11 C; 10 G; 8 T; 0 U; 0 Other;
SQ
```



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Query Match      84.0%; Score 21; DB 14; Length 39;
Best Local Similarity 100.0%; Pred.No. 4.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCAAGTCGAACGGAAGGCCT 21
    |||||:|||||
Db 19 GCAAGTCGAACGGAAGGCCT 39

RESULT 46
ID AAT45276
AC AAT45276;
DT 12-SEP-1997 (first entry)
DE Corynebacterium diphtheriae 16S rRNA.
KW Ribosomal RNA; species specific; detection; reverse transcription;
KW primer; hybridisation probe; identification; ss.
XX Corynebacterium diphtheriae.
OS
FH Key Location/Qualifiers
FT misc_feature 38..59
    /tag= a
    /note= "Defined as nucleotides 72-100"
FT misc_feature 153..170
    /tag= b
    /note= "Defined as nucleotides 195-215"
FT misc_feature 415..431
    /tag= c
    /note= "Defined as nucleotides 466-494"
FT misc_feature 544..567
    /tag= d
    /note= "Defined as nucleotides 544-567"
FT misc_feature 773..787
    /tag= e
    /note= "Defined as nucleotides 838-853"
FT misc_feature 793..808
    /tag= f
    /note= "Defined as nucleotides 859-875"
FT misc_feature 946..965
    /tag= g
    /note= "Defined as nucleotides 1013-1032"
XX
XX FR2733755-A1.
XX
XX 08-NOV-1996.
XX
XX 03-MAY-1995; 95FR-00005494.
XX
XX 03-MAY-1995; 95FR-00005494.
XX
XX (INNR ) BIO MERIEUX.
XX
XX Mabilat C, Ruimy R;
XX
XX WPI; 1997-001738/01.
XX
XX Fragments of Corynebacterium 16S RNA - useful as probes and primers for
XX identifying Corynebacterium spp.
XX
XX Claim 1; Fig 1; 60pp; French.
XX
XX Fragments covering 90 % of the sequence of 16S ribosomal RNA were
XX amplified from 28 strains of 25 different species of Corynebacterium by
XX PCR using primers specific for eubacteria. The amplification products
XX were sequenced and the sequences were aligned for comparison. It was
XX found that certain regions, i.e. those corresponding to nucleotides 72-
XX 100, 195-215, 466-494, 608-853, 859-875 and 1013-1033 in the 16S
XX ribosomal RNA of C. diphtheriae (refer to features table for the present
XX
CC sequence), vary considerably between different species. Probes and
CC primers comprising at least 5 nucleotides from one of these species-
CC specific sequences, including the present sequence, or their complements,
CC are useful to distinguish between different Corynebacterium species. DNA
CC versions of the probes and primers are also included
XX
SQ Sequence 1391 BP; 309 A; 317 C; 464 G; 1 T; 295 U; 5 Other;

Query Match      84.0%; Score 21; DB 2; Length 1391;
Best Local Similarity 90.5%; Pred.No. 7;
Matches 19; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCAAGTCGAACGGAAGGCCT 21
    |||||:|||||
Db 29 GCAAGUCGACGGAAGGCCU 49

RESULT 47
ID ADZ35975
XX ADZ35975 standard; DNA; 1440 BP.
AC ADZ35975;
DT 30-JUN-2005 (first entry)
DE Verrucosisspora sp. AB-18-032 16S rRNA gene.
XX
XX ds; antibiotic; antimalarial; protozoacide; 16S rRNA;
XX polycyclic macrolactone; abysomicin; p-Aminobenzoic acid; folic acid;
XX vitamin; abysomicin B; abysomicin C; abysomicin D;
XX Staphylococcus aureus infection; protozoal infection;
XX plasmodium infection; Leishmania infection; chagas disease;
XX Gram positive bacteria infection; mrsa infection .
XX
XX Verrucosisspora sp. AB-18-032.
OS
XX WO2005033114-A1.
XX
XX 14-APR-2005.
XX
XX 23-SEP-2004; 2004WO-EP010661.
XX
XX 01-OCT-2003; 2003DE-01047472.
XX
XX 11-NOV-2003; 2003DE-01053300.
XX
XX (UYTU-) UNIV TUEBINGEN.
XX
XX Fiedler H, Suessmuth R, Zaehner H, Bull A;
XX
XX WPI; 2005-296122/30.
XX
XX New abysomicin polycyclic macrolactone compounds, useful as antibiotics
XX and antiprotozoal agents effective against multiresistant strains,
XX prepared using bacteria of genus Verrucosisspora.
XX
XX Disclosure; SEQ ID NO 1; 47pp; German.
XX
XX This invention describes novel polycyclic macrolactones and their
XX derivatives , prepared using bacteria of genus Verrucosisspora and
XX designated abysomicins. The polycyclic macrolactones have at least one
XX oxa-bicyclo system as a partial structure and at least one Michael system
XX as double bond system. The polycyclic macrolactones are prepared by
XX culturing Verrucosisspora strain AB 18-032, recovering a culture
XX supernatant from the culture, optionally preparing a culture filtrate and
XX optionally isolating one or more polycyclic macrolactones from the
XX supernatant and/or filtrate. Alternatively the microorganism is cultured
XX followed by isolating one or more polycyclic macrolactones from the
XX microorganism. The Verrucosisspora strain AB 18-032 was isolated from
XX marine sediment collected at a depth of 1000m in Sagami bay in the
XX Japanese Sea and is deposited as DSM No. 15899. The polycyclic
XX macrolactones inhibit the biosynthesis of p-Aminobenzoic acid, (an
XX essential component in the biosynthesis of folic acid) from chorismic
XX acid, thus inhibiting folic acid biosynthesis. The vitamin folic acid is

```

CC essential to the life of microorganisms, especially prokaryotes and
 CC protozoa. The polycyclic macrolactones do not inhibit the biosynthesis of
 CC folic acid in mammals (including humans), and thus have no adverse
 CC effects on mammalian cells. Three polycyclic macrolactones are
 CC specifically claimed, i.e. abyssomicin B, abyssomicin C and abyssomicin
 CC D. Abyssomicin C strongly inhibited growth of methicillin-resistant
 CC *Staphylococcus aureus* strain N35 and vancomycin-resistant *Staphylococcus*
 CC *aureus* strain Mu50. The products of the invention are useful as
 CC antibiotics (especially effective against Gram positive bacteria) and
 CC antiprotzoal agents, specifically effective against bacteria and
 CC protozoa resistant (especially multi-resistant) to conventional
 CC antibiotics. Typically polycyclic macrolactones are useful for combating
 CC tropical protozoal diseases (e.g. malaria, leishmaniasis, sleeping
 CC sickness and Chagas disease) and infections caused by resistant Gram
 CC positive bacteria such as methicillin- and vancomycin-resistant
 CC *Staphylococcus aureus* strains. Polycyclic macrolactones are also useful
 CC as disinfectants (especially in hospitals and other medical
 CC establishments) and as lead structures for the development of further
 CC active agents. This sequence represents the *Verrucosisspora* strain AB 18-
 CC 032 16S rRNA DNA which is used to phylogenically classify the bacterial
 CC strain.
 SQ Sequence 1440 BP; 313 A; 363 C; 500 G; 264 T; 0 U; 0 Other;

Query Match 83.2%; Score 20.8; DB 14; Length 1440;
 Best Local Similarity 91.7%; Pred. No. 8.8;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAAGTCGACGGAAGGCGCTTTCG 25
 DB 1 CAAGTCGACGGAAGGCGCTTTCG 24

RESULT 48
 ABN86276
 ID ABN86276 standard; DNA; 1457 BP.
 XX
 AC ABN86276;
 XX
 DT 08-OCT-2002 (first entry)
 XX
 DE G. polyisoprenivorans P8219 16S rDNA sequence #2.
 XX
 KW Microorganism; environmental; hormone; phthalic acid; alkyl ester; ds.
 XX
 OS Gordonia polyisoprenivorans.
 XX
 PN JP2002142754-A.
 XX
 PD 21-MAY-2002.
 XX
 PF 08-NOV-2000; 2000JP-00341214.
 XX
 PR 08-NOV-2000; 2000JP-00341214.
 XX
 PA (IMBI-) IMB KK.
 XX
 DR WPI; 2002-561124/60.
 XX

PT A Gordonia sp. microorganism, useful in the eradication of the
 PT environmental hormone of phthalic acid esters for environmental
 PT protection.
 XX
 PS Disclosure; Fig 2A-D; 21pp; Japanese.
 XX
 CC The invention relates to a Gordonia sp. microorganism, capable of
 CC eradication of the environmental hormone of phthalic acid alkyl esters.
 CC The microorganism is used in the eradication of phthalic acid esters for
 CC environmental protection. The present sequence represents an alternate G.
 CC polyisoprenivorans P8219 16S rDNA sequence
 XX
 SQ Sequence 1457 BP; 323 A; 348 C; 493 G; 291 T; 0 U; 2 Other;

Query Match 83.2%; Score 20.8; DB 6; Length 1457;
 Best Local Similarity 91.7%; Pred. No. 8.8;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GCAAGTCGACGGAAGGCGCTTTC 24
 DB 40 GCAAGTCGACGGAAGGCGCTTTC 63
 RESULT 49
 ABN86275
 ID ABN86275 standard; DNA; 1457 BP.
 XX
 AC ABN86275;
 XX
 DT 08-OCT-2002 (first entry)
 XX
 DE G. polyisoprenivorans P8219 16S rDNA sequence.
 XX
 KW Microorganism; environmental; hormone; phthalic acid; alkyl ester; ds.
 XX
 OS Gordonia polyisoprenivorans.
 XX
 PN JP2002142754-A.
 XX
 PD 21-MAY-2002.
 XX
 PF 08-NOV-2000; 2000JP-00341214.
 XX
 PR 08-NOV-2000; 2000JP-00341214.
 XX
 PA (IMBI-) IMB KK.
 XX
 DR WPI; 2002-561124/60.
 XX

PT A Gordonia sp. microorganism, useful in the eradication of the
 PT environmental hormone of phthalic acid esters for environmental
 PT protection.
 XX
 PS Disclosure; Fig 2A-D; 21pp; Japanese.
 XX
 CC The invention relates to a Gordonia sp. microorganism, capable of
 CC eradication of the environmental hormone of phthalic acid alkyl esters.
 CC The microorganism is used in the eradication of phthalic acid esters for
 CC environmental protection. The present sequence represents a G.
 CC polyisoprenivorans P8219 16S rDNA sequence
 XX
 SQ Sequence 1457 BP; 322 A; 349 C; 496 G; 290 T; 0 U; 0 Other;

Query Match 83.2%; Score 20.8; DB 6; Length 1457;
 Best Local Similarity 91.7%; Pred. No. 8.8;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTCGACGGAAGGCGCTTTC 24
 DB 40 GCAAGTCGACGGAAGGCGCTTTC 63

RESULT 50
 AAS59540/c
 ID AAS59540 standard; DNA; 2743 BP.
 XX
 AC AAS59540;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Propionibacterium acnes immunogenic protein encoding DNA #35.
 XX
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant; ds.
 XX

OS Propionibacterium acnes.
 DN WO200181581-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 20-APR-2001; 2001WO-US012865.
 XX
 PR 21-APR-2000; 2000US-0199047P.
 PR 02-JUN-2000; 2000US-0208841P.
 PR 07-JUL-2000; 2000US-0216747P.
 XX
 XX (CORI-) CORIXA CORP.
 XX
 PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX
 DR WPI; 2001-616774/71.
 XX
 PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris.
 XX
 PS Claim 1; SEQ ID NO 35; 1069pp; English.
 XX
 XX Sequences AAS59506-AAS59804 represent DNA molecules encoding
 CC Propionibacterium acnes immunogenic polypeptides. The proteins and their
 CC associated DNA sequences are used in the treatment, prevention and
 CC diagnosis of medical conditions caused by P. acnes. The disorders include
 CC SAPHO syndrome (synovitis, acne, pustulosis, hyperostosis and
 CC osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in
 CC infections of bone, joints and the central nervous system, however it is
 CC particularly involved in the inflammatory lesions associated with acne
 CC vulgaris. A method for detecting the presence or absence of P. acnes in a
 CC patient comprises contacting a sample with a binding agent that binds to
 CC the proteins of the invention and determining the amount of bound protein
 CC in the sample. The polypeptides may be used as antigens in the production
 CC of antibodies specific for P. acnes proteins. These antibodies can be
 CC used to downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). This sequence encodes the
 CC polypeptides shown in AAU47822-AAU47846. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 2743 BP; 645 A; 999 C; 546 G; 551 T; 0 U; 2 Other;
 Query Match 83.2%; Score 20.8; DB 4; Length 2743;
 Best Local Similarity 91.7%; Pred. No. 9.4;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 GCAAGTCGAACGGAAGGCGCTTTC 24
 |||||
 Db 2593 GCAAGTCGAACGGAAGGCGCTGCG 2570
 |||||
 RESULT 51
 ACF64469/c
 ID ACF64469 standard; DNA; 2743 BP.
 XX
 AC ACF64469;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Propionibacterium acnes DNA contig sequence #35.
 XX
 XX Acne vulgaris; antiseborrheic; dermatological; antibacterial;
 KW immunostimulant; immune response; vaccine; ds.
 XX
 OS Propionibacterium acnes.
 XX

PN WO2003033515-A1.
 XX
 PD 24-APR-2003.
 XX
 PF 11-OCT-2002; 2002WO-US032727.
 XX
 PR 15-OCT-2001; 2001US-00978825.
 XX
 PR (CORI-) CORIXA CORP.
 XX
 PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
 PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
 PI Barth B, Vallieue-Douglas J;
 XX
 DR WPI; 2003-381789/36.
 XX
 PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX
 PS Claim 1; SEQ ID NO 35; 1481pp; English.
 XX
 XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a P. acnes DNA contig which is specifically claimed
 CC in the invention. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 2743 BP; 645 A; 999 C; 546 G; 551 T; 0 U; 2 Other;
 Query Match 83.2%; Score 20.8; DB 8; Length 2743;
 Best Local Similarity 91.7%; Pred. No. 9.4;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 GCAAGTCGAACGGAAGGCGCTTTC 24
 |||||
 Db 2593 GCAAGTCGAACGGAAGGCGCTGCG 2570
 |||||
 RESULT 52
 AAX99198
 ID AAX99198 standard; DNA; 50 BP.
 XX
 AC AAX99198;
 XX
 DT 28-SEP-1999 (first entry)
 XX
 DE M. smegmatis 16S rRNA gene fragment.
 XX
 KW Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA;
 KW shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.
 XX

```

OS Mycobacterium smegmatis.
XX WO9935284-A1.
XX
XX
PD 15-JUL-1999.
XX
XX PF 30-DEC-1997; 97WO-BR000087.
XX
XX PR 30-DEC-1997; 97WO-BR000087.
XX
XX PA (UYMI-) UNIV FEDERAL MINAS GERAIS.
XX
XX PI Peregrino Ferreira PC, Geessien Kroon E;
XX PI Bernardes Margutti Pinto ME, Aleixo AW;
XX
XX DR WPI; 1999-444201/37.
XX
XX PT Detection of mycobacteria by shift mobility assay.
XX
XX PS Disclosure; Fig 7; 20pp; English.
XX
XX CC The invention describes a new method for diagnosis, identification and
CC characterisation of Mycobacterium tuberculosis or any other mycobacteria
CC by using polymerase chain reaction (PCR) and shift mobility assay (SMA)
CC in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,
CC DNA amplification and shift mobility assay. The method is based on
CC divergence in sequences found in 16S rRNA to identify mycobacteria
CC species, since a remarkable shift of heteroduplex bands are obtained
CC between single stranded and homoduplex bands in UPAGE. The method is
CC compared with other detection methods. The sensitivity of other assays
CC suffer due to the tendency of the denatured PCR product strands to
CC reassociate and exclude oligonucleotide probes, and stearic interference
CC between the bound oligonucleotides and the solid support which impede
CC hybridization to nucleic acids in solution. Sequences AAX99193-237
CC represent 16S rRNA gene regions of some mycobacterial species
XX
XX SQ Sequence 50 BP; 13 A; 12 C; 15 G; 9 T; 0 U; 1 Other;
Query Match 81.6%; Score 20.4; DB 2; Length 50;
Best Local Similarity 91.3%; Pred. No. 9.5;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 GCAAGTCGAACGGAAGGCGCTTT 23
DB 9 GCAAGTCGAACGGAAGGCGCTT 31
RESULT 53
AAX99201
ID AAX99201 standard; DNA; 50 BP.
XX
XX AC AAX99201;
XX
XX DT 27-AUG-2003 (revised)
XX DT 28-SEP-1999 (first entry)
XX
XX DE M. simium 16S rRNA gene fragment.
XX
XX KW Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA;
XX KW shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.
XX
XX OS Mycobacterium simiae.
XX
XX PN WO9935284-A1.
XX
XX PD 15-JUL-1999.
XX
XX PF 30-DEC-1997; 97WO-BR000087.
XX
XX PR 30-DEC-1997; 97WO-BR000087.
XX
XX PA (UYMI-) UNIV FEDERAL MINAS GERAIS.
XX
XX PI Peregrino Ferreira PC, Geessien Kroon E;
XX PI Bernardes Margutti Pinto ME, Aleixo AW;
XX
XX DR WPI; 1999-444201/37.
XX
XX PT Detection of mycobacteria by shift mobility assay.
XX
XX PS Disclosure; Fig 7; 20pp; English.
XX
XX CC The invention describes a new method for diagnosis, identification and
XX characterisation of Mycobacterium tuberculosis or any other mycobacteria
XX by using polymerase chain reaction (PCR) and shift mobility assay (SMA)
XX in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,
XX DNA amplification and shift mobility assay. The method is based on
XX divergence in sequences found in 16S rRNA to identify mycobacteria
XX species, since a remarkable shift of heteroduplex bands are obtained
XX between single stranded and homoduplex bands in UPAGE. The method is
XX compared with other detection methods. The sensitivity of other assays
XX suffer due to the tendency of the denatured PCR product strands to
XX reassociate and exclude oligonucleotide probes, and stearic interference
XX between the bound oligonucleotides and the solid support which impede
XX hybridization to nucleic acids in solution. Sequences AAX99193-237
XX represent 16S rRNA gene regions of some mycobacterial species
XX
XX SQ Sequence 50 BP; 13 A; 12 C; 15 G; 9 T; 0 U; 1 Other;
Query Match 81.6%; Score 20.4; DB 2; Length 50;
Best Local Similarity 91.3%; Pred. No. 9.5;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 GCAAGTCGAACGGAAGGCGCTTT 23
DB 9 GCAAGTCGAACGGAAGGCGCTT 31
RESULT 54
ADS75567
ID ADS75567 standard; DNA; 535 BP.
XX
XX AC ADS75567;
XX
XX DT 02-DEC-2004 (first entry)
XX
XX DE Rhodococcus equi TB-60 16S rDNA sequence, SEQ ID 1.
XX
XX KW Urethane; polyurethane; 16S rDNA; ds.
XX
XX OS Rhodococcus equi; TB-60.
XX
XX PN WO2004078952-A1.
XX
XX PD 16-SEP-2004.
XX
XX PF 03-MAR-2004; 2004WO-JP002691.
XX
XX PR 03-MAR-2003; 2003JP-00055421.
XX
XX PA (NISC-) JAPAN SCI & TECHNOLOGY AGENCY.
XX
XX PI Kambe T, Shigeno Y;
XX
XX DR WPI; 2004-728402/71.
XX
XX PT Novel microorganism or its mutant belonging to Rhodococcus genus and
XX PT having ability to cleave urethane bond, useful for plastic disposal and
XX PT recycling of urethane compounds.
XX
XX PS Example 2; SEQ ID NO 1; 26pp; Japanese.
XX
XX CC The present invention relates to a novel Rhodococcus equi TB-60 strain

```


XX Microorganism; fermentation; hypercholesterolemia; 16s rDNA; antilipemic;
 KW metabolic disorder; ds.
 XX
 OS Saccharothrix; YS-44442.
 XX
 PN US2005064566-A1.
 XX
 PD 24-MAR-2005.
 XX
 XX 03-DEC-2003; 2003US-00727643.
 PF
 XX 27-FEB-2002; 2002US-00085871.
 PR
 XX (LEEF/) LEE F.
 PA (LEEM/) LEE M.
 PA (HONG/) HONG A. C.
 PA (CHIU/) CHIU S.
 XX
 PI Lee F, Lee M, Hong AC, Chiu S;
 XX
 XX WPI; 2005-252680/26.
 DR
 XX Isolation of pravastatin, used to treat hypercholesterolemia, comprises
 PT adding ammonium sulfate into a first solution to form precipitate,
 PT isolating and dissolving the precipitate to form a second solution and
 PT followed by extracting.
 XX
 XX Example 1; SEQ ID NO 1; 19pp; English.
 PS
 XX The present invention relates to two new microorganism strains of
 CC Saccharothrix, designated as YS-44442 and YS-45494. The invention also
 CC provides a method of isolating pravastatin from Saccharothrix sp and an
 CC improved process for isolation of 3-hydroxy-3-methylglutaryl-Coenzyme A
 CC (HMG CoA) reductase inhibitor. The invention is useful for the
 CC preparation of pravastatin which is useful in the treatment of
 CC hypercholesterolemia. The present sequence is the Saccharothrix YS-44442
 CC 16s rDNA.
 XX
 SQ Sequence 1437 BP; 320 A; 362 C; 495 G; 260 T; 0 U; 0 Other;
 Query Match 80.8%; Score 20.2; DB 14; Length 1437;
 Best Local Similarity 88.0%; Pred. No. 17;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GCAAGTCGAACGGAAGGCTTTTCG 25
 ||||| ||||| ||||| ||||| |||||
 Db 30 GCAAGTCGAGCGGTAAAGGCTTTTCG 54
 RESULT 58
 ADC61232
 ID ADC61232 standard; DNA; 1439 BP.
 XX
 AC ADC61232;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Baeyer-Villiger enzyme 16s rDNA gene from Rhodococcus erythropolis AN12.
 XX
 KW Baeyer-Villiger; BV; monooxygenase; ketone substrate; lactone; ester;
 KW 16s rDNA; ds.
 XX
 OS Rhodococcus erythropolis.
 XX
 PN WO2003020890-A2.
 XX
 PD 13-MAR-2003.
 XX
 PF 29-AUG-2002; 2002WO-US027549.
 XX
 XX 29-AUG-2001; 2001US-0315546P.
 PR
 XX

PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Bramucci MG, Brzostowicz PC, Kostichka KN, Nagarajan V;
 PI Rouviere PB, Thomas SM;
 XX
 DR WPI; 2003-313085/30.
 XX
 XX Novel nucleic acid fragment useful for converting ketone substrates to
 PT the corresponding lactone or ester, is isolated from Rhodococcus,
 PT Arthrobacter or Acidovorax, encoding Baeyer-Villiger monooxygenase
 PT polypeptide.
 XX
 XX Claim 54; SEQ ID NO 6; 225pp; English.
 XX
 XX The invention relates to a novel isolated nucleic acid fragment
 CC comprising a fragment encoding a Baeyer-Villiger (BV) monooxygenase
 CC polypeptide having a sequence of 542, 541, 439, 518, 462, 523, 493, 539,
 CC 649, 494, 499, 545, 532 or 538 amino acids defined in the specification;
 CC a nucleic acid molecule that hybridises with the above sequence under the
 CC hybridisation conditions; or their complements. The BV monooxygenase
 CC fragment is useful for obtaining a nucleic acid fragment encoding a BV
 CC monooxygenase polypeptide, by probing a genomic library with the
 CC fragment, identifying a DNA clone that hybridises with the fragment, and
 CC sequencing the genomic fragment that comprises the above identified
 CC clone, where the sequenced genomic fragment encodes a BV monooxygenase
 CC polypeptide. The genes and their products are useful for converting
 CC suitable ketone substrates to the corresponding lactone or ester. This
 CC polynucleotide sequence represents the 16s rDNA gene from Arthrobacter
 CC sp. BP2 relating to the Baeyer-Villiger enzymes of the invention.
 XX
 SQ Sequence 1439 BP; 333 A; 357 C; 465 G; 283 T; 0 U; 1 Other;
 Query Match 80.8%; Score 20.2; DB 10; Length 1439;
 Best Local Similarity 88.0%; Pred. No. 17;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GCAAGTCGAACGGAAGGCTTTTCG 25
 ||||| ||||| ||||| ||||| |||||
 Db 31 GCAATTCGAGCGGTAAAGGCTTTTCG 55
 RESULT 59
 ADF56671
 ID ADF56671 standard; DNA; 1471 BP.
 XX
 AC ADF56671;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE YS-45494 16s rDNA, SEQ ID 2.
 XX
 KW Pravastatin; HMG-CoA reductase inhibitor;
 KW 3-hydroxy-3-methyl glutaryl-CoA reductase inhibitor; 16s rDNA; ds.
 XX
 OS Saccharothrix sp.
 XX
 PN JP2003250532-A.
 XX
 PD 09-SEP-2003.
 XX
 PF 22-FEB-2002; 2002JP-00046750.
 XX
 XX 22-FEB-2002; 2002JP-00046750.
 PR
 XX (YUNG-) YUNG SHIN PHARM IND CO LTD.
 PA
 XX WPI; 2004-046768/05.
 DR
 XX Microorganisms Saccharothrix genus YS-44442 and YS-45494 and their
 PT mutants useful for producing pravastatin.
 XX
 XX Example 1; SEQ ID NO 2; 18pp; Japanese.
 PS
 XX

CC The present invention relates to microorganisms (I) Saccharothrix genus
CC YS-4442 and YS-45494 strains and their mutants. Also claimed is a method
CC (M1) for producing pravastatin by using (I) and isolating (M2) 3-hydroxy-
CC 3-methyl glutaryl (HMG)-CoA reductase inhibitors.

XX SQ Sequence 1471 BP; 331 A; 369 C; 506 G; 265 T; 0 U; 0 Other;

Query Match 80.8%; Score 20.2; DB 12; Length 1471;
Best Local Similarity 88.0%; Pred. No. 17;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCTTCG 25
||||||| ||||| ||||| ||||| |||||
Db 30 GCAAGTCGAGCGGTAAAGCCCTTCG 54

RESULT 60

ADG64520
ID ADG64520 standard; DNA; 1471 BP.

XX AC ADG64520;

XX DT 11-MAR-2004 (first entry)

XX DE Saccharothrix strain YS-45494 16s rDNA sequence.

XX KW Microorganism; Saccharothrix; YS-4442; YS-45494;
KW 3-hydroxy-3-methylglutaryl-CoA reductase inhibitor; HMG-CoA reductase;
KW pravastatin; fermentation; compactin; lovastatin;
KW blood cholesterol level; antilipemic; 16s rDNA; ds.

XX OS Saccharothrix sp.

XX PN US2003199047-A1.

XX PD 23-OCT-2003.

XX PF 27-FEB-2002; 2002US-00085871.

XX PR 27-FEB-2002; 2002US-00085871.

XX PA (LEEF/) LEE F.
XX PA (LEEM/) LEE M.
XX PA (HONG/) HONG A. C.
XX PA (CHIU/) CHIU S.

XX FI Lee F, Lee M, Hong AC, Chiu S;

XX DR WPI; 2004-041353/04.

XX PT Novel microorganism strains YS-4442 and YS-45494 of Saccharothrix,
XX useful for producing pravastatin.

XX FS Example 1; SEQ ID NO 2; 16pp; English.

XX CC The present invention relates to the isolation of novel microorganism
XX strains of Saccharothrix designated YS-4442 and YS-45494. Also disclosed
XX is a method for isolating 3-hydroxy-3-methylglutaryl (HMG)-CoA reductase
XX inhibitors such as pravastatin. The Saccharothrix strains YS-4442 and YS
XX -45494 are useful for producing pravastatin. The method involves
XX cultivating the strains at a suitable condition to generate a
XX fermentation broth, feeding compactin into the broth, fermenting the
XX broth for a period of time to convert the compactin to pravastatin, and
XX isolating the pravastatin from the broth. The fermentation broth is
XX cultivated for less than 2 days, preferably for 18 hours. The
XX fermentation broth is derived from a seed culture of the microorganism
XX which is cultivated at a suitable condition for 18-48 hours before
XX inoculation into the broth. The broth is fermented for less than 5 days,
XX preferably 3 days, most preferably less than 24 hours. The method of the
XX invention is useful for isolating HMG-CoA reductase inhibitor such as
XX pravastatin, compactin or lovastatin, preferably pravastatin. The
XX pravastatin or HMG-CoA reductase inhibitors are useful for reducing blood
XX cholesterol levels. The present sequence represents Saccharothrix strain

CC YS-45494 16s rDNA sequence.

XX SQ Sequence 1471 BP; 331 A; 369 C; 506 G; 265 T; 0 U; 0 Other;

Query Match 80.8%; Score 20.2; DB 12; Length 1471;
Best Local Similarity 88.0%; Pred. No. 17;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCTTCG 25
||||||| ||||| ||||| ||||| |||||
Db 30 GCAAGTCGAGCGGTAAAGCCCTTCG 54

RESULT 61

ADY86148
ID ADY86148 standard; DNA; 1471 BP.

XX AC ADY86148;

XX DT 02-JUN-2005 (first entry)

XX DE Saccharothrix YS-45494 16s rDNA, SEQ ID NO: 2.

XX KW Microorganism; fermentation; hypercholesterolemia; 16s rDNA; antilipemic;
KW metabolic disorder; ds.

XX OS Saccharothrix; YS-45494.

XX PN US2005064566-A1.

XX PD 24-MAR-2005.

XX PF 03-DEC-2003; 2003US-00727643.

XX PR 27-FEB-2002; 2002US-00085871.

XX PA (LEEF/) LEE F.

XX PA (LEEM/) LEE M.

XX PA (HONG/) HONG A. C.

XX PA (CHIU/) CHIU S.

XX FI Lee F, Lee M, Hong AC, Chiu S;

XX DR WPI; 2005-252680/26.

XX PT Isolation of pravastatin, used to treat hypercholesterolemia, comprises
XX adding ammonium sulfate into a first solution to form precipitate,
XX isolating and dissolving the precipitate to form a second solution and
XX followed by extracting.

XX PS Example 1; SEQ ID NO 2; 19pp; English.

XX CC The present invention relates to two new microorganism strains of
XX Saccharothrix, designated as YS-4442 and YS-45494. The invention also
XX provides a method for isolating pravastatin from Saccharothrix sp and an
XX improved process for isolation of 3-hydroxy-3-methylglutaryl-Coenzyme A
XX (HMG CoA) reductase inhibitor. The invention is useful for the
XX preparation of pravastatin which is useful in the treatment of
XX hypercholesterolemia. The present sequence is the Saccharothrix YS-45494
XX 16s rDNA.

XX SQ Sequence 1471 BP; 331 A; 369 C; 506 G; 265 T; 0 U; 0 Other;

Query Match 80.8%; Score 20.2; DB 14; Length 1471;
Best Local Similarity 88.0%; Pred. No. 17;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCTTCG 25
||||||| ||||| ||||| ||||| |||||
Db 30 GCAAGTCGAGCGGTAAAGCCCTTCG 54

RESULT 62

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AED47485
ID AED47485 standard; DNA; 1477 BP.
XX
AC AED47485;
XX
DT 15-DEC-2005 (first entry)
XX
DE Nocardia sp. TP-A0674 16S ribosomal DNA, SEQ ID 1.
XX
KW Analgesic; Nootropic; Antiparkinsonian; Antiasthmatic; Respiratory-Gen.;
KW Uropathic; binding inhibitor; muscarinic acetylcholine receptor;
KW analgesic; Parkinsons disease; asthma;
KW chronic obstructive pulmonary disease; bladder disease;
KW micturition disorder; 16S ribosomal RNA; 16S rRNA; gene; ds.
XX
OS Nocardia sp.
XX
PN JP2005289890-A.
XX
PD 20-OCT-2005.
XX
PF 31-MAR-2004; 2004JP-00107929.
XX
PR 31-MAR-2004; 2004JP-00107929.
XX
PA (YOSH ) YOSHITOMI PHARM IND KK.
XX
PI Furumai T, Igarashi Y, Onaka H, Ikeda Y, Nonaka H;
XX
DR WPI; 2005-738172/76.
XX
PT Binding inhibitor of muscarinic acetylcholine receptor subtype 4 or 3
PT useful for treating diseases e.g. asthma, contains chelate having TP
PT 0052A-F compound derived from Nocardia species TP-A0674 and metal ion.
XX
PS Disclosure; SEQ ID NO 1; 22pp; Japanese.
XX
CC The invention relates to a novel binding inhibitor of muscarinic
CC acetylcholine receptor subtype 4 or 3, comprising a chelate having a TP
CC 0052A-F compound or its salt and a metal ion. The invention further
CC comprises a method and a microorganism for producing the novel binding
CC inhibitor. The binding inhibitor and compound are useful as central
CC analgesics and memory improving drugs, for treating Parkinson's disease,
CC asthma, chronic obstructive pulmonary disease, overactive bladder,
CC frequent urination and urinary incontinence. This polynucleotide sequence
CC represents the 16S ribosomal DNA of a Nocardia sp. TP-A0674
CC microorganism, useful in producing a muscarinic acetylcholine receptor
CC binding inhibitor compound of the invention.
XX
SQ Sequence 1477 BP; 341 A; 357 C; 494 G; 285 T; 0 U; 0 Other;
XX
Query Match 80.8%; Score 20.2; DB 14; Length 1477;
Best Local Similarity 88.0%; Pred. No. 17;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GCAAGTCGACGCGTAAGGCCCTTCG 25
Db 47 GCAAGTCGACGCGTAAGGCCCTTCG 71
RESULT 63
ADSI17269
ID ADSI17269 standard; DNA; 1488 BP.
XX
AC ADSI17269;
XX
DT 02-DEC-2004 (first entry)
XX
DE Lechevalieria aerocolonigenes strain VK-A9 16S rDNA.
KW Plant protectant; antibiotic; thiobutacin; antifungal; antiomycete;
KW phytophthora blight; gene; ds; 16S ribosomal DNA; rDNA.
XX
OS Lechevalieria aerocolonigenes.
XX
PN US2004180960-A1.
XX
PD 16-SEP-2004.
XX
PF 13-JAN-2004; 2004US-00756683.
XX
PR 13-MAR-2003; 2003KR-00015628.
XX
PA (HWAN/) HWANG B K.
PA (LEEJ/) LEE J Y.
XX
PI Hwang BK, Lee JY;
XX
DR WPI; 2004-661528/64.
DR EMBL; AY196703.
XX
PT New antibiotic compound, thiobutacin, is used to treat plant disease e.g.
PT phytophthora blight and to control plant diseases caused by pathogens
PT e.g. Phytophthora capsici and Botrytis cinerea.
XX
PS Example 2; SEQ ID NO 1; 17pp; English.
XX
CC The invention relates to an antibiotic compound thiobutacin and
CC antifungal and antiomycete compositions comprising thiobutacin.
CC Thiobutacin is used to treat plant disease such as phytophthora blight
CC and to control plant diseases caused by pathogens e.g. Phytophthora
CC capsici and Botrytis cinerea. The present sequence is the Lechevalieria
CC aerocolonigenes strain VK-A9 16S ribosomal DNA (rDNA). L. aerocolonigenes
CC strain VK-A9 has strong antifungal and antimicrobial activity and it can
CC inhibit the growth of Phytophthora capsici.
XX
SQ Sequence 1488 BP; 339 A; 369 C; 508 G; 272 T; 0 U; 0 Other;
XX
Query Match 80.8%; Score 20.2; DB 13; Length 1488;
Best Local Similarity 88.0%; Pred. No. 17;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GCAAGTCGACGCGTAAGGCCCTTCG 25
Db 42 GCAAGTCGACGCGTAAGGCCCTTCG 66
RESULT 64
ADW12667
ID ADW12667 standard; DNA; 1514 BP.
XX
AC ADW12667;
XX
DT 07-APR-2005 (first entry)
XX
DE Rhodococcus opacus 16S rDNA, SEQ ID NO:2.
XX
KW Rhodococcus opacus.
XX
KW Stereoselective synthesis; enantiomeric enrichment;
KW beta-amino acid synthesis; cell culture; 16S ribosomal RNA; 16S rRNA; ds.
XX
OS Rhodococcus opacus.
XX
PN US2005009151-A1.
XX
PD 13-JAN-2005.
XX
PF 22-JUN-2004; 2004US-00875161.
XX
PR 10-JUL-2003; 2003US-0486032P.
PR 02-SEP-2003; 2003US-0499622P.
XX
PA (PHAA ) PHARMACIA CORP.
XX
PI Chase M, Clayton R, Landis B, Banerjee A;
XX

```


microorganism is by amplification of the complete 16S rRNA gene using primers ADP94060 and ADP94061, labelling the amplification product (a fluorescence label is preferred), and hybridising to the probe or probes of the invention. The probes may be immobilised on a DNA chip. The microorganism is selected from *Actinobacillus actinomycetemcomitans*, *Acinetobacter calcoaceticus*, *Haemophilus influenzae*, *Stenotrophomonas maltophilia*, *Proteus mirabilis*, *Streptococcus pneumoniae*, *Pseudomonas aeruginosa*, *Citrobacter freundii*, *Veillonella parvula*, *Providencia stuartii*, *Neisseria gonorrhoeae*, *Streptococcus agalactiae*, *Morganella morganii*, *Bacteroides fragilis*, *Staphylococcus hominis*, *Staphylococcus warneri*, *Staphylococcus haemolyticus*, *Enterobacter cloacae*, *Enterobacter aerogenes*, *Staphylococcus epidermidis*, *Streptococcus constellatus*, *Serratia marcescens*, *Streptococcus anginosus*, *Escherichia coli*, *Klebsiella pneumoniae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Streptococcus sanguis*, *Streptococcus mitis*, *Streptococcus intermedius*, *Listeria monocytogenes*, *Clostridium perfringens*, *Corynebacterium aquaticum*, *Streptococcus oralis*, *Staphylococcus aureus*, *Neisseria meningitidis*, *Campylobacter fetus*, *Enterococcus gallinarum*, *Enterococcus casseliflavus*, *Aeromonas hydrophila*, *Salmonella paratyphi*, *Salmonella typhi*, *Streptococcus equisimilis*, *Streptococcus canis*, *Klebsiella oxytoca*, *Staphylococcus saprophyticus*, *Pasteurella multocida*, *Eikenella corrodens*, *Streptococcus pyogenes*, *Moraxella catarrhalis*, *Legionella pneumophila*, *Mycobacterium tuberculosis*, *Mycobacterium avium*, *Mycobacterium intracellulare*, *Mycobacterium kansasii* or *Mycobacterium goodii*.

Query Match 80.0%; Score 20; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGTCGACGGAAGGCC 20
|||||

DB 1 GCAAGTCGACGGAAGGCC 20

RESULT 67
ADU66542
ID ADU66542 standard; DNA; 80 BP.
AC ADU66542;
DT 27-JAN-2005 (first entry)
DE Cut base A amplicon fragment.
KW ds; mass spectroscopy; DNA cleavage; DNA sequencing; sequencing.
XX Unidentified.
OS
XX WO2004097369-A2.
XX 11-NOV-2004.
XX 22-APR-2004; 2004WO-US012520.
XX 25-APR-2003; 2003US-0466006P.
XX (SEQU-) SEQUENOM INC.
XX (BOBC/) BOECKER S.
XX Boecker S, Van Den Boom D;
XX WPI; 2005-012656/01.
XX
XX Obtaining sequence information from target biomolecule, by fragmenting the target biomolecule by partial cleavage, performing mass spectrometry, extracting information from mass spectra, constructing sequencing graph and traversing graphs.
XX
XX Disclosure; SEQ ID NO 11; 133bp; English.
XX

This invention describes a novel method for obtaining sequence information from a target biomolecule and involves fragmenting the target biomolecule into several fragments by partial cleavage, performing mass spectrometry on fragments to produce mass spectra, extracting peak information from the produced mass spectra, constructing sequencing graphs using the extracted peak information and traversing the sequencing graphs to reconstruct sequence information of the target biomolecule. The target biomolecule is nucleic acid molecule such as DNA or RNA, or is a protein and the compositions of the two fragments are the base compositions or amino acid compositions. This method preferably involves subjecting the nucleic acid molecule to partial cleavage reactions with one or more specific cleavage reagents, thus generating two or more fragments that are specific cleavage products, determining the molecular weights of the two or more fragments, ordering the possible base compositions of the two or more fragments, determining the possible base compositions of the two or more fragments according to the number of specific cleavage sites that are not cleaved in each fragment, constructing one or more sequencing graphs that are a graph theoretical representation of the ordered base compositions for the two or more fragments, and traversing the one or more sequencing graphs to reconstruct one or more underlying sequence candidates, where each sequencing graph corresponds to the ordered base compositions derived from a partial cleavage reaction with one base-specific cleavage reagent. This method further involves scoring the one or more underlying sequence candidates and determining the rank order of fitness, where the scoring is done by statistical analysis or maximum likelihood statistical analysis. This method determines epigenetic changes in a target nucleic acid molecule relative to reference nucleic acid molecule and allows the sequencing of large biomolecules. The invention also describes a method of producing a candidate sequence of a biomolecule which involves receiving several sequencing graphs having several vertices and edges, where each vertex represents a component of the biomolecule and each edge represents a cut base of the sequencing graph and generating the candidate sequence by traversing several sequencing graphs. This second method further involves traversing several sequencing graphs by tracing through each sequencing graph, starting at a source vertex. The results of each method can be read by a program product for use in a computer that executes program instructions recorded in a computer-readable media to produce a candidate sequence of a biomolecule or to obtain sequence information in a target biomolecule. The target biomolecule contains a sequence variation, which is a mutation or a polymorphism. The target is a target nucleic acid molecule from an organism chosen from eukaryotes, prokaryotes and viruses, preferably a bacterium. The specific cleavage reagent is an RNase chosen from RNase T1, RNase U2, RNase P, RNase A, chicken liver RNase (RNase CL3) and cusavirin, or a glycosylase. The sequence variations in the target biomolecule permit genotyping a subject, forensic analysis, disease diagnosis or disease prognosis. The novel methods are useful for de novo sequencing, to identify genetic disease or chromosome abnormality, identifying a predisposition to a disease, or condition including obesity, atherosclerosis, or cancer, to identify an infection by an infectious agent, to identify a pathogen, determine haplotypes, analyze microsatellite sequences, and short tandem repeat (STR) loci, determine allelic variation and/or frequency, and analyze cellular methylation patterns. This sequence represents an amplicon used to illustrate the sequencing technique described in the invention.

Query Match 80.0%; Score 20; DB 14; Length 80;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGTCGACGGAAGGCC 20
|||||

DB 50 GCAAGTCGACGGAAGGCC 69

RESULT 68
AEB98763
ID AEB98763 standard; DNA; 209 BP.
XX AC
XX AEB98763;
XX

```
DT 06-OCT-2005 (first entry)
XX
XX Mycobacterium intracellulare partial 16S rDNA sequence, SEQ ID 5.
DE
XX microorganism detection; mycobacterium infection; antibacterial; ds.
KW
XX Mycobacterium intracellulare.
OS
XX JP2005204582-A.
PN
XX 04-AUG-2005.
PD
XX 23-JAN-2004; 2004JP-00015195.
PF
XX 23-JAN-2004; 2004JP-00015195.
XX
XX (ASAH ) ASahi KASEI KK.
PA
XX Oda N;
PI
XX WPI; 2005-526965/54.
DR
XX New single-stranded oligonucleotide, useful for amplifying the nucleic
PT acid of Mycobacterium avium, Mycobacterium intracellulare, and
PT Mycobacterium kansasii.
XX
XX Example 1; SEQ ID NO 5; 14pp; Japanese.
PS
XX The invention relates to a novel single-stranded oligonucleotide used in
CC a detection method of an atypical mycobacteria group. The invention
CC further includes: amplifying the nucleic acid of Mycobacterium avium by a
CC loop-mediated isothermal amplification (LAMP) method; amplifying the
CC nucleic acid of M. intracellulare by a LAMP method; amplifying the
CC nucleic acid of M. kansasii by a LAMP method; and a kit for detecting the
CC nucleic acid of M. avium by a LAMP method; detecting the nucleic acid of
CC M. intracellulare by a LAMP method; or detecting the nucleic acid of M.
CC kansasii by a LAMP method. The single-stranded oligonucleotide is useful
CC in medical applications. This polynucleotide represents a Mycobacterium
CC intracellulare partial 16S rDNA sequence amplified by the LAMP method of
CC the invention.
XX
XX Sequence 209 BP; 45 A; 47 C; 73 G; 44 T; 0 U; 0 Other;
SQ
Query Match 80.0%; Score 20; DB 14; Length 209;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCAAAGTCGACGGAAGGCC 20
Db 39 GCAAAGTCGACGGAAGGCC 58
RESULT 69
ABT23572
ID ABT23572 standard; DNA; 560 BP.
XX
XX ABT23572;
AC
XX
XX 22-MAY-2003 (first entry)
DT
XX
XX Stabilising reagent method related oligo SEQ ID No 24.
DE
XX
XX Stabilising reaction reagent; PCR; primer; RNaseH; long-term storage;
KW specific amplification; pathogenic microorganism; chimeric;
KW genetic engineering; clinical medicine; ss.
XX
XX Mycobacterium avium.
OS
XX WO2002101042-A1.
PN
XX
XX 19-DEC-2002.
PD
XX
XX 12-JUN-2002; 2002WO-JP005832.
PF
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```
XX 12-JUN-2001; 2001JP-00177737.
PR 20-AUG-2001; 2001JP-00249689.
XX
XX (TAKI ) TAKARA BIO INC.
PA
XX Sagawa H, Uemori T, Mukai H, Yamamoto J, Tomono J, Kobayashi E;
PI Enoki T, Asada K, Kato I;
XX
XX WPI; 2003-149805/14.
DR
XX Method for stabilizing and storing reaction reagents for specific
PT amplification and detection of nucleic acids particularly in e.g.
PT identifying pathogenic microorganisms or viruses in sample.
XX
XX Example 15; Page 110; 177pp; Japanese.
PS
XX The invention relates to a novel stabilising reaction reagent for use in
CC the amplification and/or detection of a target nucleic acid comprising:
CC preparing a reaction mixture with e.g. a nucleic acid as template, at
CC least 1 primer and RNaseH; and incubation of the reaction mixture for a
CC defined period of time to form a reaction product during the
CC amplification of such target nucleic acid. The method is useful for
CC stabilising and long-term storage of reaction reagents for highly
CC sensitive and specific amplification and detection of nucleic acids
CC particularly in identifying pathogenic microorganisms or viruses in a
CC sample using chimeric oligonucleotide primers, which is useful in genetic
CC engineering and clinical medicine. This polynucleotide sequence
CC represents an oligo relating to the novel stabilising reaction reagent
CC method of the invention
XX
XX Sequence 560 BP; 117 A; 134 C; 199 G; 110 T; 0 U; 0 Other;
SQ
Query Match 80.0%; Score 20; DB 10; Length 560;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCAAAGTCGACGGAAGGCC 20
Db 42 GCAAAGTCGACGGAAGGCC 61
RESULT 70
AEA22410
ID AEA22410 standard; DNA; 1321 BP.
XX
XX AEA22410;
AC
XX
XX 25-AUG-2005 (first entry)
DT
XX
XX Mycobacterium kubicae 16S rRNA sequence SEQ ID NO:11.
DE
XX microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
KW
XX Mycobacterium kubicae.
OS
XX US2005130168-A1.
XX
XX 16-JUN-2005.
PD
XX
XX 31-OCT-2003; 2003US-00697802.
PF
XX
XX 31-OCT-2003; 2003US-00697802.
PR
XX (HANX/) HAN X.
PA (PHAM/) PHAM A S.
XX
XX Han X, Pham AS;
PI
XX WPI; 2005-424597/43.
DR
XX
XX Determining a bacterium species comprises providing oligonucleotide
XX primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
PT
```

XX Disclosure; SEQ ID NO 11; 74pp; English.

PS The invention relates to a method (M1) for determining a bacterium

XX species. (M1) comprises: (a) culturing a bacterium from a specimen;

XX extracting a genomic nucleotide from the bacterium to provide a

CC nucleotide template; (c) annealing a region of a nucleotide template to a

CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a

CC complementary fashion, the primer set designed to provide a product

CC having a predetermined size dictated by a complementary primer set; (d)

CC amplifying the region of the nucleotide template to produce the product;

CC and (e) determining a species of a bacterium in a nucleotide sequence of

CC the product. Also described is an alternative method (M2) for determining

CC a bacterium species comprising: (a) providing a specimen or a sample

CC having a template; (b) providing a pair of primers selected from: (i) a

CC first forward primer having consecutive bases of an AFB-f comprising any

CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments

CC or variations; and a first reverse primer having consecutive bases of an

CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)

CC or their fragments or variations; (ii) a second forward primer having

CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21

CC bp (AEA22489-AEA22516) or their fragments or variations; and a second

CC reverse primer having consecutive bases of an UB-r comprising any of the

CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or

CC variations; or (iii) a first forward primer having consecutive bases of

CC an AFB-f of AEA22417-AEA22452 or their fragments or variations; and a

CC second reverse primer having consecutive bases of an UB-r of AEA22517-

CC AEA22544 or their fragments or variations; (c) the specimen; and (d)

CC comparing the product from the specimen with a nucleotide sequence from a

CC database to determine the bacterium species present in the specimen. The

CC methods are useful for determining a bacterium species. The present

CC sequence represents a Mycobacterium kansas 16S rRNA nucleotide sequence,

XX which is used in the exemplification of the present invention.

XX SQ Sequence 1321 BP; 287 A; 314 C; 457 G; 263 T; 0 U; 0 Other;

Query Match 80.0%; Score 20; DB 14; Length 1321;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGTCGACGGAAGGCC 20

DB 14 GCAAGTCGACGGAAGGCC 33

RESULT 71

AD085868/c

ID AD085868 standard; DNA; 1344 BP.

XX AC AD085868;

XX 29-JUL-2004 (first entry)

XX DE Gordonia sp. bacterium 16S rDNA.

XX microorganism; Gordonia genus; gram-positive bacillus; catalase;

KW nitrate reduction; alkali phosphatase; beta-galactosidase;

KW pyrazinamidase; pyrolidonyl allyl amidase; beta-glucuronidase;

KW alpha-glucosidase; urease; gelatin-liquefaction; esculin; glucose;

KW ribose; GR-004 strain; FERM P-18806;

XX cyclic hydrocarbon degradation agent; waste engine oil; 16S rDNA; ds.

OS Gordonia sp.

XX JP2004121068-A.

PN 22-APR-2004.

XX 01-OCT-2002; 2002JP-00288714.

XX 01-OCT-2002; 2002JP-00288714.

XX (GEIT-) GEITO KK.

XX WPI; 2004-322761/30.

XX Novel microorganism of Gordonia genus having biochemical properties

PT positive for catalase, approximately beta-galactosidase, nitrate reduction

PT ability, is useful as cyclic hydrocarbon degradation agent in waste-oil

PT treatment.

XX Claim 2; SEQ ID NO 1; 12pp; Japanese.

XX The invention relates to a novel microorganism belonging to the Gordonia

CC genus, a gram-positive bacillus. The novel microorganism having

CC biochemical properties positive for catalase, nitrate reduction ability,

CC alkali phosphatase, and beta-galactosidase, and negative for

CC pyrazinamidase, pyrolidonyl allyl amidase, beta-glucuronidase, alpha-

CC glucosidase, urease, gelatin-liquefaction ability, and esculin, glucose

CC and ribose utilisation ability. The invention further comprises: a GR-004

CC strain of Gordonia sp. having the accession number FERM P-18806; and a

CC cyclic hydrocarbon degradation agent containing the novel microorganism.

CC The Gordonia genus microorganism is useful for processing a cyclic

CC hydrocarbon-containing substance, which involves using the cyclic

CC hydrocarbon degradation agent, where the cyclic hydrocarbon-containing

CC substance is a waste engine oil. The Gordonia genus microorganism is

CC useful as a cyclic hydrocarbon degradation agent for waste-oil treatment.

CC This polynucleotide sequence represents the Gordonia sp. bacterium 16S

CC rDNA of the invention.

XX SQ Sequence 1344 BP; 276 A; 447 C; 315 G; 306 T; 0 U; 0 Other;

Query Match 80.0%; Score 20; DB 12; Length 1344;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGTCGACGGAAGGCC 20

DB 1299 GCAAGTCGACGGAAGGCC 1280

RESULT 72

AEA22413

ID AEA22413 standard; DNA; 1415 BP.

XX AC AEA22413;

XX 25-AUG-2005 (first entry)

XX DE Mycobacterium paraffinicum 16S rRNA sequence SEQ ID NO:14.

XX KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.

XX OS Mycobacterium paraffinicum.

XX PN US2005130168-A1.

XX 16-JUN-2005.

XX 31-OCT-2003; 2003US-00697802.

XX 31-OCT-2003; 2003US-00697802.

XX (HANYX/) HAN X.

PA (PHAM/) PHAM A S.

XX Han X, Pham AS;

XX WPI; 2005-424597/43.

XX Determining a bacterium species comprises providing oligonucleotide

PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.

XX Disclosure; SEQ ID NO 14; 74pp; English.

XX The invention relates to a method (M1) for determining a bacterium

CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
 CC extracting a genomic nucleotide from the bacterium to provide a
 CC nucleotide template; (c) annealing a region of a nucleotide template to a
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
 CC complementary fashion, the primer set designed to provide a product
 CC having a predetermined size dictated by a complementary primer set; (d)
 CC amplifying the region of the nucleotide template to produce the product;
 CC and (e) determining a species of a bacterium in a nucleotide sequence of
 CC the product. Also described is an alternative method (M2) for determining
 CC a bacterium species comprising: (a) providing a specimen or a sample
 CC having a template; (b) providing a pair of primers selected from: (i) a
 CC first forward primer having consecutive bases of an AFB-f comprising any
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
 CC or variations and a first reverse primer having consecutive bases of an
 CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
 CC or their fragments or variations, (ii) a second forward primer having
 CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
 CC bp (AEA22489-AEA22516) or their fragments or variations and a second
 CC reverse primer having consecutive bases of an UB-r comprising any of the
 CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
 CC variations, or (iii) a first forward primer having consecutive bases of
 CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
 CC second reverse primer having consecutive bases of an UB-r of AEA22517-
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)
 CC comparing the product from the specimen with a nucleotide sequence from a
 CC database to determine the bacterium species present in the specimen. The
 CC methods are useful for determining a bacterium species. The present
 CC sequence represents a Mycobacterium paraffinicum 16S rRNA nucleotide
 CC sequence, which is used in the exemplification of the present invention.

XX
 SQ Sequence 1415 BP; 307 A; 343 C; 480 G; 285 T; 0 U; 0 Other;

Query Match 80.0%; Score 20; DB 14; Length 1415;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCAAGTCGAACGGAAGGCC 20
 |||||
 Db 15 GCAAGTCGAACGGAAGGCC 34

RESULT 73
 AA222765
 ID AA222765 standard; DNA; 1460 BP.

AC AA222765;

XX 15-MAR-2000 (first entry)

DT Corynebacterium sp. NK-1 16S rRNA gene.

XX Seasoning liquor; flavour; vegetable; pickling; salted rice bran paste;
 KW microorganism; gamma-dodecalactone; gamma-dodecalactone; lactic acid;
 KW propionic acid; 16S rRNA; pickle; ss.

XX Corynebacterium sp.

XX WO9962347-A1.

XX 09-DEC-1999.

XX 28-MAY-1999; 99WO-JP002854.

XX 29-MAY-1998; 98JP-00166226.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Saitoh C, Yoshiro A, Tokunaga C, Ozawa K, Yokoi A, Ogata N;

XX Ochiai K, Ando K, Katakira H;

XX WPI; 2000-062809/05.

XX Production of seasoning liquors with the flavor of vegetables pickled in

PT salted rice bran.
 XX
 PS Disclosure; Page 41-43; 45pp; Japanese.

XX The invention relates to a method of producing seasoning liquors with the
 CC flavour of vegetables pickled in salted rice bran paste by culturing a
 CC microorganism in a rice bran dispersion to produce gamma-dodecalactone
 CC and/or gamma-dodecalactone. The microorganism produces lactic acid,
 CC propionic acid, gamma-dodecalactone and/or gamma-dodecalactone. The
 CC microorganism is especially a novel strain of Corynebacterium (strain NK-
 CC 1, FERM BP-6329) with properties defined in the specification. This
 CC sequence represents the 16S rRNA gene from the novel Corynebacterium
 CC strain. The seasoning liquor is used for preparing a salted rice bran
 CC pickle bed which provides pickles

SQ Sequence 1460 BP; 320 A; 342 C; 492 G; 305 T; 0 U; 1 Other;

Query Match 80.0%; Score 20; DB 3; Length 1460;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCAAGTCGAACGGAAGGCC 20
 |||||
 Db 38 GCAAGTCGAACGGAAGGCC 57

RESULT 74
 AEA22415
 ID AEA22415 standard; DNA; 1462 BP.

XX AC AEA22415;

DT 25-AUG-2005 (first entry)

XX Mycobacterium szulgai 16S rRNA sequence SEQ ID NO:16.

XX microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.

XX Mycobacterium szulgai.

XX US2005130168-A1.

XX 16-JUN-2005.

XX 31-OCT-2003; 2003US-00697802.

XX 31-OCT-2003; 2003US-00697802.

XX (HANK/) HAN X.

XX (PHAM/) PHAM A S.

XX Han X, Pham AS;

XX WPI; 2005-424597/43.

XX Determining a bacterium species comprises providing oligonucleotide
 PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.

XX Disclosure; SEQ ID NO 16; 74pp; English.

XX The invention relates to a method (M1) for determining a bacterium
 CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
 CC extracting a genomic nucleotide from the bacterium to provide a
 CC nucleotide template; (c) annealing a region of a nucleotide template to a
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
 CC complimentary fashion, the primer set designed to provide a product
 CC having a predetermined size dictated by a complimentary primer set; (d)
 CC amplifying the region of the nucleotide template to produce the product;
 CC and (e) determining a species of a bacterium in a nucleotide sequence of
 CC the product. Also described is an alternative method (M2) for determining
 CC a bacterium species comprising: (a) providing a specimen or a sample
 CC having a template; (b) providing a pair of primers selected from: (i) a
 CC first forward primer having consecutive bases of an AFB-f comprising any

CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
 CC or variations and a first reverse primer having consecutive bases of an
 CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
 CC or their fragments or variations, (ii) a second forward primer having
 CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
 CC bp (AEA22489-AEA22516) or their fragments or variations and a second
 CC reverse primer having consecutive bases of an UB-r comprising any of the
 CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
 CC variations, or (iii) a first forward primer having consecutive bases of
 CC an AFB-f of AEA22417-AEA22517-AEA22544) or their fragments or
 CC second reverse primer having consecutive bases of an UB-r of AEA22517-
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)
 CC comparing the product from the specimen with a nucleotide sequence from a
 CC database to determine the bacterium species present in the specimen. The
 CC methods are useful for determining a bacterium species. The present
 CC sequence represents a Mycobacterium szulgai 16S rRNA nucleotide sequence,
 CC which is used in the exemplification of the present invention.
 XX
 SQ Sequence 1462 BP; 314 A; 350 C; 507 G; 291 T; 0 U; 0 Other;
 Query Match 80.0%; Score 20; DB 14; Length 1462;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCAAGTCGAACGAAAGGCC 20
 DB 20 GCAAGTCGAACGAAAGGCC 39
 RESULT 75
 ID AEA22414 standard; DNA; 1484 BP.
 AC AEA22414;
 DT 25-AUG-2005 (first entry)
 DE Mycobacterium simiae 16S rRNA sequence SEQ ID NO:15.
 DX microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
 KW Mycobacterium simiae.
 OS
 XX US2005130168-A1.
 XX 16-JUN-2005.
 XX 31-OCT-2003; 2003US-00697802.
 XX 31-OCT-2003; 2003US-00697802.
 XX (HANK/) HAN X.
 PA (PHAM/) PHAM A S.
 XX Han X, Pham AS;
 PI WPI; 2005-424597/43.
 DR
 XX Determining a bacterium species comprises providing oligonucleotide
 PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
 XX Disclosure; SEQ ID NO 15; 74pp; English.
 PS The invention relates to a method (M1) for determining a bacterium
 CC species (M1) comprises: (a) culturing a bacterium from a specimen; (b)
 CC extracting a genomic nucleotide from the bacterium to provide a
 CC nucleotide template; (c) annealing a region of a nucleotide template to a
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
 CC complimentary fashion, the primer set designed to provide a product
 CC having a predetermined size dictated by a complimentary primer set; (d)
 CC amplifying the region of the nucleotide template to produce the product;
 CC and (e) determining a species of a bacterium in a nucleotide sequence of
 CC the product. Also described is an alternative method (M2) for determining

CC a bacterium species comprising: (a) providing a specimen or a sample
 CC having a template; (b) providing a pair of primers selected from: (i) a
 CC first forward primer having consecutive bases of an AFB-f comprising any
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
 CC or variations and a first reverse primer having consecutive bases of an
 CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
 CC or their fragments or variations, (ii) a second forward primer having
 CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
 CC bp (AEA22489-AEA22516) or their fragments or variations and a second
 CC reverse primer having consecutive bases of an UB-r comprising any of the
 CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
 CC variations, or (iii) a first forward primer having consecutive bases of
 CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
 CC second reverse primer having consecutive bases of an UB-r of AEA22517-
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)
 CC comparing the product from the specimen with a nucleotide sequence from a
 CC database to determine the bacterium species present in the specimen. The
 CC methods are useful for determining a bacterium species. The present
 CC sequence represents a Mycobacterium simiae 16S rRNA nucleotide sequence,
 CC which is used in the exemplification of the present invention.
 XX
 SQ Sequence 1484 BP; 320 A; 362 C; 509 G; 293 T; 0 U; 0 Other;
 Query Match 80.0%; Score 20; DB 14; Length 1484;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCAAGTCGAACGAAAGGCC 20
 DB 20 GCAAGTCGAACGAAAGGCC 39
 RESULT 76
 ADM92517
 ID ADM92517 standard; DNA; 1517 BP.
 XX
 AC ADM92517;
 DT 03-JUN-2004 (first entry)
 DX Gordononia genus Actinomycetes DNA sequence SeqID1.
 DE
 XX Gordononia genus; Actinomycetes; ammonia; nitrous acid oxidation;
 KW purifying fresh water; purifying seawater; ayu fish; flatfish; blowfish;
 KW gold fish; ds.
 XX Gordononia.
 OS
 XX JP2004081109-A.
 XX 18-MAR-2004.
 XX 27-AUG-2002; 2002JP-00247166.
 XX 27-AUG-2002; 2002JP-00247166.
 XX (KANM-) KANMONKAI KK.
 XX WPI; 2004-233309/22.
 XX Gordononia genus Actinomycetes for purifying fresh water and seawater useful
 PT in raising ayu fish, flatfish, blowfish and gold fish, has ammonia
 PT utilizing ability and nitrous acid oxidation ability.
 XX Disclosure; SEQ ID NO 1; 16pp; Japanese.
 PS This invention relates to a novel Gordononia genus Actinomycetes which has
 CC ammonia utilising ability and nitrous acid oxidation ability. The
 CC invention may be useful for purifying fresh water and seawater, of
 CC particular use in raising ayu fish, flatfish, blowfish and gold fish. The
 CC Gordononia genus actinomycetes effectively suppresses concentration of
 CC ammonia and nitrous acid in fresh water and seawater, and provides
 CC purified water that is favourable for raising fishes.

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XX SQ Sequence 1517 BP; 334 A; 363 C; 515 G; 304 T; 0 U; 1 Other;
Query Match      80.0%; Score 20; DB 12; Length 1517;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCC 20
Db 53 GCAAGTCGAACGGAAGGCC 72

RESULT 77
AD071823
ID AD071823 standard; DNA; 1517 BP.
XX AC
XX AD071823;
XX DT
XX 15-JUL-2004 (first entry)
XX DE DNA of RNA isolated from Gordonia sp. Kanmonkai-1129 SeqID 1.
XX KW astaxanthin; canthaxanthine; microbial; livestock fodder; fish breeding;
XX KW ds.
XX OS Gordonia sp.
XX PN JP2004089015-A.
XX PD 25-MAR-2004.
XX PF 29-AUG-2002; 2002JP-00251165.
XX PR 29-AUG-2002; 2002JP-00251165.
XX PA (KANM-) KANMONKAI KK.
XX DR WPI; 2004-253025/24.
XX PT Production of astaxanthin and canthaxanthine useful as fodder and feed
XX PT for livestock, domestic fowl and fish, involves cultivating Actinomyces
XX PS belonging to Gordonia genus.
XX PS Disclosure; SEQ ID NO 1; 13pp; Japanese.
XX CC This invention relates to a novel method for producing astaxanthin and
XX CC canthaxanthine. Specifically, it refers to the cultivation of Actinomyces
XX CC microbial cells belonging to the Gordonia genus using a fresh water or
XX CC sea water mineral nutrition containing culture medium. The present
XX CC invention describes producing astaxanthin and canthaxanthine for use as a
XX CC fodder for livestock and domestic fowl, as well as a feed for fish
XX CC breeding. The production method uses natural products and is efficient at
XX CC a low cost. This polynucleotide sequence is a DNA copy of RNA isolated
XX CC from the Gordonia sp. Kanmonkai-1129 microorganism of the invention.
XX SQ Sequence 1517 BP; 334 A; 363 C; 515 G; 304 T; 0 U; 1 Other;
Query Match      80.0%; Score 20; DB 12; Length 1517;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCC 20
Db 53 GCAAGTCGAACGGAAGGCC 72

RESULT 78
AEA22407
ID AEA22407 standard; DNA; 1527 BP.
XX AC
XX AEA22407;
XX DT 25-AUG-2005 (first entry)

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XX DE Mycobacterium heckeshornense 16S rRNA sequence SEQ ID NO:8.
XX KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
XX OS Mycobacterium heckeshornense.
XX PN US2005130168-A1.
XX PD 16-JUN-2005.
XX PF 31-OCT-2003; 2003US-00697802.
XX PR 31-OCT-2003; 2003US-00697802.
XX PA (HANX/) HAN X.
XX PA (PHAM/) PHAM A S.
XX PI Han X, Pham AS;
XX DR WPI; 2005-424597/43.
XX PT Determining a bacterium species comprises providing oligonucleotide
XX PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
XX PS Disclosure; SEQ ID NO 8; 74pp; English.
XX CC The invention relates to a method (M1) for determining a bacterium
XX CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
XX CC extracting a genomic nucleotide from the bacterium to provide a
XX CC nucleotide template; (c) annealing a region of a nucleotide template to a
XX CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
XX CC complimentary fashion, the primer set designed to provide a product
XX CC having a predetermined size dictated by a complimentary primer set; (d)
XX CC amplifying the region of the nucleotide template to produce the product;
XX CC and (e) determining a species of a bacterium in a nucleotide sequence of
XX CC the product. Also described is an alternative method (M2) for determining
XX CC a bacterium species comprising: (a) providing a specimen or a sample
XX CC having a template; (b) providing a pair of primers selected from: (i) a
XX CC first forward primer having consecutive bases of an AFB-f comprising any
XX CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
XX CC or variations and a first reverse primer having consecutive bases of an
XX CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
XX CC or their fragments or variations, (ii) a second forward primer having
XX CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
XX CC bp (AEA22489-AEA22516) or their fragments or variations and a second
XX CC reverse primer having consecutive bases of an UB-r comprising any of the
XX CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
XX CC variations, or (iii) a first forward primer having consecutive bases of
XX CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
XX CC second reverse primer having consecutive bases of an UB-r of AEA22517-
XX CC AEA22544 or their fragments or variations; (c) the specimen; and (d)
XX CC comparing the product from the specimen with a nucleotide sequence from a
XX CC database to determine the bacterium species present in the specimen. The
XX CC methods are useful for determining a bacterium species. The present
XX CC sequence represents a Mycobacterium heckeshornense 16S rRNA nucleotide
XX CC sequence, which is used in the exemplification of the present invention.
XX SQ Sequence 1527 BP; 325 A; 365 C; 534 G; 303 T; 0 U; 0 Other;
Query Match      80.0%; Score 20; DB 14; Length 1527;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCC 20
Db 44 GCAAGTCGAACGGAAGGCC 63

RESULT 79
AAD11264
ID AAD11264 standard; DNA; 32 BP.
XX

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AC AAD11264;
XX
DT 24-SEP-2001 (first entry)
XX
DE Mycobacterium 16S rRNA amplifying primer #8.
XX
KW Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
KW Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
XX
OS Mycobacterium sp.
XX
PN WO200144510-A2.
XX
PD 21-JUN-2001.
XX
PF 17-DEC-1999; 99WO-US030346.
XX
PR 17-DEC-1999; 99WO-US030346.
XX
PA (GENP-) GEN-PROBE INC.
PA (INNR ) BIOMERIEUX SA.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
DR WPI; 2001-398170/42.
XX
PT Detecting Mycobacterium species, involves in vitro amplification of 16S
PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using
PT specific primers, and detecting the amplified nucleic acid.
XX
PS Claim 1; Page 35; 44pp; English.
XX
CC The invention relates to a method of detecting Mycobacterium species,
CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture
CC comprising a polymerase, and at least two primers, and then detecting the
CC amplified nucleic acid. The method is relatively simple and useful for
CC detecting the presence of various Mycobacterium species in a biological
CC sample, and thus important for diagnosis of infections resulting from
CC them. The method is especially important for screening opportunistic
CC infections caused by M. tuberculosis or a Mycobacterium other than
CC tuberculosis (MOTT). The present sequence is a PCR primer used for
CC amplifying Mycobacterium 16S rRNA
XX
SQ Sequence 32 BP; 10 A; 6 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 79.2%; Score 19.8; DB 4; Length 32;
Best Local Similarity 91.3%; Pred. No. 17;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTT 23
Db 1 GCAAGTCGAACGGAAGGCTCT 23

RESULT 80
ADG88345
ID ADG88345 standard; DNA; 32 BP.
XX
AC ADG88345;
XX
DT 11-MAR-2004 (first entry)
XX
DE Mycobacterium amplifying PCR primer #14.
XX
KW In vitro amplification; PCR; primer; ss.
XX
OS Mycobacterium sp.
XX
PN US2003165824-A1.
XX
PD 04-SEP-2003.
XX

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PF 15-DEC-2000; 2000US-00738274.
XX
PR 17-DEC-1999; 99US-0172190P.
XX
PA (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZAT P.
PA (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
DR WPI; 2003-898044/82.
XX
PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample comprises performing in vitro nucleic acid
PT amplification and detection of amplified products.
XX
PS Claim 1; SEQ ID NO 14; 20pp; English.
XX
CC The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample comprises performing an in vitro
CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
CC detecting the amplified Mycobacterium nucleic acid. The present sequence
CC is Mycobacterium amplifying PCR primer.
XX
SQ Sequence 32 BP; 10 A; 6 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 79.2%; Score 19.8; DB 10; Length 32;
Best Local Similarity 91.3%; Pred. No. 17;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTT 23
Db 1 GCAAGTCGAACGGAAGGCTCT 23

RESULT 81
AEA08220
ID AEA08220 standard; DNA; 32 BP.
XX
AC AEA08220;
XX
DT 14-JUL-2005 (first entry)
XX
DE Mycobacterium tuberculosis 16SrRNA amplifying PCR primer, SEQ ID NO: 14.
XX
KW Microorganism detection; DNA amplification; 16S ribosomal RNA; 16S rRNA;
KW PCR; primer; ss.
XX
OS Mycobacterium tuberculosis; ATCC 27294.
XX
PN US2005100915-A1.
XX
PD 12-MAY-2005.
XX
PF 18-SEP-2003; 2003US-00665708.
XX
PR 17-DEC-1999; 99US-0172190P.
PR 15-DEC-2000; 2000US-00738274.
XX
PA (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZAT P.
PA (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
DR WPI; 2005-345392/35.
XX
PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample, comprises using in vitro nucleic acid

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PT amplification and detection of amplified products.
XX
PS Example 1; SEQ ID NO 14; 21pp; English.
XX
CC The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample. The method involves using in
CC vitro nucleic acid amplification and detection of amplified products. The
CC invention is useful for diagnostic detection of pathogenic bacteria such
CC as Mycobacterium species. The present sequence is the Mycobacterium
CC tuberculosis (ATCC 27294) 16S ribosomal RNA (16S rRNA) amplifying PCR
CC primer.
XX
SQ Sequence 32 BP; 10 A; 6 C; 10 G; 6 T; 0 U; 0 Other;
XX
XX
XX Query Match 79.2%; Score 19.8; DB 14; Length 32;
XX Best Local Similarity 91.3%; Pred. No. 17;
XX Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 1 GCAAGTCGAACGGAAGGCGCTTT 23
XX |||||
Db 1 GCAAGTCGAACGGAAGGCTCTCT 23
XX |||||
XX
XX RESULT 82
XX AAX99199
XX ID AAX99199 standard; DNA; 50 BP.
XX
XX AC AAX99199;
XX
XX DT 28-SEP-1999 (first entry)
XX
XX DE M. kansasii 16S rRNA gene fragment.
XX
XX KW Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA;
XX shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.
XX
XX OS Mycobacterium kansasii.
XX
XX PN WO9935284-Al.
XX
XX PD 15-JUL-1999.
XX
XX PF 30-DEC-1997; 97WO-BR000087.
XX
XX PR 30-DEC-1997; 97WO-BR000087.
XX
XX PA (UWMI-) UNIV FEDERAL MINAS GERAIS.
XX
XX PI Peregrino Ferreira PC, Geessien Kroon E;
XX Bernardes Margutti Pinto ME, Aleixo AW;
XX
XX DR WPI; 1999-444201/37.
XX
XX PT Detection of mycobacteria by shift mobility assay.
XX
XX PS Disclosure; Fig 7; 20pp; English.
XX
XX CC The invention describes a new method for diagnosis, identification and
XX characterisation of Mycobacterium tuberculosis or any other mycobacteria
XX by using polymerase chain reaction (PCR) and shift mobility assay (SMA)
XX in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,
XX DNA amplification and shift mobility assay. The method is based on
XX divergence in sequences found in 16S rRNA to identify mycobacteria
XX species, since a remarkable shift of heteroduplex bands are obtained
XX between single stranded and homoduplex bands in UPAGE. The method is
XX fast, simple and can produce information not easily obtained when
XX compared with other detection methods. The sensitivity of other assays
XX suffer due to the tendency of the denatured PCR product strands to
XX reassociate and exclude oligonucleotide probes, and steric interference
XX between the bound oligonucleotides and the solid support which impede
XX hybridization to nucleic acids in solution. Sequences AAX99193-237
XX represent 16S rRNA gene regions of some mycobacterial species
XX
XX
XX SQ Sequence 50 BP; 14 A; 12 C; 14 G; 10 T; 0 U; 0 Other;
XX
XX
XX Query Match 79.2%; Score 19.8; DB 2; Length 50;
XX Best Local Similarity 91.3%; Pred. No. 18;
XX Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 1 GCAAGTCGAACGGAAGGCGCTTT 23
XX |||||
Db 9 GCAAGTCGAACGGAAGGCTCTCT 31
XX |||||
XX
XX RESULT 83
XX AAX99194
XX ID AAX99194 standard; DNA; 50 BP.
XX
XX AC AAX99194;
XX
XX DT 28-SEP-1999 (first entry)
XX
XX DE M. bovis 16S rRNA gene fragment.
XX
XX KW Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA;
XX shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.
XX
XX OS Mycobacterium bovis.
XX
XX PN WO9935284-Al.
XX
XX PD 15-JUL-1999.
XX
XX PF 30-DEC-1997; 97WO-BR000087.
XX
XX PR 30-DEC-1997; 97WO-BR000087.
XX
XX PA (UWMI-) UNIV FEDERAL MINAS GERAIS.
XX
XX PI Peregrino Ferreira PC, Geessien Kroon E;
XX Bernardes Margutti Pinto ME, Aleixo AW;
XX
XX DR WPI; 1999-444201/37.
XX
XX PT Detection of mycobacteria by shift mobility assay.
XX
XX PS Disclosure; Fig 7; 20pp; English.
XX
XX CC The invention describes a new method for diagnosis, identification and
XX characterisation of Mycobacterium tuberculosis or any other mycobacteria
XX by using polymerase chain reaction (PCR) and shift mobility assay (SMA)
XX in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,
XX DNA amplification and shift mobility assay. The method is based on
XX divergence in sequences found in 16S rRNA to identify mycobacteria
XX species, since a remarkable shift of heteroduplex bands are obtained
XX between single stranded and homoduplex bands in UPAGE. The method is
XX fast, simple and can produce information not easily obtained when
XX compared with other detection methods. The sensitivity of other assays
XX suffer due to the tendency of the denatured PCR product strands to
XX reassociate and exclude oligonucleotide probes, and steric interference
XX between the bound oligonucleotides and the solid support which impede
XX hybridization to nucleic acids in solution. Sequences AAX99193-237
XX represent 16S rRNA gene regions of some mycobacterial species
XX
XX
XX SQ Sequence 50 BP; 15 A; 11 C; 14 G; 10 T; 0 U; 0 Other;
XX
XX
XX Query Match 79.2%; Score 19.8; DB 2; Length 50;
XX Best Local Similarity 91.3%; Pred. No. 18;
XX Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 1 GCAAGTCGAACGGAAGGCGCTTT 23
XX |||||
Db 9 GCAAGTCGAACGGAAGGCTCTCT 31
XX |||||
XX
XX RESULT 84
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AAX99193
ID AAX99193 standard; DNA; 50 BP.
XX
AC AAX99193;
XX
DT 28-SEP-1999 (first entry)
XX
DE M. tuberculosis 16S rRNA gene fragment.
XX
KW Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA;
KW shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9935284-A1;
XX
PD 15-JUL-1999.
XX
PF 30-DEC-1997; 97WO-BR000087.
XX
PR 30-DEC-1997; 97WO-BR000087.
XX
PA (UYMI-) UNIV FEDERAL MINAS GERAIS.
XX
PI Peregrino Ferreira PC, Geessien Kroon E;
PI Bernardes Margutti Pinto ME, Aleixo AW;
XX
DR WPI; 1999-444201/37.
XX
PT Detection of mycobacteria by shift mobility assay.
XX
PS Disclosure; Fig 7; 20pp; English.
XX
CC The invention describes a new method for diagnosis, identification and
CC characterisation of Mycobacterium tuberculosis or any other mycobacteria
CC by using polymerase chain reaction (PCR) and shift mobility assay (SMA)
CC in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,
CC DNA amplification and shift mobility assay. The method is based on
CC divergence in sequences found in 16S rRNA to identify mycobacteria
CC species, since a remarkable shift of heteroduplex bands are obtained
CC between single stranded and homoduplex bands in UPAGE. The method is
CC fast, simple and can produce information not easily obtained when
CC compared with other detection methods. The sensitivity of other assays
CC suffer due to the tendency of the denatured PCR product strands to
CC reassociate and exclude oligonucleotide probes, and steric interference
CC between the bound oligonucleotides and the solid support which impede
CC hybridization to nucleic acids in solution. Sequences AAX99193-237
CC represent 16S rRNA gene regions of some mycobacterial species
XX
SQ Sequence 50 BP; 15 A; 11 C; 14 G; 10 T; 0 U; 0 Other;
Query Match 79.2%; Score 19.8; DB 2; Length 50;
Best Local Similarity 91.3%; Pred No. 18;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCAAGTCGAACGGAAGGCTTT 23
Db 9 GCAAGTCGAACGGAAGGCTCT 31
|||||
RESULT 85
ID ADF94055
ID ADF94055 standard; DNA; 50 BP.
XX
AC ADF94055;
XX
DT 11-MAR-2004 (first entry)
XX
DE Microorganism detection probe, SEQ ID 148.
XX
KW Probe; detection; identification; microorganism; food; drug;
KW 16S rRNA V1 region; 16S rRNA V2 region; 16S rRNA V3 region; ss.
XX

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OS Mycobacterium kansasii.
XX
PN WO2003106676-A1.
XX
PD 24-DEC-2003.
XX
PF 16-JUN-2003; 2003WO-JP007620.
XX
PR 14-JUN-2002; 2002JP-00174564.
XX
PA (HISF) HITACHI SOFTWARE ENG CO LTD.
PA (MITS-) MITSUBISHI KAGAKU BIO-CLINICAL LAB INC.
XX
PI Hashida J, Ueno S, Muto I, Naruse K, Tamura M, Matsuda K;
PI Shimadzu M, Kobayashi I, Ishiko H;
XX
DR WPI; 2004-071565/07.
XX
CC 20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a
CC microorganism for specific detection and identification of the
CC microorganism in foods and drug compositions.
XX
PS Claim 2; SEQ ID NO 148; 150pp; Japanese.
XX
CC The present invention relates to probes (ADF93908-ADF94059) for the
CC specific detection and identification of harmful microorganisms in
CC samples of foods and drug compositions. The probe sequences are derived
CC from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism,
CC or its complementary sequence. Detection and identification of the
CC microorganism is by amplification of the complete 16S rRNA gene using
CC primers ADF94060 and ADF94061, labelling the amplification product (a
CC fluorescence label is preferred), and hybridising to the probe or probes
CC of the invention. The probes may be immobilised on a DNA chip. The
CC microorganism is selected from Actinobacillus actinomycetemcomitans,
CC Acinetobacter calcoaceticus, Haemophilus influenzae, Stenotrophomonas
CC maltophilia, Proteus mirabilis, Streptococcus pneumoniae, Pseudomonas
CC aeruginosa, Citrobacter freundii, Veillonella parvula, Providencia
CC stuartii, Neisseria gonorrhoeae, Streptococcus agalactiae, Morganella
CC morganii, Bacteroides fragilis, Staphylococcus hominis, Staphylococcus
CC warneri, Staphylococcus haemolyticus, Enterobacter cloacae, Enterobacter
CC aerogenes, Staphylococcus epidermidis, Streptococcus constellatus,
CC Serratia marcescens, Streptococcus anginosus, Escherichia coli,
CC Klebsiella pneumoniae, Enterococcus faecalis, Enterococcus faecium,
CC Streptococcus sanguis, Streptococcus mitis, Streptococcus intermedius,
CC Listeria monocytogenes, Clostridium perfringens, Corynebacterium
CC aquaticum, Streptococcus oralis, Staphylococcus aureus, Neisseria
CC meningitidis, Campylobacter fetus, Enterococcus gallinarum, Enterococcus
CC caseeliflavus, Aeromonas hydrophila, Salmonella paratyphi, Salmonella
CC typhi, Streptococcus equisimilis, Streptococcus canis, Klebsiella
CC oxytoca, Staphylococcus saprophyticus, Pasteurella multocida, Eikenella
CC corrodens, Streptococcus pyogenes, Moraxella catarrhalis, Legionella
CC pneumophila, Mycobacterium tuberculosis, Mycobacterium avium,
CC Mycobacterium intracellulare, Mycobacterium kansasii or Mycobacterium
CC Gordonae.
XX
SQ Sequence 50 BP; 13 A; 11 C; 18 G; 8 T; 0 U; 0 Other;
Query Match 79.2%; Score 19.8; DB 12; Length 50;
Best Local Similarity 91.3%; Pred No. 18;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCAAGTCGAACGGAAGGCTTT 23
Db 1 GCAAGTCGAACGGAAGGCTCT 23
|||||
RESULT 86
ID ADF94047
ID ADF94047 standard; DNA; 50 BP.
XX
AC ADF94047;
XX
DT 11-MAR-2004 (first entry)

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XX DE Microorganism detection probe, SEQ ID 140.
 XX KW Probe; detection; identification; microorganism; food; drug;
 XX KW 16S rRNA V1 region; 16S rRNA V2 region; 16S rRNA V3 region; ss.
 XX OS Mycobacterium tuberculosis.
 XX PN WO2003106676-A1.
 XX PD 24-DEC-2003.
 XX PF 16-JUN-2003; 2003WO-JP007620.
 XX PR 14-JUN-2002; 2002JP-00174564.
 XX PA (HISF) HITACHI SOFTWARE ENG CO LTD.
 XX PA (MITS-) MITSUBISHI KAGAKU BIO-CLINICAL LAB INC.
 XX PI Hashida J, Ueno S, Muto I, Naruse K, Tamura M, Matsuda K;
 XX PI Shimadzu M, Kobayashi I, Ishiko H;
 XX DR WPI; 2004-071565/07.
 XX XX 20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a
 XX PT microorganism for specific detection and identification of the
 XX PT microorganism in foods and drug compositions.
 XX PS Claim 2; SEQ ID NO 140; 150pp; Japanese.
 XX CC The present invention relates to probes (ADF93908-ADF94059) for the
 CC specific detection and identification of harmful microorganisms in
 CC samples of foods and drug compositions. The probe sequences are derived
 CC from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism,
 CC or its complementary sequence. Detection and identification of the
 CC microorganism is by amplification of the complete 16S rRNA gene using
 CC primers ADF94060 and ADF94061, labelling the amplification product (a
 CC fluorescence label is preferred), and hybridising to the probe or probes
 CC of the invention. The probes may be immobilised on a DNA chip. The
 CC microorganism is selected from *Actinobacillus actinomycetemcomitans*,
 CC *Acinetobacter calcoaceticus*, *Haemophilus influenzae*, *Stenotrophomonas*
 CC *malophilia*, *Proteus mirabilis*, *Streptococcus pneumoniae*, *Pseudomonas*
 CC *aeruginosa*, *Citrobacter freundii*, *Veillonella parvula*, *Providencia*
 CC *stuartii*, *Neisseria gonorrhoeae*, *Streptococcus agalactiae*, *Morganella*
 CC *morganii*, *Bacteroides fragilis*, *Staphylococcus hominis*, *Staphylococcus*
 CC *warneri*, *Staphylococcus haemolyticus*, *Enterobacter cloacae*, *Enterobacter*
 CC *aerogenes*, *Staphylococcus epidermidis*, *Streptococcus constellatus*,
 CC *Serratia marcescens*, *Streptococcus anginosus*, *Escherichia coli*,
 CC *Klebsiella pneumoniae*, *Enterococcus faecalis*, *Enterococcus faecium*,
 CC *Streptococcus sanguis*, *Streptococcus mitis*, *Streptococcus intermedius*,
 CC *Listeria monocytogenes*, *Clostridium perfringens*, *Corynebacterium*
 CC *aquaticum*, *Streptococcus oralis*, *Staphylococcus aureus*, *Neisseria*
 CC *meningitidis*, *Campylobacter fetus*, *Enterococcus gallinarum*, *Enterococcus*
 CC *caseliflavus*, *Aeromonas hydrophila*, *Salmonella paratyphi*, *Salmonella*
 CC *typhi*, *Streptococcus equisimilis*, *Streptococcus canis*, *Klebsiella*
 CC *oxytoca*, *Staphylococcus saprophyticus*, *Pasteurella multocida*, *Eikenella*
 CC *corrodens*, *Streptococcus pyogenes*, *Moraxella catarrhalis*, *Legionella*
 CC *pneumophila*, *Mycobacterium tuberculosis*, *Mycobacterium avium*,
 CC *Mycobacterium intracellulare*, *Mycobacterium kansasii* or *Mycobacterium*
 CC *Gordonae*.
 XX SQ Sequence 50 BP; 13 A; 10 C; 18 G; 9 T; 0 U; 0 Other;

Query Match 79.2%; Score 19.8; DB 12; Length 50;
 Best Local Similarity 91.3%; Pred. No. 18;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCTTT 23
 |||||
 Db 1 GCAAGTCGACGGAAGGCCTTT 23
 |||||

RESULT 87

AAQ94742
 ID AAQ94742 standard; DNA; 203 BP.
 XX AC AAQ94742;
 XX DT 26-FEB-1996 (first entry)
 XX DE DNA fragment of 16S rRNA gene of *M. tuberculosis*.
 XX KW hybridisation; *Mycobacteria*; acid-fast; 16S rRNA; ribosomal RNA; probe;
 KW detection; identification; ss.
 XX OS *Mycobacterium tuberculosis*.
 XX FH Key Location/Qualifiers
 FT misc_binding complement(1..20)
 FT FT /*tag= a
 FT /*note= "probe binding (see AAQ94743)"
 FT FT 41..60
 FT /*tag= b
 FT /*note= "probe binding (see AAQ94745)"
 FT FT 92..113
 FT /*tag= c
 FT /*note= "probe binding (see AAQ94746)"
 FT FT 183..203
 FT /*tag= d
 FT /*note= "probe binding (see AAQ94744)"
 XX JP07155200-A.
 XX PN 20-JUN-1995.
 XX PF 10-DEC-1993; 93JP-00310865.
 XX PR 10-DEC-1993; 93JP-00310865.
 XX PA (TOYM) TOYOSO KK.
 XX DR WPI; 1995-250746/33.
 XX XX Novel oligo-nucleotide(s) which hybridise with the 16S rRNA gene of
 PT bacteria - used for detection and identification of acid-fast bacteria,
 PT eg. *Mycobacterium*.
 XX PS Claim 1; Page 10; 13pp; Japanese.
 CC AAQ94743-46 are oligonucleotides used for the detection and
 CC identification of acid-fast bacteria (pref. *Mycobacterium*) by hybridising
 CC with the base sequence of the 16S rRNA gene of the bacteria. The
 CC oligonucleotides can be represented by all or a part of the 203 base
 CC sequence shown here. *Mycobacteria* are gram-positive bacteria which grow
 CC very slowly and require a lot of time for culture for detection (longer
 CC than one month). The probes provide a simple, rapid and exact method for
 CC detection and identification of the bacteria. The method can be applied
 CC directly to sputum or blood samples and the result obtd. within one day.
 CC AAQ94747-60 are specific probes for different *Mycobacteria* species
 XX SQ Sequence 203 BP; 44 A; 42 C; 72 G; 45 T; 0 U; 0 Other;
 Query Match 79.2%; Score 19.8; DB 2; Length 203;
 Best Local Similarity 91.3%; Pred. No. 21;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 GCAAGTCGACGGAAGGCCTTT 23
 |||||
 Db 5 GCAAGTCGACGGAAGGCCTTT 27
 |||||
 RESULT 88
 AEB98764
 ID AEB98764 standard; DNA; 209 BP.
 XX AC AEB98764;

```
XX 06-OCT-2005 (first entry)
XX Mycobacterium kansasii partial 16S rDNA sequence, SEQ ID 6.
XX microorganism detection; mycobacterium infection; antibacterial; ds.
XX Mycobacterium kansasii.
XX JP2005204582-A.
XX 04-AUG-2005.
XX 23-JAN-2004; 2004JP-00015195.
XX 23-JAN-2004; 2004JP-00015195.
XX (ASAH ) ASahi KASEI KK.
XX Oda N;
XX WPI; 2005-526965/54.
XX New single-stranded oligonucleotide, useful for amplifying the nucleic
XX acid of Mycobacterium avium, Mycobacterium intracellulare, and
XX Mycobacterium kansasii.
XX Example 1; SEQ ID NO 6; 14pp; Japanese.
XX The invention relates to a novel single-stranded oligonucleotide used in
XX a detection method of an atypical mycobacteria group. The invention
XX further includes: amplifying the nucleic acid of Mycobacterium avium by a
XX loop-mediated isothermal amplification (LAMP) method; amplifying the
XX nucleic acid of M. intracellulare by a LAMP method; amplifying the
XX nucleic acid of M. kansasii by a LAMP method; and a kit for detecting the
XX nucleic acid of M. avium by a LAMP method; detecting the nucleic acid of
XX M. intracellulare by a LAMP method; or detecting the nucleic acid of
XX kansasii by a LAMP method. The single-stranded oligonucleotide is useful
XX in medical applications. This polynucleotide represents a Mycobacterium
XX kansasii partial 16S rDNA sequence amplified by the LAMP method of the
XX invention.
XX Sequence 209 BP; 47 A; 49 C; 72 G; 41 T; 0 U; 0 Other;
XX Query Match 79.2%; Score 19.8; DB 14; Length 209;
XX Best Local Similarity 91.3%; Pred. No. 21;
XX Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCAAGTCGAACGGAAGGCTTT 23
Db 39 GCAAGTCGAACGGAAGGCTCT 61
RESULT 89
ID AEB98761 standard; DNA; 211 BP.
XX AEB98761;
XX 06-OCT-2005 (first entry)
XX Mycobacterium tuberculosis partial 16S rDNA sequence, SEQ ID 3.
XX microorganism detection; mycobacterium infection; antibacterial; ds.
XX Mycobacterium tuberculosis.
XX JP2005204582-A.
XX 04-AUG-2005.
XX 23-JAN-2004; 2004JP-00015195.
XX
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PR 23-JAN-2004; 2004JP-00015195.
XX (ASAH ) ASahi KASEI KK.
XX Oda N;
XX WPI; 2005-526965/54.
XX New single-stranded oligonucleotide, useful for amplifying the nucleic
XX acid of Mycobacterium avium, Mycobacterium intracellulare, and
XX Mycobacterium kansasii.
XX Example 1; SEQ ID NO 3; 14pp; Japanese.
XX The invention relates to a novel single-stranded oligonucleotide used in
XX a detection method of an atypical mycobacteria group. The invention
XX further includes: amplifying the nucleic acid of Mycobacterium avium by a
XX loop-mediated isothermal amplification (LAMP) method; amplifying the
XX nucleic acid of M. intracellulare by a LAMP method; amplifying the
XX nucleic acid of M. kansasii by a LAMP method; and a kit for detecting the
XX nucleic acid of M. avium by a LAMP method; detecting the nucleic acid of
XX M. intracellulare by a LAMP method; or detecting the nucleic acid of
XX kansasii by a LAMP method. The single-stranded oligonucleotide is useful
XX in medical applications. This polynucleotide represents a Mycobacterium
XX tuberculosis partial 16S rDNA sequence amplified by the LAMP method of
XX the invention.
XX Sequence 211 BP; 48 A; 45 C; 74 G; 44 T; 0 U; 0 Other;
XX Query Match 79.2%; Score 19.8; DB 14; Length 211;
XX Best Local Similarity 91.3%; Pred. No. 21;
XX Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCAAGTCGAACGGAAGGCTTT 23
Db 39 GCAAGTCGAACGGAAGGCTCT 61
RESULT 90
ID ADV99481 standard; DNA; 349 BP.
XX ADV99481;
XX 24-FEB-2005 (first entry)
XX Meningitis causing bacteria DNA fragment #9.
XX ds; antibacterial; antiinflammatory; inflammation; neurological disease;
XX diagnosis; meningitis; biochip.
XX Mycobacterium tuberculosis.
XX CN1420123-A.
XX 28-MAY-2003.
XX 16-NOV-2001; 2001CN-00137478.
XX 16-NOV-2001; 2001CN-00137478.
XX (JING-) JINGQI BIO CHEM SCI & TECH CO LTD.
XX Xu B, Jiang Y, Huang X;
XX WPI; 2004-044307/05.
XX A nucleic acid sequence useful for diagnosing pathogenic bacteria for
XX meningitides.
XX Disclosure; Page 18; 24pp; Chinese.
XX The invention relates to a nucleic acid sequence group for quickly
```

CC diagnosing 20 kinds of pathogenic bacteria for meningitis. Its method
CC includes comparing the DNA sequences of different pathogenic bacteria,
CC choosing special fragments, finding out common primer, designing 3
CC specific probe fragments for each pathogenic bacterium, dotting them on
CC high-molecular polymer to obtain chip, sampling the DNA of pathogenic
CC bacterium of patient, labeling, amplification, and reacting with said
CC chip for visually recognizing the pathogenic bacterium. Its advantages are
CC high speed and low cost. The present sequence represents a meningitis
CC causing bacteria DNA fragment.

XX SQ Sequence 349 BP; 75 A; 82 C; 125 G; 67 T; 0 U; 0 Other;

Query Match 79.2%; Score 19.8; DB 13; Length 349;
Best Local Similarity 91.3%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
Db 52 GCAAGTCGAACGGAAGGCTCT 74

RESULT 91

AAV24293
ID AAV24293 standard; DNA; 1271 BP.

XX AC AAV24293;

DT 14-SEP-1998 (first entry)

DE Mycobacterium tuberculosis 16S ribosomal RNA gene.

XX KW Antibacterial; antimycobacterial; oligonucleotide; infection; therapy;
KW ribosome binding site; Shine-Dalgarno; ribosomal RNA; cystic fibrosis;
KW tuberculosis; ss.

XX OS Mycobacterium tuberculosis.

XX PN WO9814567-A2.

XX PD 09-APR-1998.

XX PF 30-SEP-1997; 97WO-US018094.

XX PR 01-OCT-1996; 96US-0027729P.

XX PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.

XX PI Martin WJ, Wisniewski P;

XX DR WPI; 1998-240079/21.

XX PT Use of oligo:nucleotide(s) corresponding to bacterial 16S rRNA - for
XX inhibiting bacterial protein expression and treating bacterial infection.

XX PS Claim 26; Page 60-61; 73pp; English.

XX CC This polynucleotide comprises the 16S ribosomal RNA (rRNA) gene of
XX Mycobacterium tuberculosis. The invention relates to methods and
XX compositions for the treatment of Gram-negative bacterial infections
XX employing novel oligonucleotides as antimicrobial agents. The
XX oligonucleotides are targeted to the Shine-Dalgarno (SD) region of
XX prokaryotes to inhibit bacterial expression and hence inhibit bacterial
XX infection. They preferably comprise 10-35 consecutive bases of the 3' end
XX of a bacterial 16S rRNA (see also AAV24291-95). An oligonucleotide may
XX also include a transport moiety and may have DNA phosphate modifications
XX to increase nuclease resistance, or may be formulated in a liposome. A
XX claimed method for treating a bacterial infection of a patient comprises
XX administering a liposomal formulation of such an oligonucleotide. The
XX oligonucleotides can be used particularly for treating bacterial
XX infections in pulmonary diseases such as cystic fibrosis or tuberculosis.
XX Since the SD sequence is not present in eukaryotic cells, the
XX oligonucleotides provide a pathogen-specific therapeutic method

SQ Sequence 1271 BP; 260 A; 281 C; 430 G; 300 T; 0 U; 0 Other;
Query Match 79.2%; Score 19.8; DB 2; Length 1271;
Best Local Similarity 91.3%; Pred. No. 26;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
Db 442 GCAAGTCGAACGGAAGGCTCT 464

RESULT 92

AEA22416
ID AEA22416 standard; DNA; 1416 BP.

XX AC AEA22416;

DT 25-AUG-2005 (first entry)

DE Mycobacterium tuberculosis 16S rRNA sequence SEQ ID NO:17.

XX KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.

XX OS Mycobacterium tuberculosis.

XX PN US2005130168-A1.

XX PD 16-JUN-2005.

XX PF 31-OCT-2003; 2003US-00697802.

XX PR 31-OCT-2003; 2003US-00697802.

XX PA (HANX/) HAN X.

XX PI (PHAM/) PHAM A S.

XX PI Han X, Pham AS;

XX DR WPI; 2005-424597/43.

XX PT Determining a bacterium species comprises providing oligonucleotide
XX primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.

XX PS Disclosure; SEQ ID NO 17; 74pp; English.

XX CC The invention relates to a method (M1) for determining a bacterium
XX species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
XX extracting a genomic nucleotide from the bacterium to provide a
XX nucleotide template; (c) annealing a region of a nucleotide template to a
XX specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
XX complimentary fashion, the primer set designed to provide a product
XX having a predetermined size dictated by a complementary primer set; (d)
XX amplifying the region of the nucleotide template to produce the product;
XX and (e) determining a species of a bacterium in a nucleotide sequence of
XX the product. Also described is an alternative method (M2) for determining
XX a bacterium species comprising: (a) providing a specimen or a sample
XX having a template; (b) providing a pair of primers selected from: (i) a
XX first forward primer having consecutive bases of an AFB-f comprising any
XX of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
XX or variations, and a first reverse primer having consecutive bases of an
XX AFB-f comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
XX or their fragments or variations, (ii) a second forward primer having
XX consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
XX bp (AEA22489-AEA22516) or their fragments or variations, and a second
XX reverse primer having consecutive bases of an UB-r comprising any of the
XX 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
XX variations, or (iii) a first forward primer having consecutive bases of
XX an AFB-f of AEA22417-AEA22452 or their fragments or variations, and a
XX second reverse primer having consecutive bases of an UB-r of AEA22517-
XX AEA22544 or their fragments or variations; (c) the specimen; and (d)
XX comparing the product from the specimen with a nucleotide sequence from a
XX database to determine the bacterium species present in the specimen. The
XX methods are useful for determining a bacterium species. The present

CC sequence represents a *Mycobacterium tuberculosis* 16S rRNA nucleotide
CC sequence, which is used in the exemplification of the present invention.
XX
SQ Sequence 1416 BP; 309 A; 341 C; 481 G; 285 T; 0 U; 0 Other;

Query Match 79.2%; Score 19.8; DB 14; Length 1416;
Best Local Similarity 91.3%; Pred. No. 26;
Matches 21; Conservative 0; Mismatches 2; Indels 0;

Qy 1 GCAAGTCGAACGGAAAGGCTTT 23
20 GCAAGTCGAACGGAAAGGCTCT 42

RESULT 93
AEA22402
ID AEA22402 standard; DNA; 1421 BP.

AC AEA22402;

DT 25-AUG-2005 (first entry)

DE Mycobacterium bovis 16S rRNA sequence SEQ ID NO:3.

KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.

OS *Mycobacterium bovis*.

PN US2005130168-A1.

PD 16-JUN-2005.

31-OCT-2003; 2003US-00697802.

PR 31-OCT-2003; 2003US-00697802.

PA (HANX/) HAN X.

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PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.

PS Disclosure; SEQ ID NO 3; 74pp; English.

The invention relates to a method (M1) for determining a bacterium species. (M1) comprises: (a) culturing a bacterium from a specimen; (b) extracting a genomic nucleotide from the bacterium to provide a nucleotide template; (c) annealing a region of a nucleotide template to a specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a complementary fashion, the primer set designed to provide a product having a predetermined size dictated by a complementary primer set; (d) amplifying the region of the nucleotide template to produce the product; and (e) determining a species of a bacterium in a nucleotide sequence of the product. Also described is an alternative method (M2) for determining a bacterium species comprising: (a) providing a specimen or a sample having a template; (b) providing a pair of primers selected from: (i) a first forward primer having consecutive bases of an AFB-f comprising any of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments or variations and a first reverse primer having consecutive bases of an AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488) or their fragments or variations, (ii) a second forward primer having consecutive bases of an UB-f comprising any of the 28 sequences of 15-21 bp (AEA22489-AEA22516) or their fragments or variations and a second reverse primer having consecutive bases of an UB-r comprising any of the 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or variations, or (iii) a first forward primer having consecutive bases of an AFB-f of AEA22417-AEA22452 or their fragments or variations and a second reverse primer having consecutive bases of an UB-r of AEA22517-AEA22544 or their fragments or variations; (c) the specimen and (d)

CC comparing the product from the specimen with a nucleotide sequence from a
CC database to determine the bacterium species present in the specimen. The
CC methods are useful for determining a bacterium species. The present
CC sequence represents a *Mycobacterium bovis* 16S rRNA nucleotide sequence,
CC which is used in the exemplification of the present invention.

SQ Sequence 1421 BP; 310 A; 341 C; 484 G; 286 T; 0 U; 0 Other;
Query Match 79.2%; Score 19.8; DB 14; Length 1421;

Qy 1 GCAAGTCGAACGGAAAGGCCTT 23
|||
Db 20 GCAAGTCGAACGGAAAGGTCTCT 42

RESULT 94
AEA22409
ID AEA22409 standard; DNA; 1463 BP.

AC AEA22409;

DT 25-AUG-2005 (first entry)

DE Mycobacterium kansasii 16S rRNA sequence SEQ ID NO:10.

KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.

OS *Mycobacterium kansasii*.

PN US2005130168-A1.

PD 16-JUN-2005.

PF 31-OCT-2003; 2003US-00697802.

PR 31-OCT-2003; 2003US-00697802.

PA (HANX/) HAN X.

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PS Disclosure; SEQ ID NO 10; 74pp; English.

The invention relates to a method (M1) for determining a bacterium species. (M1) comprises: (a) culturing a bacterium from a specimen; (b) extracting a genomic nucleotide from the bacterium to provide a nucleotide template; (c) annealing a region of a nucleotide template to a specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a complementary fashion, the primer set designed to provide a product having a predetermined size dictated by a complementary primer set; (d) amplifying the region of the nucleotide template to produce the product; and (e) determining a species of a bacterium in a nucleotide sequence of the product. Also described is an alternative method (M2) for determining a bacterium species comprising: (a) providing a specimen or a sample having a template; (b) providing a pair of primers selected from: (i) a first forward primer having consecutive bases of an AFB-f comprising any of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments or variations and a first reverse primer having consecutive bases of an AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488) or their fragments or variations, (ii) a second forward primer having consecutive bases of an UB-f comprising any of the 28 sequences of 15-21 bp (AEA22489-AEA22516) or their fragments or variations and a second reverse primer having consecutive bases of an UB-r comprising any of the 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or variations, or (iii) a first forward primer having consecutive bases of

CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
CC second reverse primer having consecutive bases of an UB-r of AEA22517-
CC AEA22544 or their fragments or variations; (c) the specimen; and (d)
CC comparing the product from the specimen with a nucleotide sequence from a
CC database to determine the bacterium species present in the specimen. The
CC methods are useful for determining a bacterium species. The present
CC sequence represents a Mycobacterium kansasii 16S rRNA nucleotide
CC sequence, which is used in the exemplification of the present invention.
XX
XX
SQ Sequence 1463 BP; 318 A; 354 C; 500 G; 291 T; 0 U; 0 Other;

Query Match 79.2%; Score 19.8; DB 14; Length 1463;
Best Local Similarity 91.3%; Pred. No. 26;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
Db 19 GCAAGTCGAACGGAAGGTCCT 41

RESULT 95
AAZ35571
ID AAZ35571 standard; DNA; 1464 BP.

XX AAZ35571;

XX 28-JAN-2000 (first entry)

DE Mycobacterium tuberculosis 16S rRNA gene.

KW 16S rRNA gene; oligonucleotide primer; amplify; genus specific;
KW diagnosis; Mycobacterium; ss.

OS Mycobacterium tuberculosis.

XX US985569-A.

XX 16-NOV-1999.

XX 26-SEP-1997; 97US-00938858.

XX 26-SEP-1997; 97US-00938858.

XX (BECT) BECTON DICKINSON & CO.

XX Foxall PA, Kumar H;

XX WPI; 2000-012779/01.

XX Oligonucleotide primers useful for detecting microorganisms of the genus
PT Mycobacterium.

XX Example; Fig 3; 2lpp; English.

CC This sequence is the Mycobacterium tuberculosis 16S rRNA gene. This
CC sequence is used in an example of a method using oligonucleotide primers
CC for amplification of a genus specific sequence of the 16S rRNA gene. The
CC method of the invention consists of using primers AAZ35572-235586 to
CC amplify M. tuberculosis DNA and then detecting the amplified nucleic
CC acids. The oligonucleotides are useful for the detection of species of
CC medical interest of the genus Mycobacterium. In particular the detection
CC can be used for human and veterinary diagnosis from samples of biological
CC fluids or tissue e.g. sputum, bronchial washings, gastric washings.
CC blood, milk, lymph, skin and soft tissues. Identifying the mycobacterium
CC using the nucleic acid based diagnostic assay reduces the time required
CC for an accurate diagnosis as cultivation of the organisms is not required
XX

SQ Sequence 1464 BP; 321 A; 349 C; 502 G; 292 T; 0 U; 0 Other;

Query Match 79.2%; Score 19.8; DB 3; Length 1464;
Best Local Similarity 91.3%; Pred. No. 26;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
Db 20 GCAAGTCGAACGGAAGGTCCT 42

RESULT 96

AAZ11027
ID AAZ11027 standard; DNA; 1464 BP.

XX AAZ11027;

XX 24-OCT-2001 (first entry)

DE Mycobacterium tuberculosis 16S ribosomal RNA gene.

XX Antisense; bacterial 16S ribosomal RNA; rRNA; bacterial infection; human;
KW food grain supplement; livestock; poultry; therapeutic; ds.

OS Mycobacterium tuberculosis.

XX WO200142457-A2.

XX 14-JUN-2001.

XX 29-NOV-2000; 2000WO-US042391.

XX 29-NOV-1999; 99US-0168150P.

XX (AVIB-) AVI BIOPHARMA INC.

XX Iversen PL;

XX WPI; 2001-457295/49.

XX Antibacterial compound, useful for treating bacterial infections and as
PT livestock and poultry food supplement, comprises antisense
PT oligonucleotides complementary to bacterial 16S and 23S rRNA.

XX Disclosure; Page; 62pp; English.

XX AAS11021-AAS11034 represent the coding sequences of bacterial 16S
CC ribosomal RNA (rRNA) genes. The sequences were used to design anti-
CC bacterial compounds comprising substantially uncharged antisense
CC oligomers containing 8-40 nucleotide subunits, including a targeting
CC nucleic acid sequence at least 10 nucleotides in length which is
CC complementary to a bacterial 16S or 23S rRNA nucleic acid sequence. The
CC antisense oligomers are used for treating a bacterial infection in a
CC human or a mammalian animal produced by Escherichia coli, Salmonella
CC typhimurium, Pseudomonas aeruginosa, Vibrio cholera, Neisseria
CC gonorrhoea, Helicobacter pylori, Bartonella henselae, Haemophilus
CC influenza, Shigella dysenteriae, Staphylococcus aureus, Mycobacterium
CC tuberculosis, Streptococcus pneumoniae, Treponema palladium and Chlamydia
CC trachomatis. The antibacterial compound may be used as a food grain
CC supplement in livestock and poultry food composition. Note: The present
CC sequence is not shown in the specification but has been accessed from
CC GenBank using the appropriate accession number given in the specification
XX

SQ Sequence 1464 BP; 321 A; 349 C; 502 G; 292 T; 0 U; 0 Other;

Query Match 79.2%; Score 19.8; DB 5; Length 1464;
Best Local Similarity 91.3%; Pred. No. 26;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
Db 20 GCAAGTCGAACGGAAGGTCCT 42

RESULT 97

ADR90574
ID ADR90574 standard; DNA; 1469 BP.

XX ADR90574;

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XX 02-DEC-2004 (first entry)
XX M kansasii 16S rRNA gene sequence SeqID3.
XX acid-fast bacterium; differentiation; 16S rRNA; M avium complex; MAC;
XX taxonomic-tree analysis; atypical-mycobacteria; gene; ds.
XX Mycobacterium kansasii.
XX JP2004254591-A.
XX 16-SEP-2004.
XX 26-FEB-2003; 2003JP-00048654.
XX 26-FEB-2003; 2003JP-00048654.
XX (MTP) MITSUBISHI YUKA BCL KK.
XX WPI; 2004-664464/65.
XX Differentiating acid-fast bacterium e.g., Mycobacterium avium complex,
XX useful for detecting mutant of M.avium complex, and for grouping strains
XX of M.kansasii, involves detecting mutation in 16S rRNA gene of acid-fast
XX bacterium.
XX Claim 3; SEQ ID NO 3; 23pp; Japanese.
XX This invention relates to a novel method of differentiating acid-fast
XX bacterium, which involves detecting a mutation in the 16S rRNA gene of
XX the acid-fast bacterium. The method is useful for differentiating acid-
XX fast bacterium such as M avium complex (MAC) or M kansasii, in particular
XX for detecting mutants of MAC, and for grouping strains of M kansasii. The
XX method is also useful for carrying out taxonomic-tree analysis of
XX atypical-mycobacteria and enables detection of MAC accurately and
XX reliably. The present sequence is that of a Mycobacterium 16S rRNA gene
XX which may be used in the method of the invention.
XX Sequence 1469 BP; 321 A; 355 C; 502 G; 291 T; 0 U; 0 Other;
Query Match 79.2%; Score 19.8; DB 13; Length 1469;
Best Local Similarity 91.3%; Pred. No. 26;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCAAGTCGAACGGAAGGCTTT 23
DB 30 GCAAGTCGAACGGAAGGCTCT 52
RESULT 98
AAS30719
ID AAS30719 standard; DNA; 1524 BP.
XX AC AAS30719;
XX 04-DEC-2001 (first entry)
XX Mycobacterium tuberculosis 16S ribosomal gene partial sequence.
XX Mycobacterium; species-specific bacterial identification;
XX 16S ribosomal gene; ds.
XX Mycobacterium tuberculosis.
XX WO200166797-A2.
XX 13-SEP-2001.
XX 01-MAR-2001; 2001WO-US006731.
XX 03-MAR-2000; 2000US-0186840P.
XX

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PA (BECI) BECKMAN COULTER INC.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (USSH) US NAT INST OF HEALTH.
XX Fischer SH, Rampal JB, Fahle GA, Conville PS;
XX WPI; 2001-514847/56.
XX Species-specific bacterial identification, used particularly to identify
XX Mycobacterium species, involves hybridizing bacterial genus-selective or
XX specific primers to a sample.
XX Example 2; Page 42-43; 43pp; English.
XX The invention relates to a method of species-specific bacterial
XX identification, comprising hybridising a bacterial genus-selective or
XX specific primer to a sample and amplifying nucleic acids. This is
XX followed by hybridising the amplified nucleic acid to a solid phase array
XX comprising bacterial species specific probe oligonucleotides chemically
XX linked to a polymeric support in a predetermined pattern. This method is
XX used for species-specific identification of a bacterium, particularly a
XX Mycobacterium, especially M. gordonae, M. intracellulare, M. avium, M.
XX tuberculosis, M. marinum, or M. kansasii. The method provides rapid
XX identification of multiple species of Mycobacterium. AAS30686-AAS30720
XX represent Mycobacterium species-specific primers and probes used in the
XX method of the invention. The present sequence may be used in the
XX invention as a target sequence for amplification
XX Sequence 1524 BP; 333 A; 365 C; 520 G; 306 T; 0 U; 0 Other;
Query Match 79.2%; Score 19.8; DB 4; Length 1524;
Best Local Similarity 91.3%; Pred. No. 26;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCAAGTCGAACGGAAGGCTTT 23
DB 50 GCAAGTCGAACGGAAGGCTCT 72
RESULT 99
ADB61681
ID ADB61681 standard; DNA; 1536 BP.
XX AC ADB61681;
XX 04-DEC-2003 (first entry)
XX 16S rRNA of Mycobacterium tuberculosis DNA sequence.
XX enriching mRNA; high quality bacterial mRNA; bacterial gene expression;
XX poly-A tail; mRNA purification; oligo-dT capture;
XX prokaryote mRNA purification; bridging oligonucleotide; targeting region;
XX capture oligonucleotide; prokaryotic 16S rRNA; prokaryotic 23S rRNA;
XX eukaryotic 17S rRNA; eukaryotic 18S rRNA; eukaryotic 28S rRNA;
XX 28S eukaryotic rRNA bridging oligonucleotide; ds.
XX Mycobacterium tuberculosis.
XX WO2003054162-A2.
XX 03-JUL-2003.
XX 19-DEC-2002; 2002WO-US041014.
XX 20-DEC-2001; 2001US-00029397.
XX (AMBI-) AMBION INC.
XX Murphy GL, Whitley JP;
XX WPI; 2003-663255/62.
XX Depleting or isolating targeted nucleic acids e.g. rRNA, involves using a
XX

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PT bridging oligonucleotide comprising bridging region and a targeting
PT region complementary to a targeted nucleic acid, and a capture
XX oligonucleotide.
XX
PS Claim 4; Page 168-169; 208pp; English.
XX
CC This invention relates to a novel method for isolating, depleting or
CC separating a targeted nucleic acid, such as rRNA, from a sample
CC comprising targeted and non-targeted nucleic acids. It effects a way of
CC enriching for non-targeted nucleic acids such as mRNAs. Isolating
CC sufficient quantities of high quality bacterial mRNA is a demanding
CC process which impedes analysis of bacterial gene expression in the
CC presence of host cells. A small percentage of bacterial mRNAs may be poly
CC -A tailed, but these are targeted for degradation and tend to be
CC unstable. As a result, the commonly employed method for mRNA purification
CC with eukaryotic cells, oligo-dT capture, is ineffective. The present
CC invention provides an alternative, more suitable method for mRNA
CC purification from prokaryotes. The method of the invention comprises the
CC incubation of a sample with a bridging oligonucleotide (containing a
CC targeting region) and subsequently incubating with a capture
CC oligonucleotide allowing the isolation of the target from the sample. The
CC method is useful for depleting or isolating targeted nucleic acid, for
CC example rRNA such as prokaryotic 16S or prokaryotic 23S, eukaryotic 17S
CC or 18S or eukaryotic 28S rRNA, from a sample. The rRNA sequence may
CC comprise any one of 64 fully defined sequences as given in the
CC specification. The present sequence is that of a DNA sequence which
CC represents the sequence of 16S rRNA of Mycobacterium tuberculosis related
CC to the invention.
XX
SQ Sequence 1536 BP; 333 A; 366 C; 523 G; 314 T; 0 U; 0 Other;

Query Match 79.2%; Score 19.8; DB 10; Length 1536;
Best Local Similarity 91.3%; Pred. No. 26;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAAGGCCTTT 23
|||||
Db 59 GCAAGTCGAACGGAAAGGTCTCT 81

RESULT 100
ADB61682
ID ADB61682 standard; DNA; 1536 BP.
XX
AC ADB61682;
XX
DT 04-DEC-2003 (first entry)
XX
DE 16S rRNA of Escherichia coli DNA sequence.
XX
KW enriching mRNA; high quality bacterial mRNA; bacterial gene expression;
KW poly-A tail; mRNA purification; oligo-dT capture;
KW prokaryote mRNA purification; bridging oligonucleotide; targeting region;
KW capture oligonucleotide; prokaryotic 16S rRNA; prokaryotic 23S rRNA;
KW eukaryotic 17S rRNA; eukaryotic 18S rRNA; eukaryotic 28S rRNA;
KW 28S eukaryotic rRNA bridging oligonucleotide; ds.
XX
OS Escherichia coli.
XX
FN WO2003054162-A2.
XX
PD 03-JUL-2003.
XX
PF 19-DEC-2002; 2002WO-US041014.
XX
PR 20-DEC-2001; 2001US-00029397.
XX
PA (AMBI-) AMBION INC.
XX
PI Murphy GL, Whitley JP;
XX
DR WPI; 2003-663255/62.
XX

PT Depleting or isolating targeted nucleic acids e.g. rRNA, involves using a
PT bridging oligonucleotide comprising bridging region and a targeting
PT region complementary to a targeted nucleic acid, and a capture
XX oligonucleotide.
XX
PS Claim 4; Page 169; 208pp; English.
XX
CC This invention relates to a novel method for isolating, depleting or
CC separating a targeted nucleic acid, such as rRNA, from a sample
CC comprising targeted and non-targeted nucleic acids. It effects a way of
CC enriching for non-targeted nucleic acids such as mRNAs. Isolating
CC sufficient quantities of high quality bacterial mRNA is a demanding
CC process which impedes analysis of bacterial gene expression in the
CC presence of host cells. A small percentage of bacterial mRNAs may be poly
CC -A tailed, but these are targeted for degradation and tend to be
CC unstable. As a result, the commonly employed method for mRNA purification
CC with eukaryotic cells, oligo-dT capture, is ineffective. The present
CC invention provides an alternative, more suitable method for mRNA
CC purification from prokaryotes. The method of the invention comprises the
CC incubation of a sample with a bridging oligonucleotide (containing a
CC targeting region) and subsequently incubating with a capture
CC oligonucleotide allowing the isolation of the target from the sample. The
CC method is useful for depleting or isolating targeted nucleic acid, for
CC example rRNA such as prokaryotic 16S or prokaryotic 23S, eukaryotic 17S
CC or 18S or eukaryotic 28S rRNA, from a sample. The rRNA sequence may
CC comprise any one of 64 fully defined sequences as given in the
CC specification. The present sequence is that of a DNA sequence which
CC represents the sequence of 16S rRNA of Escherichia coli related to the
CC invention.
XX
SQ Sequence 1536 BP; 333 A; 366 C; 523 G; 314 T; 0 U; 0 Other;

Query Match 79.2%; Score 19.8; DB 10; Length 1536;
Best Local Similarity 91.3%; Pred. No. 26;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAAGGCCTTT 23
|||||
Db 59 GCAAGTCGAACGGAAAGGTCTCT 81

Search completed: May 19, 2006, 04:18:54
Job time : 304.729 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 02:24:46 ; Search time 1671.99 Seconds
(without alignments)
836.120 Million cell updates/sec

Title: US-10-665-708-21

Perfect score: 25

Sequence: 1 gcaagtcgaacggaaggcttctcg 25

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est3:*

3: gb_est4:*

4: gb_est5:*

5: gb_est6:*

6: gb_hnc:*

7: gb_est2:*

8: gb_est7:*

9: gb_est8:*

10: gb_est9:*

11: gb_gss1:*

12: gb_gss2:*

13: gb_gss3:*

14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21.8	87.2	657	8	CN208729 Tor9226 G
2	20.8	83.2	356	4	CD122074 ME1-0071G
3	20.2	80.8	312	7	BB241896 BB241896
4	20.2	80.8	683	14	DU818647 OG_ABA009
5	20.0	80.0	650	8	CN204419 Tor7810 G
6	20.0	80.0	874	8	CN365133 RTK1_23 G
7	20.0	80.0	885	8	CN201712 Tor1780 G
8	19.2	76.8	452	11	AQ627316 CITBI-E1-
9	19.2	76.8	540	11	AQ549361 RPCI-11-3
10	18.8	75.2	903	12	CC453191 ZMMBC034
11	18.8	75.2	910	9	DN561788 92178421
12	18.6	74.4	399	3	BQ104075 991205.e
13	18.6	74.4	513	4	CA282280 SCAGSD204
14	18.6	74.4	526	2	BM131991 TgESTzyb0
15	18.6	74.4	806	2	BI157204 602923403
16	18.4	73.6	591	8	CN207299 Tor7720 G
17	18.4	73.6	735	5	CF882404 trico88xm
18	18.4	73.6	788	4	CB908942 trico88xm
19	18.4	73.6	817	8	CN207539 Tor7952 G

DR421359	CHHS5E05	DR421359	907	10	DR421359
DY091901	010128BEM	DY091901	327	10	DY091901
BY457153	BY457153	BY457153	421	4	BY457153
DN526979	1271790 M	DN526979	475	9	DN526979
CA934753	MTUSTS.P2	CA934753	609	4	CA934753
CB378019	rq08a11.y	CB378019	630	4	CB378019
CK950118	4075090 B	CK950118	719	5	CK950118
DN283722	1183944 M	DN283722	835	9	DN283722
CR077081	Reverse s	CR077081	835	14	CR077081
DN282351	1182408 M	DN282351	843	9	DN282351
DU746898	ASNC3551	DU746898	906	14	DU746898
ALJ39578	T3 end of	ALJ39578	929	14	CNS06FX8
DM640758	CLJ372-G0	DM640758	943	10	DM640758
ALJ392423	T3 end of	ALJ392423	994	14	CNS06CEP
DU760208	ASNG3054	DU760208	1043	14	DU760208
DQ213078	Taeniopyg	DQ213078	1052	6	DQ213078
CL645653	CH213-99C	CL645653	1242	13	CL645653
BF537535	602553182	BF537535	938	7	BF537535
BX342644	BX342644	BX342644	994	4	BX342644
W10183	ma43f03.r1	W10183	223	10	W10183
AA815626	vt03c06.r	AA815626	273	1	AA815626
BG147420	mac03g07	BG147420	337	2	BG147420
CB705072	AMGNNUC.S	CB705072	347	4	CB705072
W65078	me01d06.r1	W65078	357	10	W65078
CF425395	lad53e09	CF425395	384	5	CF425395
ALJ36386	ALJ36386	ALJ36386	400	1	ALJ36386
AI050353	ub29f09.r	AI050353	419	1	AI050353
AI713707	UI-R-AGI-	AI713707	420	1	AI713707
AA818546	UI-R-A0-a	AA818546	424	1	AA818546
BU743860	mai49f01	BU743860	444	3	BU743860
W47680	mc89h02.r1	W47680	446	10	W47680
AI593186	vt03c06.y	AI593186	473	1	AI593186
CN692701	E0326F01-	CN692701	492	8	CN692701
AA014214	mh18g10.r	AA014214	500	1	AA014214
AA509546	vh50c08.r	AA509546	502	1	AA509546
CG036380	PULV37TD	CG036380	502	12	CG036380
BE863637	UI-N-BHO-	BE863637	527	7	BE863637
BQ569727	gil33c11.y	BQ569727	532	3	BQ569727
BF022607	uy51d11.y	BF022607	542	7	BF022607
AI603423	UI-R-ACI-	AI603423	543	1	AI603423
AZ024985	RPCI-23-3	AZ024985	566	11	AZ024985
CN692527	E0324C02-	CN692527	571	8	CN692527
BE288370	601094841	BE288370	577	9	BE288370
DN215604	MEST971.D	DN215604	600	9	DN215604
DR968997	ZM_BFB009	DR968997	602	10	DR968997
AW914801	EST346105	AW914801	613	7	AW914801
BI648126	603278444	BI648126	622	2	BI648126
CA734384	jbo1e11.y	CA734384	635	9	CA734384
BI331633	602983168	BI331633	641	2	BI331633
CF897511	A0226B05-	CF897511	641	5	CF897511
DV169729	ZM_BFB016	DV169729	643	10	DV169729
BF237353	602025026	BF237353	647	7	BF237353
CF898433	A0239B05-	CF898433	651	5	CF898433
DV023955	ZM_BFB014	DV023955	680	10	DV023955
CN525338	UI-N-HKO-	CN525338	682	8	CN525338
DT945027	ZM_BFB013	DT945027	685	10	DT945027
CA429338	UI-N-HWO-	CA429338	695	8	CA429338
BI649774	603279966	BI649774	700	2	BI649774
DV541234	ZM_BFB023	DV541234	710	10	DV541234
DT954257	ZM_BFB012	DT954257	711	10	DT954257
BF099995	601752156	BF099995	714	10	DT945215
BQ445033	UI-N-ERO-	BQ445033	729	3	BQ445033
CO383984	AGENCOURT	CO383984	738	8	CO383984
BI414831	602990771	BI414831	739	2	BI414831
EX855983	EX855983	EX855983	740	4	EX855983
BY732037	BY732037	BY732037	745	4	BY732037
DV942547	1000137-E	DV942547	746	10	DV942547
DR794419	ZM_BFB001	DR794419	752	10	DR794419
DV164476	ZM_BFB016	DV164476	753	10	DV164476
DR786717	ZM_BFB000	DR786717	777	10	DR786717
DR954333	ZM_BFB004	DR954333	777	10	DR954333
DV164117	ZM_BFB016	DV164117	780	10	DV164117

93	17.8	71.2	808	4	CB953248	CB953248	AGENCOURT	166	17.6	70.4	410	2	BI275046	BI275046	UI-R-CX0-
94	17.8	71.2	816	10	DR794420	ZM_BF001	167	17.6	70.4	410	4	BY435007	BY435007	BY435007	
95	17.8	71.2	820	10	DV164477	ZM_BF016	168	17.6	70.4	410	5	CJ210358	CJ210358	CJ210358	
96	17.8	71.2	824	10	DY361640	ZO_E0000	169	17.6	70.4	414	4	BY458657	BY458657	BY458657	
97	17.8	71.2	827	10	DR786718	ZM_BF000	170	17.6	70.4	416	3	BQ748621	UJ-M-FA0-	BQ748621	
98	17.8	71.2	848	10	DR966931	ZM_BF008	171	17.6	70.4	417	5	CJ210067	CJ210067	CJ210067	
99	17.8	71.2	851	10	DT876921	AGENCOURT	172	17.6	70.4	421	1	AA655960	vs49f08.r	AA655960	
100	17.8	71.2	856	2	BI664538	603290164	173	17.6	70.4	422	1	AI043633	UI-R-C0-j	AI043633	
101	17.8	71.2	862	5	CF551692	AGENCOURT	174	17.6	70.4	423	5	CJ317470	CJ317470	CJ317470	
102	17.8	71.2	874	3	BU522312	AGENCOURT	175	17.6	70.4	426	1	AV011735	AV011735	AV011735	
103	17.8	71.2	891	10	DT942318	ZM_BF012	176	17.6	70.4	434	5	CJ228806	CJ228806	CJ228806	
104	17.8	71.2	894	7	BE367787	601217408	177	17.6	70.4	435	3	BU961211	AGENCOURT	BU961211	
105	17.8	71.2	906	3	BO944677	AGENCOURT	178	17.6	70.4	443	4	BY452887	BY452887	BY452887	
106	17.8	71.2	912	10	DR815819	ZM_BF004	179	17.6	70.4	444	4	BY432547	BY432547	BY432547	
107	17.8	71.2	918	2	BG247267	602360162	180	17.6	70.4	447	4	CA563760	K0317010-	CA563760	
108	17.8	71.2	945	10	DV062398	NEONATAL	181	17.6	70.4	452	8	CR470938	CR470938	CR470938	
109	17.8	71.2	995	12	CL029182	CH216-28J	182	17.6	70.4	462	4	BY599571	BY599571	BY599571	
110	17.8	71.2	1199	9	DR045951	FP-11_G06	183	17.6	70.4	465	1	AI235898	EST232460	AI235898	
111	17.6	70.4	121	11	AZ891427	RPCI-24-1	184	17.6	70.4	466	7	BB833557	BB833557	BB833557	
112	17.6	70.4	193	1	AA204210	mu60h11.r	185	17.6	70.4	468	1	AI372548	EST175439	AI372548	
113	17.6	70.4	233	3	BQ322138	FM3-CT081	186	17.6	70.4	473	7	BB283360	BB283360	BB283360	
114	17.6	70.4	239	1	AV366949	AV366949	187	17.6	70.4	476	9	DN856279	4153009 B	DN856279	
115	17.6	70.4	242	3	BU899169	ma146g11.	188	17.6	70.4	478	10	W54232	mc94c12.r1	W54232	
116	17.6	70.4	247	1	AV314699	AV314699	189	17.6	70.4	485	1	AA832954	uc93d10.r	AA832954	
117	17.6	70.4	247	7	BB015618	BB015618	190	17.6	70.4	490	4	CA834145	610733 MA	CA834145	
118	17.6	70.4	256	1	AV264774	AV264774	191	17.6	70.4	490	4	CB437180	684620 MA	CB437180	
119	17.6	70.4	257	1	AV140604	AV140604	192	17.6	70.4	490	4	CB438188	686678 MA	CB438188	
120	17.6	70.4	266	1	AV268640	AV268640	193	17.6	70.4	493	1	AJ678405	AJ678405	AJ678405	
121	17.6	70.4	270	1	AV074580	AV074580	194	17.6	70.4	496	3	BU579473	im85b11.y	BU579473	
122	17.6	70.4	277	1	AV105856	AV105856	195	17.6	70.4	496	4	BY448707	BY448707	BY448707	
123	17.6	70.4	279	1	AV078336	AV078336	196	17.6	70.4	499	2	BM121724	L0500H07-	BM121724	
124	17.6	70.4	282	1	AV351905	AV351905	197	17.6	70.4	502	2	CX598149	CT020020A	CX598149	
125	17.6	70.4	290	3	BQ840493	ma68h007.	198	17.6	70.4	504	7	AW361919	FM3-CT026	AW361919	
126	17.6	70.4	291	1	AV066368	AV066368	199	17.6	70.4	504	9	DN363141	LI83628-0	DN363141	
127	17.6	70.4	293	1	AV144872	AV144872	200	17.6	70.4	505	2	BM232039	K0317F10-	BM232039	
128	17.6	70.4	293	7	BB516293	BB516293	201	17.6	70.4	507	1	AA000190	mg33d09.r	AA000190	
129	17.6	70.4	295	7	BB028015	BB028015	202	17.6	70.4	509	5	CD790755	EST662116	CD790755	
130	17.6	70.4	295	7	BB511052	BB511052	203	17.6	70.4	517	5	CK283328	CK283328	CK283328	
131	17.6	70.4	297	7	BB031763	BB031763	204	17.6	70.4	517	5	CK840680	UI-R-C0-j	CK840680	
132	17.6	70.4	300	1	AV147017	AV147017	205	17.6	70.4	521	11	B61927	TL91919F 1A	B61927	
133	17.6	70.4	305	1	AV088825	AV088825	206	17.6	70.4	524	7	AW435159	UI-R-BU0p	AW435159	
134	17.6	70.4	305	1	AV258314	AV258314	207	17.6	70.4	529	1	AI838320	UI-M-A00-	AI838320	
135	17.6	70.4	305	4	BY432536	BY432536	208	17.6	70.4	529	2	BG012793	QV1-GN034	BG012793	
136	17.6	70.4	305	8	CX2113854	MNS20950	209	17.6	70.4	532	7	BF017987	uw85h08.x	BF017987	
137	17.6	70.4	311	1	AV310522	AV310522	210	17.6	70.4	539	1	BE989007	UI-M-CG0p	BE989007	
138	17.6	70.4	312	1	BB361078	BB361078	211	17.6	70.4	569	1	AA542056	vk43d12.r	AA542056	
139	17.6	70.4	319	1	AA374314	EST86475	212	17.6	70.4	569	5	CK902574	im95b11.y	CK902574	
140	17.6	70.4	324	1	AV216218	AV216218	213	17.6	70.4	574	2	BM383870	BM383870	BM383870	
141	17.6	70.4	334	8	C0939094	UMC-pd20f	214	17.6	70.4	580	5	CF968672	laq10g04.	CF968672	
142	17.6	70.4	335	7	AW014662	UI-H-B10p	215	17.6	70.4	596	3	BM878400	if43e03.x	BM878400	
143	17.6	70.4	343	7	AW524972	UI-R-BU0p	216	17.6	70.4	600	2	EG806032	2013-13 M	EG806032	
144	17.6	70.4	353	4	CB779991	AMGNNUC:S	217	17.6	70.4	601	1	AA930910	v255d01.r	AA930910	
145	17.6	70.4	353	10	DR409871	EST000056	218	17.6	70.4	601	3	CB735102	MONO1_16-	CB735102	
146	17.6	70.4	359	4	BY445959	BY445959	219	17.6	70.4	620	4	BM337903	laa30h09.	BM337903	
147	17.6	70.4	361	7	BB991892	UI-M-B21-	220	17.6	70.4	656	14	DE193783	Branchios	DE193783	
148	17.6	70.4	362	4	BY426276	BY426276	221	17.6	70.4	660	11	BH794488	ME_M8a000	BH794488	
149	17.6	70.4	369	4	BY663759	BY663759	222	17.6	70.4	674	9	DN120598	1130627 M	DN120598	
150	17.6	70.4	371	1	AA796799	vp31c07.r	223	17.6	70.4	674	9	DN120950	1121011 M	DN120950	
151	17.6	70.4	377	1	BB791326	BB791326	224	17.6	70.4	675	4	CD058105	HO05015	CD058105	
152	17.6	70.4	380	2	BB803041	BB803041	225	17.6	70.4	675	5	CJ746041	CJ746041	CJ746041	
153	17.6	70.4	390	2	BG146385	mab91b09.	226	17.6	70.4	676	4	BY755829	BY755829	BY755829	
154	17.6	70.4	390	14	DE200714	Branchios	227	17.6	70.4	680	9	DN116917	1116534 M	DN116917	
155	17.6	70.4	392	4	BY625882	BY625882	228	17.6	70.4	681	7	AW967239	EST379313	AW967239	
156	17.6	70.4	394	4	CA976745	AGENCOURT	229	17.6	70.4	684	9	DR027116	bda010011	DR027116	
157	17.6	70.4	395	4	BY626963	BY626963	230	17.6	70.4	694	2	B1184236	UNL-P-PN-	B1184236	
158	17.6	70.4	398	4	BY434099	BY434099	231	17.6	70.4	697	2	EG477861	603522512	EG477861	
159	17.6	70.4	400	4	BY420961	BY420961	232	17.6	70.4	698	3	BU291509	603608101	BU291509	
160	17.6	70.4	401	1	AI372546	EST175437	233	17.6	70.4	713	2	BG478164	602522813	BG478164	
161	17.6	70.4	401	4	BY625353	BY625353	234	17.6	70.4	721	7	BE384503	601277871	BE384503	
162	17.6	70.4	405	8	CO053683	esc_k_bre	235	17.6	70.4	725	14	CR921765	Sus_8c0rof	CR921765	
163	17.6	70.4	409	5	CJ199163	CJ199163	236	17.6	70.4	744	9	CK605206	CT02040B2	CK605206	
164	17.6	70.4	409	7	BE173992	QV1-HT057	237	17.6	70.4	755	4	BX667075	BX667075	BX667075	
165	17.6	70.4	409	10	R49381	yg60b05.e1	238	17.6	70.4	763	2	BG764347	602736263	BG764347	

c 239	17.6	70.4	770	1	AU167594	AU167594	AU167594
240	17.6	70.4	772	3	BQ716203	AGENCOURT	
241	17.6	70.4	778	5	CJ457834	CJ457834	
242	17.6	70.4	790	2	BG767613	BG767613	
243	17.6	70.4	792	8	CV650066	B07_010c	
244	17.6	70.4	792	8	CX242558	NMA00345-	
245	17.6	70.4	794	3	BU962186	AGENCOURT	
246	17.6	70.4	798	2	BI224442	602940807	
c 247	17.6	70.4	801	14	AY410663	Mus muscu	
c 248	17.6	70.4	805	12	CE2113009	tigr-gss-	
c 249	17.6	70.4	812	2	BG426521	602493431	
c 250	17.6	70.4	813	9	DR105701	JHU095C03	
c 251	17.6	70.4	822	5	CD789253	EST660614	
c 252	17.6	70.4	839	9	DR030570	bda020220	
253	17.6	70.4	842	2	BI415736	602988821	
254	17.6	70.4	848	2	BG769503	602742479	
255	17.6	70.4	851	5	CD790756	EST662117	
c 256	17.6	70.4	855	3	BU239599	603321930	
c 257	17.6	70.4	856	3	BU457366	603768264	
c 258	17.6	70.4	859	5	CD789655	EST661016	
c 259	17.6	70.4	879	3	BU853415	AGENCOURT	
c 260	17.6	70.4	882	5	CD793487	EST664848	
261	17.6	70.4	907	2	BI526517	602924939	
c 262	17.6	70.4	916	5	CD782407	EST653768	
263	17.6	70.4	918	10	DV043823	DAY10_16	
c 264	17.6	70.4	920	13	DU046239	158666 To	
265	17.6	70.4	940	12	CC597932	ZMMBBc040	
266	17.6	70.4	942	10	DV043460	DAY10_15	
267	17.6	70.4	943	2	BG761740	602717935-	
268	17.6	70.4	949	6	AK009715	Mus muscu	
269	17.6	70.4	951	7	BF688762	602184926	
c 270	17.6	70.4	952	6	AK160217	Mus muscu	
c 271	17.6	70.4	953	12	CL065269	CH216-104	
272	17.6	70.4	955	6	AK166410	Mus muscu	
273	17.6	70.4	955	2	BI903760	603167822	
274	17.6	70.4	957	6	AK011011	Mus muscu	
275	17.6	70.4	967	3	BU509953	AGENCOURT	
c 276	17.6	70.4	996	12	CC934245	ZMMBBc054	
c 277	17.6	70.4	1003	14	CNS04EXR	AL287640 Tetraodon	
c 278	17.6	70.4	1019	14	DU772735	APKG3109.	
c 279	17.6	70.4	1057	3	BQ057059	AGENCOURT	
280	17.6	70.4	1085	3	BM803090	AGENCOURT	
281	17.6	70.4	1535	6	CR596731	full-leng	
282	17.6	70.4	1610	6	CR591390	full-leng	
283	17.6	70.4	1634	6	CR599521	full-leng	
284	17.6	70.4	1641	6	CR620180	full-leng	
285	17.6	70.4	1669	6	CR619642	full-leng	
286	17.6	70.4	1673	6	CR614333	full-leng	
287	17.6	70.4	1699	6	CR623628	full-leng	
288	17.6	70.4	1715	6	CR605450	full-leng	
289	17.6	70.4	1722	6	CR621364	full-leng	
290	17.6	70.4	1723	6	CR594015	full-leng	
291	17.6	70.4	1723	6	CR603520	full-leng	
292	17.6	70.4	1728	6	CR605258	full-leng	
293	17.6	70.4	1740	6	CR613057	full-leng	
294	17.6	70.4	1741	6	CR622122	full-leng	
295	17.6	70.4	1765	6	CR592980	full-leng	
296	17.6	70.4	1772	6	CR620296	full-leng	
297	17.6	70.4	1802	6	CR859228	Pongo pyg	
298	17.6	70.4	1827	6	AY609775	Sus scrof	
299	17.6	70.4	1832	6	CR592602	full-leng	
300	17.6	70.4	1986	6	CR605577	full-leng	

ALIGNMENTS

RESULT 1
 CN208729
 LOCUS Tor226 Gametophyte rehydration Library Tortula ruralis cDNA, mRNA
 DEFINITION
 ACCESSION CN208729

VERSION CN208729.1 GI:46905460
 KEYWORDS EST.
 SOURCE Tortula ruralis
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Dicranidae; Pottiaceae; Tortula.
 REFERENCE 1 (Bases 1 to 657)
 AUTHORS Oliver, M.J., Dowd, S.E., Zaragosa, J., Mauget, S.A. and Payton, P.R.
 TITLE The rehydration transcriptome of the desiccation-tolerant bryophyte Tortula ruralis: transcript classification and analysis
 JOURNAL BMC Genomics 5 (1), 89 (2004)
 PUBMED 15546486
 COMMENT Contact: Oliver Melvin J
 Plant Stress Lab
 USDA-ARS
 3810 4th St, Lubbock, TX 79415, USA
 Tel: 806-749-5560
 Fax: 806-723-5272
 Email: moliver@lbrk.ars.usda.gov
 PCR Primers
 FORWARD: GTTTCCAGTCAGTCAGC
 BACKWARD: CAGGAACAGCTATGAC
 Location/Qualifiers
 1..657
 /organism="Tortula ruralis"
 /mol_type="mRNA"
 /db_xref="taxon:38588"
 /clone_lib="Gametophyte rehydration Library"
 /note="Organ: Green Gametophyte; Vector: pSport1; Site_1: Sali; Site_2: NotI"

ORIGIN
 Query Match 87.2%; Score 21.8; DB 8; Length 657;
 Best Local Similarity 92.0%; Pred. No. 25;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 GCAAGTCGAACGGAAAGCCCTTCG 25
 |||||
 Db 239 GCAAGTCGAGCGAAAGGCCCTTCG 263

RESULT 2
 CD122074/c
 LOCUS
 DEFINITION ME1-0071G-Al60-E04-1.B ME1-0071 Schistosoma mansoni cDNA clone
 ACCESSION CD122074
 VERSION CD122074.1 GI:34660126
 KEYWORDS EST.
 SOURCE Schistosoma mansoni
 ORGANISM Schistosoma mansoni
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 Strigidae; Schistosomatidae; Schistosomidae.
 1 (Bases 1 to 356)
 REFERENCE Verjovski-Almeida, S., DeMarco, R., Martins, E.A.L., Guimaraes, P.E.M.,
 Ojopi, E.P.B., Paquella, A.C.M., Piazza, J.P., Nishiyama, M.Y. Jr.,
 Kitajima, J.P., Adamson, R.E., Ashton, P.D., Bonaldo, M.F.,
 Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho, P.L.,
 Leite, R.A., Malaquias, L.C.C., Marques, R.C.P., Miyasato, P.A.,
 Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A.,
 Sa, R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T.,
 Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M.,
 Seubal, J.C., Leite, L.C.C. and Dias-Neto, E.
 Transcriptional analysis of the acoelomate human parasite Schistosoma mansoni
 Nat. Genet. 35 (2), 148-157 (2003)
 JOURNAL 12973350
 PUBMED
 COMMENT Other ESTs: ME1-0071G-Al60-E04-2.B
 Contact: Dr. Sergio Verjovski-Almeida
 Departamento de Bioquímica
 Instituto de Química - Universidade de São Paulo
 Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 São Paulo - SP,
 Brasil

Tel: +55-11-3091-2173
 Fax: +55-11-3091-2186
 Email: verjoe@iq.usp.br

This sequence was derived from the FAPESP Schistosoma mansoni EST Genome Project. All sequences in the project were assembled and annotated. This entry and all the assembled sequences can be seen in the following URL <http://bioinfo.iq.usp.br/schisto/>
 Plate: ME1-0071G-A160 row: 4 column: E.

FEATURES

Location/Qualifiers
 1..356
 /organism="Schistosoma mansoni"
 /mol_type="mRNA"
 /db_xref="taxon:6183"
 /clone="ME1-0071G-A160-E04.B"
 /sex="mixed pool"
 /dev_stage="egg"
 /lab_host="Mus musculus"
 /clone_lib="ME1-0071"
 /note="Vector: pGEM T-easy"

ORIGIN

Query Match 83.2%; Score 20.8; DB 4; Length 356;
 Best Local Similarity 91.7%; Pred. No. 70;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCTTTC 24

Db 295 GCAAAGTCGACGGAAGGCCTTC 272

RESULT 3

BB241896/C

LOCUS BB241896 RIKEN full-length enriched, 3 days neonate thymus Mus
 DEFINITION musculus cDNA clone A630089H08 3', mRNA sequence.

ACCESSION BB241896

VERSION BB241896.1 GI:8934642

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Konno,H., Alzawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kuakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tomimaga,N., Toya,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.

RIKEN Mouse ESTs (Konno,H., et al.)

Unpublished (2000)

TITLE

JOURNAL

COMMENT

Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216

Email: genome-res@sc.riken.jp, URL:<http://genome.gsc.riken.jp/>

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Thermoalabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh,M., Kitsuunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,

Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
 Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
 Carninci,P. and Hayashizaki,Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES

Location/Qualifiers
 1..312
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="A630089H08"
 /tissue_type="thymus"
 /dev_stage="3 days neonate"
 /lab_host="DH10B"
 /clone_lib="RIKEN full-length enriched, 3 days neonate thymus"

/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'-GAGAGAGAGATCCAAAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5'-GAGAGAGATCTCGAGTTAATAATATCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

ORIGIN

Query Match 80.8%; Score 20.2; DB 7; Length 312;
 Best Local Similarity 88.0%; Pred. No. 1.3e+02;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCTTTCG 25

Db 75 GTAAAGTCCTAACCGAAGGCCTTACG 51

RESULT 4

DUB18647

LOCUS DUB18647 683 bp DNA linear GSS 13-DEC-2005
 DEFINITION OG_Aba0092L10.r OG_Aba Oryza granulata genomic clone OG_Aba0092L10 3', genomic survey sequence.

ACCESSION DUB18647

VERSION DUB18647.1 GI:83614306

KEYWORDS GSS.

SOURCE Oryza granulata

ORGANISM Oryza granulata

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

SanMiguel,P., Westerman,R., Kim,H., Yu,Y., Wissotski,M., Yost,D., Scum,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C., Wing,R. and Jackson,S.A.

OMAP (Oryza Map Alignment Project) - Purdue University

JOURNAL

COMMENT

Contact: Scott A. Jackson

Jackson Laboratory

Purdue University

915 W. State St., West Lafayette, IN 47907, USA

Tel: 7654963621

Fax: 7654967255

QY 1 GCAAGTCGAACGGAAAGCC 20

Db

RESULT 7
CN201712
LOCUS
DEFINITION Tort1780 Gametophyte rehydration Library Tortula ruralis cDNA, mRNA
sequence.
ACCESSION CN201712
VERSION CN201712
KEYWORDS CN201712.1 GI:46898443
SOURCE EST.
ORGANISM Tortula ruralis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Dicranidae; Pottiales; Pottiaceae; Tortula.
REFERENCE 1 (bases 1 to 885)
AUTHORS Oliver, M.J., Dowd, S.E., Zaragosa, J., Mauget, S.A. and Payton, P.R.
TITLE The rehydration transcriptome of the desiccation-tolerant bryophyte
Tortula ruralis: transcript classification and analysis
JOURNAL BMC Genomics 5 (1), 89 (2004)
PUBMED 15546486
COMMENT Contact: Oliver Melvin J
Plant Stress Lab
USDA-ARS
3810 4th St, Lubbock, TX 79415, USA
Tel: 806-749-5560
Fax: 806-723-5272
Email: moliver@lbrk.ars.usda.gov
PCR Primers
FORWARD: GTTTTCCAGTCACGAC
BACKWARD: CAGAAACAGCTATGAC.
Location/Qualifiers
1..885
/organism="Tortula ruralis"
/db_xref="taxon:38588"
/clone_lib="Gametophyte rehydration Library"
/note="Organ: Green Gametophyte; Vector: pSport1; Site_1:
Salt; Site_2: NoI"

FEATURES
source
Query Match 80.0%; Score 20; DB 8; Length 885;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAAGTCGACGGAAAGGCC 20
Db 53 GCAAGTCGACGGAAAGGCC 72

ORIGIN
Query Match 80.0%; Score 20; DB 8; Length 885;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAAGTCGACGGAAAGGCC 20
Db 53 GCAAGTCGACGGAAAGGCC 72

RESULT 8
AQ627316
LOCUS
DEFINITION AQ627316 452 bp DNA linear GSS 16-JUN-1999
CITBI-EI-2650I13.TR CITBI-EI Homo sapiens genomic clone 2650I13,
genomic survey sequence.
ACCESSION AQ627316
VERSION AQ627316.1 GI:5089708
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 452)
AUTHORS Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and
Venter, J.C.
TITLE Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
Map Building
JOURNAL Unpublished (1997)
COMMENT Other GSSs: CITBI-EI-2650I13.TF
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers
1..452
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="2650I13"
/sex="male"
/cell_type="sperm"
/clone_lib="CITBI-EI"
/notes="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
CalTech Human BAC Library D"

FEATURES
source

ORIGIN

Query Match 76.8%; Score 19.2; DB 11; Length 452;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GCAAGTCGACGGAAAGGCCCTTC 24
Db 191 GCAAGTCGACCTGAAAGGCCCTTC 214

RESULT 9
AQ549361
LOCUS

DEFINITION AQ549361 540 bp DNA linear GSS 28-MAY-1999
RPCI-11-371H1.TV RPCI-11 Homo sapiens genomic clone RPCI-11-371H1,
genomic survey sequence.
ACCESSION AQ549361
VERSION AQ549361.1 GI:4908538
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 540)
Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and
Venter, J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
Unpublished (1997)
Other GSSs: RPCI-11-371H1.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieterdejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1..540
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7642248"
/db_xref="taxon:9606"
/clone="RPCI-11-371H1"
/sex="Male"

FEATURES
source

ORIGIN

```

/clone_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
RPCI11 Human Male BAC Library"

ORIGIN

Query Match          76.8%;   Score 19.2;   DB 11;   Length 540;
Best Local Similarity 87.5%;   Pred. No. 4.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  1  GCAAGTCGAACGGAAGGCGCTTTC 24
      |||||  |||||  |||||  |||||  |||||
Db   171  GCAAGTGGACCTGAAGGCGCTTTC 194

RESULT 10
CC453191/c
LOCUS      CC453191          903 bp      DNA      linear      GSS 22-MAY-2003
DEFINITION ZMMBbc0347A07f ZMMBbc Zea mays genomic clone ZMMBbc0347A07 5',
            genomic survey sequence.
ACCESSION  CC453191
VERSION     CC453191.1  GI:31000754
KEYWORDS   GSS.
SOURCE     Zea mays
            Zea mays
ORGANISM   Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 903)
AUTHORS    Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
            Rouzard,K., Fuks,G., Yu,Y., Wang,R. and Messing,J.
TITLE      Sequencing of the maize genome at PGRI (2003b)
JOURNAL    Unpublished (2003)
COMMENT    Contact: Bharti,A.K.
            Dr.Joachim Messing's lab
            The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
            University
            190 Frelinghuysen Road, Piscataway, NJ 08854, USA
            Tel: 732 445 3801
            Fax: 732 445 5735
            Email: bharti@waksman.rutgers.edu
            Seq primer: T7
            Class: BAC ends
            High quality sequence start: 398.
FEATURES   Location/Qualifiers
            source          1..903
            /organism="Zea mays"
            /mol_type="genomic DNA"
            /cultivar="B73"
            /db_xref="taxon:4577"
            /clone="ZMMBbc0347A07"
            /lab_host="E. coli DH10B"
            /clone_lib="ZMMBbc"
            /note="Vector: pTARBAC1.3; Site 1: BamHI; Site 2: BamHI"

ORIGIN

Query Match          75.2%;   Score 18.8;   DB 12;   Length 903;
Best Local Similarity 90.9%;   Pred. No. 6.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2  CAAGTCGAACGGAAGGCGCTTT 23
      |||||  |||||  |||||  |||||  |||||
Db   75  CAAGTGTGATCGGAAGGCGCTTT 54

RESULT 11
DN561788
LOCUS      DN561788          910 bp      mRNA      linear      EST 14-MAR-2005
DEFINITION 92178421 Sea Urchin primary mesenchyme cell cDNA library
            Strongylocentrotus purpuratus cDNA clone PMCSPR2-102A16 5', mRNA
            sequence.
ACCESSION  DN561788
VERSION     DN561788.1  GI:61120827

/clone_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
RPCI11 Human Male BAC Library"

ORIGIN

Query Match          75.2%;   Score 18.8;   DB 9;   Length 910;
Best Local Similarity 90.9%;   Pred. No. 6.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  4  ACTCGAACGGAAGGCGCTTTC 25
      |||||  |||||  |||||  |||||  |||||
Db   790  AGCGCAACGGAAGGCGCTTTC 811

RESULT 12
BQ104075
LOCUS      BQ104075          399 bp      mRNA      linear      EST 16-APR-2002
DEFINITION gg1205.e Rose Petals (Golden Gate) Lambda Zap Express Library Rosa
            hybrid cultivar cDNA clone gg1205.e 5', mRNA sequence.
ACCESSION  BQ104075
VERSION     BQ104075.1  GI:20153737
KEYWORDS   EST.
SOURCE     Rosa hybrid cultivar
            Rosa hybrid cultivar
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.
            Guterman,I., Shalit,M., Menda,N., Piestun,D., Dafny-Yelin,M.,
            Shalev,G., Bar,E., Davydov,O., Ovadis,M., Emanuel,M., Wang,J.,
            Adam,Z., Fichtersky,E., Lewinsohn,E., Zamir,D., Vainstein,A. and
            Weiss,D.
REFERENCE  1 (bases 1 to 399)
AUTHORS    Guterman,I., Shalit,M., Menda,N., Piestun,D., Dafny-Yelin,M.,
            Shalev,G., Bar,E., Davydov,O., Ovadis,M., Emanuel,M., Wang,J.,
            Adam,Z., Fichtersky,E., Lewinsohn,E., Zamir,D., Vainstein,A. and
            Weiss,D.
TITLE      Rose Scent: Genomics Approach to Discovering Novel Floral
            Fragrance-Related Genes
JOURNAL    Plant Cell 14 (10), 2325-2338 (2002)
COMMENT    Contact: Naama Menda
            Petal Genomics
            Faculty of Agricultural, Food and Environmental Quality Sciences,
            The Hebrew University of Jerusalem
            P.O. Box 12, Rehovot, 76100, Israel

```


Tel: 972 8 9489 683
 Fax: 972 8 9468 265
 Email: shaham@agri.huji.ac.il
 Seq primer: T3 forward.

FEATURES

source

```

1. .399
/organism="Rosa hybrid cultivar"
/mol_type="mRNA"
/strain="Golden Gate"
/db_xref="taxon:128735"
/clone="gg1205.e"
/tissue_type="Petals"
/dev_stage="Young open flower at stage four"
/clone_lib="Rose Petals (Golden Gate) Lambda Zap Express Library"
/note="Vector: pBKCWV; Site_1: EcoRI; Site_2: XhoI"

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ORIGIN

```

Query Match          74.4%; Score 18.6; DB 3; Length 399;
Best Local Similarity 84.0%; Pred. No. 7.8e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 GCAAGTCGAACGGAAGCCCTTCG 25
      ||||| ||||| ||||| ||||| |||||
Db 262 GCAAGTTGACCGGAATGCGCTTCG 286

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RESULT 13

CA282280

LOCUS

```

DEFINITION CA282280.513 bp mRNA linear EST 26-SEP-2003
            SCAGSD2042H09, g SD2 Saccharum officinarum cDNA clone SCAGSD2042H09
            5', mRNA sequence.

```

ACCESSION

CA282280

VERSION

CA282280.1

KEYWORDS

GI:36013534

SOURCE

Saccharum officinarum

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.

1 (bases 1 to 513)

Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.

The libraries that made SUCEST

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: parruda@unicamp.br

Clone distribution: clone distribution information can be found

through the Brazilian Clone Collection Center (BCCC) at

http://www.bcccenter.fcav.unesp.br

Plate: 042 row: H column: 09

Seq primer: T7 Promoter Primer.

Location/Qualifiers

1. .513

/organism="Saccharum officinarum"

/mol_type="mRNA"

/db_xref="taxon:4547"

/clone="SCAGSD2042H09"

/lab_host="DH10B"

/clone_lib="SD2"

/note="Organ: Developing seeds (small insert library); Vector: pSport1; Site 1: SalI; Site 2: NotI; An

unidirectional cDNA library generated from [Developing

seeds (small insert library)]. cDNA was prepared from

polyA+ mRNA using SuperScript Plasmid System kit

(Invitrogen). The double-strand cDNAs were fractionated

in a sepharose CL-2B 40cm-columns and fragments sizing

between 0.8 and 1.5 Kb were directionally cloned into the

vector. Details of each source of RNA and library construction can be obtained at <http://sucest.lad.ic.unicamp.br/public>

ORIGIN

```

Query Match          74.4%; Score 18.6; DB 4; Length 513;
Best Local Similarity 84.0%; Pred. No. 8e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 GCAAGTCGAACGGAAGCCCTTCG 25
      ||||| ||||| ||||| ||||| |||||
Db 27 GCAAGTCGAACGGAAGCCCTTCG 51

```

RESULT 14

BM131991/c

LOCUS

```

DEFINITION BM131991.526 bp mRNA linear EST 27-NOV-2001
            TgESTzyb05b12.y1 TGRH Tachyzoite Subtracted cDNA Library Toxoplasma gondii cDNA clone TgESTzyb05b12.y1 5', similar to TR:O15793 O15793
            STRAIN DD2 HEAT SHOCK PROTEIN 86 ;, mRNA sequence.

```

ACCESSION

BM131991

VERSION

BM131991.1

KEYWORDS

GI:17126543

SOURCE

Toxoplasma gondii

ORGANISM

Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae; Toxoplasma.

1 (bases 1 to 526)

Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajioke, J.A., White, M., Clifton, S., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Waterston, R. and Wilson, R.

Toxoplasma EST Project

Unpublished (2001)

Contact: Clifton, S.

Toxoplasma EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: toxo@watson.wustl.edu

Contact David Sibley (toxost@borcim.wustl.edu) for further

information relating to organism, libraries, or clone availability.

Seq primer: -40RP from Gibco

High quality sequence stop: 421.

Location/Qualifiers

1. .526

/organism="Toxoplasma gondii"

/mol_type="mRNA"

/strain="RH (Type I)"

/db_xref="taxon:5811"

/clone="TgESTzyb05b12.y1"

/dev_stage="Tachyzoite"

/lab_host="DH10B (GeneHog, Invitrogen, Inc.)"

/clone_lib="TGRH Tachyzoite Subtracted cDNA Library"

/note="Vector: pBluscript SK-; Site 1: EcoRI; Site 2:

XhoI; Toxoplasma RH strain tachyzoites were grown in human

foreskin fibroblast cultures in vitro. The library was

originally constructed by K.L.Wan, Cambridge University.

cDNAs were synthesized from polyA RNAs by oligo d(T)

priming and directionally cloned into the EcoRI to XhoI

sites of the Lambda ZapII vector using the ZAP-cDNA

synthesis kit (Stratagene). The primary cDNA library was

mass excised as phagemid using Exassist helper phage

(Stratagene). Phagemid DNA was extracted by

phenol-chloroform method, and hybridized against a pool of

over-represented ESTs (N>=12, from 5596 previous reads).

The subtracted library was electroporated into DH10B

(GeneHog, Invitrogen, Inc.). WARNING: the library contains

a small percentage of cDNAs derived from the human host

cells. Library Source: David Sibley, Washington

University."

ORIGIN

Query Match 74.4%; Score 18.6; DB 2; Length 526;
 Best Local Similarity 84.0%; Pred. No. 8e+02; Mismatches 0; Gaps 0;
 Matches 21; Conservative 0; Indels 4; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCGCTTTTCG 25
 ||||| || || ||||| |||||
 Db 478 GCAAGACGCACAGAAAGTCCTTTTCG 454

RESULT 15

BI157204
 LOCUS 602923403F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5063424 5',
 DEFINITION mRNA sequence.

ACCESSION BI157204

VERSION BI157204.1 GI:14617205

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LHAM1171 row: f column: 01

High quality sequence stop: 667.

FEATURES

source

1..806
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129,C57BL/6J,FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:5063424"
 /tissue_type="tumor, gross tissue"
 /dev_stage="10 months"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP Mam3"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies Investigators.
 Providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
 Reference for transgenic model: Xu et al., Nature Genetics
 22, 37-43 (1999)."

ORIGIN

Query Match 74.4%; Score 18.6; DB 2; Length 306;
 Best Local Similarity 84.0%; Pred. No. 8.5e+02; Mismatches 4; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Indels 4; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCGCTTTTCG 25
 ||||| || || ||||| |||||

Db 601 GCAAGACGCACAGAAAGGCGCTTTTCG 625

RESULT 16

CN207299
 LOCUS Tor7720 Gametophyte rehydration library Tortula ruralis cDNA, mRNA
 DEFINITION sequence.
 ACCESSION CN207299

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

CONTACT: Oliver Melvin J

Plant Stress Lab

USDA-ARS

3810 4th St, Lubbock, TX 79415, USA

Tel: 806-749-5560

Fax: 806-723-5272

Email: moliver@lbk.ars.usda.gov

PCR Primers

FORWARD: GTTTCCTCAGTCACGAC

BACKWARD: CAGGAACAGCTATGAC

Location/Qualifiers

1..591

/organism="Tortula ruralis"

/mol_type="mRNA"

/db_xref="taxon:38588"

/clone_lib="Gametophyte rehydration Library"

/note="Organ: Green Gametophyte; Vector: pSport1; Site_1:

SalI; Site_2: NotI"

ORIGIN

Query Match 73.6%; Score 18.4; DB 8; Length 591;

Best Local Similarity 95.0%; Pred. No. 1e+03; Mismatches 19; Conservative 0; Indels 1; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCGC 20
 ||||| ||||| ||||| |||||

Db 274 GCAAGTCGACGGAAGGCGC 293

RESULT 17

CF882404

LOCUS

DEFINITION

Hypocrea jecorina cDNA clone trico086xm16, mRNA sequence.

CF882404

ACCESSION

CF882404.1 GI:38137086

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

CONTACT: Ralph A. Dean

Fungal Genomics Laboratory

North Carolina State University

Campus Box 7251, Raleigh, NC 27695, USA

Tel: 919-513-0020

Fax: 919-513-0024

Email: ralph.dean@ncsu.edu

Seq primer: LT-Fl primer.

Location/Qualifiers

1..735

/organism="Hypocrea jecorina"

/mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
/clone="tric086xm16"
/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 6 October 2003"
/note="Vector; prep3v; Site_1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

ORIGIN

Query Match 73.6%; Score 18.4; DB 5; Length 735;
Best Local Similarity 95.0%; Pred. No. 1e+03; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 1

Qy 5 GTCGAACGGAAGCGCTTTC 24
|||||
Db 58 GTCGAACGGAACGCTTTC 77

RESULT 18

CB908942

LOCUS

DEFINITION

tric086xm16 T.reesei mycelial culture, Version 3 april Hypocrea

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Hypocrea jecorina (anamorph: Trichoderma reesei)

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

REFERENCE

AUTHORS

FOREMAN, P.K., BROWN, D.E., DANKMEYER, L., DEAN, R., DIENER, S., DUNN-COLEMAN, N.S., GOEDEGEBUUR, F., HOUFEK, T.D., ENGLAND, G.J., KELLEY, A.S., MEERMAN, H.J., MITCHELL, T., MITCHINSON, C., OLIVARES, H.A., TEUNISSEN, P.J., YAO, J. and WARD, M.

TITLE

Transcriptional regulation of biomass-degrading enzymes in the filamentous fungus Trichoderma reesei

JOURNAL

PUBLISHED

COMMENT

J. Biol. Chem. 278 (34), 31988-31997 (2003)

Contact: Pamela K. Foreman
Genencor Intl.
925 Page Mill Road, Palo Alto, CA 94304, USA
Tel: (650) 846-7635
Fax: (650) 621-7817
Email: Pforeman@genencor.com
Seq primer: LT-F1 primer.

FEATURES

source

1..788

/organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
/clone="tric086xm16"
/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 3 april"
/note="Vector; prep3v; Site_1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

ORIGIN

Query Match 73.6%; Score 18.4; DB 4; Length 788;
Best Local Similarity 95.0%; Pred. No. 1e+03; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 1

Qy 5 GTCGAACGGAAGCGCTTTC 24
|||||
Db 111 GTCGAACGGAACGCTTTC 130

RESULT 19

CN207539

LOCUS

DEFINITION

Tor7952 Gametophyte rehydration Library Tortula ruralis cDNA, mRNA

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Tortula ruralis

Tortula ruralis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Dicranidae; Pottiales; Pottiaceae; Tortula.

REFERENCE

AUTHORS

OLIVER, M.J., DOWD, S.E., ZARAGOSA, J., MAUGET, S.A. and PAYTON, P.R.

TITLE

The rehydration transcriptome of the desiccation-tolerant bryophyte Tortula ruralis: transcript classification and analysis

JOURNAL

PUBLISHED

COMMENT

BMC Genomics 5 (1), 89 (2004)

Contact: Oliver Melvin J
Plant Stress Lab
USDA-ARS
3810 4th St, Lubbock, TX 79415, USA
Tel: 806-749-5560
Fax: 806-723-5272
Email: moliver@lbrk.ars.usda.gov
PCR Primers
FORWARD: GTTTTCCAGTCACGAC
BACKWARD: CAGGAACAGCTATGAC.

FEATURES

source

1..817

/organism="Tortula ruralis"
/mol_type="mRNA"
/db_xref="taxon:38598"
/clone_lib="Gametophyte rehydration Library"
/note="Organ: Green Gametophyte; Vector: pSport1; Site_1: SalI; Site_2: NotI"

ORIGIN

Query Match 73.6%; Score 18.4; DB 8; Length 817;
Best Local Similarity 95.0%; Pred. No. 1.1e+03; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 1

Qy 1 GCAAGTCGAACGGAAGGCC 20
|||||
Db 50 GCAAGTCGAACGGAAGGCC 69

RESULT 20

DR421359

LOCUS

DEFINITION

CCHSSE05 Coprinus cinereus heat-shocked mycelia cDNAs Coprinopsis

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Coprinopsis cinerea (Coprinus cinereus)

Coprinopsis cinerea

Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes; Agaricales; Psathyrellaceae; Coprinopsis.

REFERENCE

AUTHORS

1 (bases 1 to 907)
CARLSON, M.D., BART, C., MURPHY, B., WILKE, S.K., GATHMAN, A.C., LILLY, W.W. and PUKKILA, P.J.

TITLE

Expressed sequence tags from Coprinus cinereus (Coprinopsis cinerea) cDNAs, spring 2005

JOURNAL

COMMENT

Unpublished (2005)
Contact: Gathman AC
Biology Department
Southeast Missouri State University
1 University Plaza, Cape Girardeau, MO 63701, USA
Tel: 5736512361
Fax: 573 651 2382
Email: agathman@semo.edu.

FEATURES

source

1..907

```

/organism="Coprinopsis cinerea"
/mol_type="mRNA"
/strain="Okayama7#130"
/db_xref="taxon:5346"
/dev_stage="vegetative monokaryotic mycelium"
/lab_host="E. coli XL10-Gold"
/clone_lib="Coprinus cinereus heat-shocked mycelia cDNAs"
/notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; Mycelia grown for three days at 37 degrees on
minimal medium, then transferred to pre-warmed minimal
media and incubated at 42 degrees for one hour before
harvesting."

ORIGIN
Query Match      73.6%; Score 18.4; DB 10; Length 907;
Best Local Similarity 95.0%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCC 20
    ||||| ||||| ||||| |||||
Db 716 GCAAGTCGAACGGAAGGCC 735

RESULT 21
DY091901
LOCUS DY091901 327 bp mRNA linear EST 31-JAN-2006
DEFINITION 010128BEMN06222HT BEMN Bos taurus CDNA, mRNA sequence.
ACCESSION DY091901
VERSION DY091901.1 GI:86238488
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 327)
AUTHORS McCulloch,A., Wilson,T., Molenaar,A., Grigor,M., Davis,S.,
Glenn,M., Havukala,I., Watson,J., Crawford,A., Wheeler,T.,
Hagemann,L., Lee,R., Hein,W., Johnstone,P., Magbool,N., McMahon,C.,
McCracken,J., Stelwagen,K., Farr,V., Singh,K., Whitley,J.,
Nicholas,K., Savin,K., Mather,A., McPartlan,H., Whitley,J.,
Wells,M., Bowman,P., Goddard,M., Langford,C., McEwan,J. and
Atkinson,P.
AGResearch, Genesis and Primary Industry Victoria Bovine EST
project
JOURNAL Unpublished (2006)
COMMENT Contact: Magbool N
AGResearch Ltd.
Invermay Agricultural Centre, Puddle Alley, Private Bag 50034,
Mosgiel, New Zealand
Email: nauman.magbool@agresearch.co.nz.
FEATURES
Source
Location/Qualifiers
1..327
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue type="Life Tech Normalised library"
/clone_lib="BEMN"
/notes="Vector: pCMV-Sport6; Life Tech Normalised library"

ORIGIN
Query Match      72.8%; Score 18.2; DB 10; Length 327;
Best Local Similarity 87.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCTTTC 24
    ||||| ||||| ||||| |||||
Db 106 CAAGTCGAACGGAAGGACTGTC 128

RESULT 22
BY457153
LOCUS BY457153 421 bp mRNA linear EST 13-DEC-2002

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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

```

BY457153 RIKEN full-length enriched, 15 days pregnant adult female
amion Mus musculus cDNA clone K63096B19 3', mRNA sequence.

BY457153
BY457153.1 GI:36755296

EST.
Mus musculus (house mouse)

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 421)

Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuoka,H.,
Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusica,V.,
Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
Petrowsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
Itoh,W., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
Rogers,J., Birney,E. and Hayashizaki,Y.

Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

12466851

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for

```

further details.
FEATURES
  source
    Location/Qualifiers
      1..421
        /organism="Mus musculus"
        /mol_type="mRNA"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="K630096B19"
        /sex="female"
        /tissue_type="amnion"
        /dev_stage="15 days pregnant adult"
        /clone_lib="RIKEN full-length enriched, 15 days pregnant
        adult female amnion"

ORIGIN
  Query Match      72.8%; Score 18.2; DB 4; Length 421;
  Best Local Similarity 87.0%; Pred. No. 1.2e+03;
  Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2  CAAGTCGAACGGAAGGCCTTC 24
      ||||| ||||| ||||| |||||
Db  272 CAAGTCGAGCAGAAAGTCCTTC 294

RESULT 23
LOCUS      DN526979              475 bp      mRNA      linear      EST 11-MAR-2005
DEFINITION 1271790 MARC 7BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  DN526979
VERSION     DN526979.1 GI:60972211
KEYWORDS   EST.
SOURCE     Bos taurus (cattle)
ORGANISM   Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE  1 (bases 1 to 475)
AUTHORS   Smith,T.P.L., Roberts,J.W., Echtenkamp,S.E., Chitko-McKown,C.G.,
Wray,J.E. and Keele,J.W.
TITLE     A second set of bovine ESTs from pooled-tissue normalized libraries
JOURNAL   Unpublished (2003)
COMMENT   Contact: Smith TPL
          USDA, ARS, US Meat Animal Research Center
          PO Box 166, Clay Center, NE 68933-0166, USA
          Tel: 402 762 4366
          Fax: 402 762 4390
          Email: smith@email.marc.usda.gov
          Single pass sequencing. Bases called with phred v0.020425.c and
          trimmed with the aid of the trim_alt option. Vector identified with
          cross_match v0.990329.
          Plate: RUK8046 row: I column: 10
          Seq primer: GTAATACGACTCACTATAGG.

FEATURES
  source
    Location/Qualifiers
      1..475
        /organism="Bos taurus"
        /mol_type="mRNA"
        /db_xref="taxon:9913"
        /tissue_type="pooled"
        /lab_host="DH10B"
        /clone_lib="MARC 7BOV"
        /note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
        Library made with RNA pooled from multiple tissues
        including ovary, hindbrain, uterus, and day-30 whole
        embryos."

ORIGIN
  Query Match      72.8%; Score 18.2; DB 9; Length 475;
  Best Local Similarity 87.0%; Pred. No. 1.2e+03;
  Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2  CAAGTCGAACGGAAGGCCTTC 24
      ||||| ||||| ||||| |||||
Db  163 CAAGTCGAACTGAAGGACTGTC 185

```

```

RESULT 24
LOCUS      CA934753/c              609 bp      mRNA      linear      EST 30-DEC-2002
DEFINITION MTU5TS.P23.C06 Aspen stem cDNA Library Populus tremuloides cDNA,
mRNA sequence.
ACCESSION  CA934753
VERSION     CA934753.1 GI:27423233
KEYWORDS   EST.
SOURCE     Populus tremuloides (quaking aspen)
ORGANISM   Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.
REFERENCE  1 (bases 1 to 609)
AUTHORS   Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and
Tsai,C.-J.
TITLE     Expressed sequence tags from Aspen
JOURNAL   Unpublished (2003)
COMMENT   Contact: Tsai C-J
          Plant Biotech Research Center
          Michigan Technological University, School of Forest Resources &
          Environmental Science
          1400 Townsend Drive, Houghton, MI 49931-1295, USA
          Tel: 906 487 2914
          Fax: 906 487 2915
          Email: chtsai@mtu.edu.

FEATURES
  source
    Location/Qualifiers
      1..609
        /organism="Populus tremuloides"
        /mol_type="mRNA"
        /db_xref="taxon:3693"
        /clone_lib="Aspen stem cDNA Library"
        /note="Organ: stem"

ORIGIN
  Query Match      72.8%; Score 18.2; DB 4; Length 609;
  Best Local Similarity 87.0%; Pred. No. 1.3e+03;
  Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  1  GCAAGTCGAACGGAAGGCCTTT 23
      ||||| ||||| ||||| |||||
Db  276 GAAAGTCGTTCCGGAAGGCCTTT 254

RESULT 25
LOCUS      CB378019              630 bp      mRNA      linear      EST 16-MAY-2003
DEFINITION rg06a11.y1 Heterodera glycines J3 Heterodera glycines cDNA 5',
similar to WP:CE23823 H24K24.4 RNA-binding protein,, mRNA
sequence.
ACCESSION  CB378019
VERSION     CB378019.1 GI:29127315
KEYWORDS   EST.
SOURCE     Heterodera glycines
ORGANISM   Heterodera glycines
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.
REFERENCE  1 (bases 1 to 630)
AUTHORS   McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,
Taagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
Underwood,K., Sceptoe,M., Allen,M., Person,B., Swaller,T.,
Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
TITLE     The Washington Univ. Nematode EST Project, 1999
JOURNAL   Unpublished (1999)
COMMENT   Contact: McCarter JP
          The Washington Univ. Nematode EST Project, 1999
          Washington University School of Medicine
          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

```

Query Match 72.8%; Score 18.2; DB 9; Length 835;
Best Local Similarity 87.0%; Pred. No. 1.3e+03;

Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCGCTTTC 24
|||||
Db 552 CAAGTCGAACGGAAGGACTGTC 574

RESULT 28
LOCUS CR077081 835 bp DNA linear GSS 05-JUL-2004
DEFINITION Reverse strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHP284c21, genomic survey sequence.
ACCESSION CR077081.1 GI:49810669
VERSION GSS; genome survey sequence; MICR.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 835)
REFERENCE Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y., Rogers,J. and Bradley,A.
AUTHORS Direct Submission
TITLE Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
JOURNAL CB10 15A, UK. <http://www.sanger.ac.uk/MICR>
FEATURES Location/Qualifiers
source 1..835
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHP284c21"
/clone_lib="MHP"

ORIGIN
Query Match 72.8%; Score 18.2; DB 14; Length 835;
Best Local Similarity 87.0%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGTCGAACGGAAGGCGCTTCG 25
|||||
Db 519 AATTAGAAAGGAAGGCGCTTCG 541

RESULT 29
LOCUS DN282351/c 843 bp mRNA linear EST 02-MAR-2005
DEFINITION 1182408 MARC 7BOV Bos taurus CDNA 3', mRNA sequence.
ACCESSION DN282351
VERSION DN282351.1 GI:60450961
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 843)
REFERENCE Smith,T.P.L., Roberts,A.J., Ehternkamp,S.E., Chitko-McKown,C.G., Wray,J.E. and Keele,J.W.
AUTHORS A second set of bovine ESTs from pooled-tissue normalized libraries Unpublished (2003)
JOURNAL Contact: Smith TPL
COMMENT USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329.
Plate: RLK8014 row: J column: 12
Seq primer: TAGAAGGCACAGTCGAGG.

FEATURES source
Location/Qualifiers
1..843
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH108"
/clone_lib="MARC 7BOV"
/note="Vector: pCDNA3.1; Site_1: EcoRI; Site_2: NotI; Library made with RNA pooled from multiple tissues including ovary, hindbrain, uterus, and day-30 whole embryos."

ORIGIN
Query Match 72.8%; Score 18.2; DB 9; Length 843;
Best Local Similarity 87.0%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCGCTTTC 24
|||||
Db 284 CAAGTCGAACGGAAGGACTGTC 262

RESULT 30
LOCUS DU746898/c 906 bp DNA linear GSS 27-JAN-2006
DEFINITION ASNC3551.b2 HF10 10-07-02 uncultured marine microorganism HF10_10-07-02 genomic clone HF0010_049G12, genomic survey sequence.
ACCESSION DU746898
VERSION DU746898.1 GI:85756734
KEYWORDS GSS.
SOURCE uncultured marine microorganism HF10_10-07-02
ORGANISM uncultured marine microorganism HF10_10-07-02
unclassified sequences; environmental samples.
1 (bases 1 to 906)
REFERENCE DeLong,E.F., Preston,C.M., Mincer,T., Rich,V., Hallam,S.J., Frigaard,N.U., Martinez,A., Sullivan,M., Edwards,R., Chisholm,S.W. and Karl,D.M.
AUTHORS Comparative genomics reveals ecological trends in stratified microbial communities in the ocean's interior Science (2006) In press
JOURNAL Contact: Susan Lucas, Alex Copeland, Sam Pitluck, Alla Lapidus, Kerrie Barry, Tijana Glavinadelio, David Bruce, Paul Richardson and Edward DeLong
COMMENT US DOE Joint Genome Institute
US DOE Joint Genome Institute
2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA
Tel: 617-253-5271
Fax: 617-253-2679
Email: PMRichardson@lbl.gov; delong@mit.edu
North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid DNA library prepared from marine picoplankton in the less than 1.6 um, greater than 0.22 um fraction. Sample Date: 10/7/2002
Coordinates: 22.45 N, 158 W Depth: 10 m Temperature: 26.4 C
Salinity 35.08 psu Oxygen: 204.6 umol/kg
Class: fosmid ends.
Location/Qualifiers
1..906
/organism="uncultured marine microorganism HF10_10-07-02"
/mol_type="genomic DNA"
/db_xref="taxon:361145"
/clone="HF0010_049G12"
/cell_type="marine picoplankton, less than 1.8 um, greater than 0.22 um fraction"
/clone_lib="HF10_10-07-02"
/note="Vector: pCC1FOS; North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid DNA library prepared from marine picoplankton in the less than 1.6 um, greater than 0.22 um fraction. Picoplankton collected at 10 m depth on 10/7/2002, Coordinates: 22.45 N,158 W. Sample Date: 10/7/2002 Coordinates: 22.45 N, 158 W Depth: 10 m Temperature: 26.4 C Salinity 35.08 psu Oxygen: 204.6 umol/kg"

ORIGIN

Query Match 72.8%; Score 18.2; DB 14; Length 906;
 Best Local Similarity 87.0%; Pred. No. 1.3e+03;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGTCGAACGGAAGGCCTTCG 25
 |||||
 DB 421 AAGTCGAACGCGAGCCTTCG 399
 |||||

RESULT 31,
CN506FX8/c

LOCUS CN506FX8 929 bp DNA linear GSS 17-JUN-2001
 DEFINITION T3 end of clone XAR0AA001H08 of library XAR0AA from strain CBS 732
 of Zygosaccharomyces rouxii, genomic survey sequence.

ACCESSION AL396978
 VERSION AL396978.1 GI:12149467

KEYWORDS

SOURCE GSS.

ORGANISM

Zygosaccharomyces rouxii
 Zygosaccharomyces rouxii
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Zygosaccharomycetes.

1 (bases 1 to 929)

Souci t,J.L., Aigle,M., Artiguenave,F., Blandin,G.,

Boiotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,

de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Liorente,B.,

Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,

Saurin,W., Tekai ,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,

Winkler,P. and Weissenbach,J.

Genomic exploration of the hemiascomycetous yeasts: 1. A set of

yeast species for molecular evolution studies

FEMS Lett. 487 (1), 3-12 (2000)

1152876

2 (bases 1 to 929)

de Montigny,J., Straub,M., Potier,S., Tekai ,F., Dujon,B.,

Winkler,P., Artiguenave,F. and Souci t,J.

Genomic exploration of the hemiascomycetous yeasts: 8.

Zygosaccharomyces rouxii

FEMS Lett. 487 (1), 52-55 (2000)

1152883

3 (bases 1 to 929)

Genoscope.

Direct Submission

Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :

secref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen

yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces

exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,

Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces

lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia

angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,

Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to

5 kb were prepared and both extremities were sequenced. See

keywords for description of this sequence and for the sequence of

the other extremity of this insert.

Location/Qualifiers

1..929

/organism="Zygosaccharomyces rouxii"

/mol_type="genomic DNA"

/strain="CBS 732"

/db_xref="taxon:4956"

/clone="XAR0AA001H08"

/clone_lib="XAR0AA"

/note="end : 73"

complement(<1..>927)

/inferences="non-experimental evidence, no additional

details recorded"

/note="similar to Saccharomyces cerevisiae ORF YLR399C [

BDF1 ; sporulation protein]

1 putative frameshift(s)"

complement(<16..>927)

misc_feature

/inference="non-experimental evidence, no additional
 details recorded"

/note="similar to Saccharomyces cerevisiae ORF YDL070w [

BDF2 ; similarity to bromodomain protein Bdf1p]

1 putative frameshift(s)"

ORIGIN

Query Match 72.8%; Score 18.2; DB 14; Length 929;
 Best Local Similarity 87.0%; Pred. No. 1.3e+03;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCCTTT 23
 |||||

DB 902 GCAAGTTGACGTAATAGCCTTT 880
 |||||

RESULT 32,
DM640758/c

LOCUS

DEFINITION DM640758 943 bp mRNA linear EST 19-JAN-2006

CLJ372-G02 3', mRNA sequence.

ACCESSION DM640758

VERSION DM640758.1 GI:85406860

KEYWORDS EST.

SOURCE Gasterosteus aculeatus (three spined stickleback)

ORGANISM Gasterosteus aculeatus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;

Gasterosteidae; Gasterosteus.

1 (bases 1 to 943)

Kingsley,D.M., Peichel,C., Knecht,A., Balabhadra,S., Grimwood,J.,

Dickson,M., Schmutz,J. and Myers,R.M.

Expressed sequence tags from Gasterosteus aculeatus (2004)

Unpublished (2004)

Contact: Grimwood, Jane

Stanford Human Genome Center

Stanford University School of Medicine

975 S California Ave, Palo Alto, CA 94304, USA

Tel: 650 320 5917

Fax: 650 320 5801

Email: jane@hgc.stanford.edu

Plate: 372

High quality sequence stop: 751.

Location/Qualifiers

1..943

/organism="Gasterosteus aculeatus"

/mol_type="mRNA"

/strain="Bittuufjordur marine sticklebacks, Iceland"

/db_xref="taxon:69293"

/clones="CLJ372-G02"

/sex="mixed male and female"

/tissue_type="whole larva"

/dev_stage="21 day old larvae collected at Swarup Stage 30

(J. Embryol. Exp. Morphol 6: 373-383,1958)"

/lab_host="DH10B (T1 phage resistant)"

/clone_lib="SHGC-CLJ2"

/note="Vector: Express 1: Total and poly A+ RNA was

isolated from the indicated stickleback tissue, and a cDNA

library was constructed in the Express 1 plasmid vector by

Open Biosystems. First strand cDNA synthesis was primed

with an 54 bp linker primer containing an oligodT sequence

preceded by a synthetic NotI site (first strand primer:

5'-GACTAGTTCATGATCGGCGGCC(T)25-3'). Following

second strand synthesis, cDNAs were made blunt at the end

corresponding to the original 5 prime end of mRNA, and

cloned directionally into the NotI and EcoRV sites of

Express 1. Note that the EcoRV site is typically destroyed

in the blunt end cloning, leaving a junction of the form

'xxATC' (where is ATC is the second half of the EcoRV

site, and xxx is derived from the cDNA sequence). A map of

the Express 1 vector is available at:

http://www.openbiosystems.com/cdna_library_construction_fa

misc_feature

q.php#8 The primary library was transformed and amplified in DH10B (T1 phage resistant) bacteria."

```

ORIGIN
Query Match          72.8%; Score 18.2; DB 10; Length 943;
Best Local Similarity 87.0%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCTTT 23
    ||||| ||||| ||||| ||||| |||||
Db 893 GCAAAATTGACGGAAGGGCTTT 871

RESULT 33
CNS06CEP/c          994 bp DNA linear GSS 14-JUN-2001
LOCUS               T3 end of clone AR0AA004E02 of library AR0AA from strain CBS 732 of
DEFINITION          Zygosaccharomyces rouxii, genomic survey sequence.
ACCESSION            AL392423.1 GI:12141725
VERSION              AL392423
KEYWORDS              Zygosaccharomyces rouxii
SOURCE               Zygosaccharomyces rouxii
ORGANISM              Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
REFERENCE            Saccharomycetales; Saccharomycetaceae; Zygosaccharomyces.
AUTHORS              Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
                    Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
                    de-Montigny,J., DuJon,B., Durrens,P., Lepingle,A., Illorente,B.,
                    Malpertuy,A., Neuvelisse,C., Ozier-Kalogeropoulos,O., Potier,S.,
                    Saurin,W., Tekaiia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
                    Winkler,P. and Weissenbach,J.
TITLE                Genomic exploration of the hemiascomycetous yeasts: 1. A set of
                    yeast species for molecular evolution studies
JOURNAL              FEBS Lett. 487 (1), 3-12 (2000)
PUBMED               11152876
REFERENCE            2 (bases 1 to 994)
AUTHORS              de Montigny,J., Straub,M., Potier,S., Tekaiia,F., DuJon,B.,
                    Winkler,P., Artiguenave,F. and Souciet,J.
TITLE                Genomic exploration of the hemiascomycetous yeasts: 8.
JOURNAL              Zygosaccharomyces rouxii
PUBMED               FEBS Lett. 487 (1), 52-55 (2000)
REFERENCE            11152883
AUTHORS              3 (bases 1 to 994)
GENOSCOPE            Genoscope.
DIRECT SUBMISSION    Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage,
                    2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
                    sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT              This GSS is part of a random genomic sequencing program of thirteen
                    yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
                    exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii,
                    Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
                    lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
                    angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
                    Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
                    5 kb were prepared and both extremities were sequenced. See
                    keywords for description of this sequence and for the sequence of
                    the other extremity of this insert.
FEATURES
    source            1. .994
                    /organism="Zygosaccharomyces rouxii"
                    /mol_type="genomic DNA"
                    /strain="CBS 732"
                    /db_xref="taxon:4956"
                    /clone="AR0AA004E02"
                    /clone_lib="AR0AA"
                    /note="end : T3"
                    complement(<2..964)
                    /inference="non-experimental evidence, no additional
                    details recorded"
                    /note="similar to Saccharomyces cerevisiae ORF YLR399c [
                    BDF1 ; sporulation protein ]"

misc_feature
Query Match          72.8%; Score 18.2; DB 14; Length 1043;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCTTCG 25
    ||||| ||||| ||||| ||||| |||||
Db 79 GCCAGNCGNCCGGAAGGCCTTTG 103

ORIGIN
Query Match          72.8%; Score 18.2; DB 14; Length 1043;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCTTCG 25
    ||||| ||||| ||||| ||||| |||||
Db 79 GCCAGNCGNCCGGAAGGCCTTTG 103

FEATURES
    source            1. .1043
                    /organism="uncultured marine microorganism HF200_10-06-02"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:361147"
                    /clone="HF200_090F10"
                    /cell_type="marine picoplankton, less than 1.8 um, greater
                    than 0.22 um fraction"
                    /clone_lib="HF200_10-06-02"
                    /notes="Vector: pCifOS; North Pacific Subtropical Gyre
                    (Hawaii) picoplankton genomic fosmid DNA library prepared
                    from marine picoplankton in the less than 1.6 um, greater
                    than 0.22 um fraction. Picoplankton collected at 200 m
                    depth on 10/6/2002, Coordinates: 22.45 N, 158 W. Sample
                    Date: 10/6/2002 Coordinates: 22.45 N, 158 W Depth 200 m
                    Temperature: 18.53 C Salinity: 35.04 psu Oxygen: 198.8
                    umol/kg"

```

ORIGIN

Query Match 72.8%; Score 18.2; DB 14; Length 994;
Best Local Similarity 87.0%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCTTT 23

Db 921 GCAAGTTGAACGTAATGCCTTT 899

RESULT 34

DU760208

LOCUS DU760208 1043 bp DNA linear GSS 27-JAN-2006
DEFINITION ASNG3054.b2 HF200_10-06-02 uncultured marine microorganism
HF200_10-06-02 genomic clone HF0200_090F10, genomic survey
sequence.

ACCESSION DU760208

VERSION DU760208.1 GI:857770044

KEYWORDS GSS.
SOURCE uncultured marine microorganism HF200_10-06-02
uncultured marine microorganism HF200_10-06-02
unclassified sequences; environmental samples.

ORGANISM

REFERENCE 1 (bases 1 to 1043)

AUTHORS

DeLong,E.F., Preston,C.M., Mincer,T., Rich,V., Hallam,S.J.,
Frigaard,N.U., Martinez,A., Sullivan,M., Edwards,R., Chisholm,S.W.
and Karl,D.W.

TITLE Comparative genomics reveals ecological trends in stratified
microbial communities in the ocean's interior

JOURNAL

Science (2006) In press
Contact: Susan Lucas, Alex Copeland, Sam Pitluck, Alla Lapidus,
Kerrie Barry, Tijana Glavinadelrio, David Bruce, Paul Richardson
and Edward DeLong

US DOE Joint Genome Institute

2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA

Tel: 617-253-5271

Fax: 617-253-2679

Email: PRRichardson@lbl.gov; delong@mit.edu

North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid
DNA library prepared from marine picoplankton in the less than 1.6
um, greater than 0.22 um fraction. Sample Date: 10/6/2002

Coordinates: 22.45 N, 158 W Depth 200 m Temperature: 18.53 C

Salinity: 35.04 psu Oxygen: 198.8 umol/kg

Class: fosmid ends.

FEATURES

source

1. .1043

/organism="uncultured marine microorganism HF200_10-06-02"

/mol_type="genomic DNA"

/db_xref="taxon:361147"

/clone="HF200_090F10"

/cell_type="marine picoplankton, less than 1.8 um, greater

than 0.22 um fraction"

/clone_lib="HF200_10-06-02"

/notes="Vector: pCifOS; North Pacific Subtropical Gyre

(Hawaii) picoplankton genomic fosmid DNA library prepared

from marine picoplankton in the less than 1.6 um, greater

than 0.22 um fraction. Picoplankton collected at 200 m

depth on 10/6/2002, Coordinates: 22.45 N, 158 W. Sample

Date: 10/6/2002 Coordinates: 22.45 N, 158 W Depth 200 m

Temperature: 18.53 C Salinity: 35.04 psu Oxygen: 198.8

umol/kg"

ORIGIN

Query Match 72.8%; Score 18.2; DB 14; Length 1043;

Best Local Similarity 80.0%; Pred. No. 1.3e+03;

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCTTCG 25

Db 79 GCCAGNCGNCCGGAAGGCCTTTG 103

misc_feature

/inference="non-experimental evidence, no additional

details recorded"

/note="similar to Saccharomyces cerevisiae ORF YLR399c [

BDF1 ; sporulation protein]"

```

RESULT 35
LOCUS      DQ213078
DEFINITION Taeniopygia guttata clone 0058P0007D03 gephyrin-like mRNA, complete
            sequence.
ACCESSION  DQ213078
VERSION     DQ213078.1
KEYWORDS    GI:76152437
SOURCE      HTc.
ORGANISM    Taeniopygia guttata (Poephila guttata)
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Passeriformes; Estrilidae;
            Estrilidae; Taeniopygia.
REFERENCE   1 (bases 1 to 1052)
AUTHORS     Wada,K., Howard,J.T., McConnell,P., Lints,T., Rivas,R.V.,
            Whitney,O.B., Horita,H., Patterson,M., White,S., Zhao,S.,
            Sakaguchi,H., Hagiwara,M., Toshiyuki,S., Hirozane-Kishikawa,T.,
            Skene,P., Hayashizaki,Y., Carninci,P. and Jarvis,E.D.
TITLE       A molecular neuroethological approach for identifying and
            characterizing a melody of behaviorally regulated genes
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 1052)
AUTHORS     Wada,K. and Jarvis,E.D.
TITLE       Direct Submission
JOURNAL     Submitted (21-SEP-2005) Neurobiology, Duke University Medical
            Center, Box 3209, Durham, NC 27710, USA
FEATURES   source
            1..1052
            /organism="Taeniopygia guttata"
            /mol_type="mRNA"
            /db_xref="taxon:59729"
            /clone="0058P0007D03"
            /sex="female"
            /tissue_type="whole brain"
            /clone_lib="normalized (50 mix pooled juveniles + adults)"
            /dev_stage="P88"
            /note="common: zebra finch; authority: Taeniopygia guttata
            Vieillot (1817); synonym: Poephila guttata"
            1..1052
            /note="similar to gephyrin"
            misc_feature

ORIGIN
Query Match      72.8%; Score 18.2; DB 6; Length 1052;
Best Local Similarity 87.0%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 CAAGTCGAACGGAAGGCGCTTTC 24
        ||||| ||||| ||||| ||||| |||||
Db      193 CAAGTCAACACGCAAGGCGCTTTC 215

RESULT 36
LOCUS      CL645653/c
DEFINITION CH213-99C02.SP6 CH213 Gasterosteus aculeatus genomic clone
            CH213-99C02 3', genomic survey sequence.
ACCESSION  CL645653
VERSION     CL645653.1
KEYWORDS    GI:49665077
SOURCE      GSS.
ORGANISM    Gasterosteus aculeatus (three spined stickleback)
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
            Gasterosteidae; Gasterosteus.
REFERENCE   1 (bases 1 to 1242)
AUTHORS     Kingsley,D., Grimwood,J., Dickinson,M., Schmutz,J. and Myers,R.M.
TITLE       Expressed sequence tags from Gasterosteus aculeatus
JOURNAL     Unpublished (2004)
COMMENT     Contact: Grimwood, Jane
            Stanford Human Genome Center
            Stanford University School of Medicine
            975 S California Avenue, Palo Alto, CA 94304, USA

```

```

Tel: 650 320 5917
Fax: 650 320 5801
Email: jane@hgsc.stanford.edu
Plate: 99
Class: BAC ends
High quality sequence start: 18
High quality sequence stop: 933.
Location/Qualifiers
1..1242
/organism="Gasterosteus aculeatus"
/mol_type="genomic DNA"
/strain="Salmon River"
/db_xref="taxon:69293"
/clone="CH213-99C02"
/sex="Mixed"
/cell_type="Blood"
/clone_lib="CH213"
/note="vector: pTARBAC2.1; Site 1: EcoRI; The sequence of
the clone was established as a mapping and sequencing
collaboration at the Stanford Genome Evolution Center,
funded by the NIH Centers of Excellence in Genomic Science
(CEGS) initiative (http://cegs.stanford.edu). The clone
was isolated from the BAC library CHORI-213 built by
Pieter deJong in collaboration with the Stanford Genome
Evolution Center (http://www.chori.org/bacpac). Clones
may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering\_information.html)."
```

FEATURES source

Query Match 72.8%; Score 18.2; DB 13; Length 1242;
Best Local Similarity 87.0%; Pred. No. 1.4e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGTCGAACGGAAGGCGCTTTCG 25
 ||||| ||||| ||||| ||||| |||||
Db 517 AAGTCGAACGGAAGGCGCTTTCG 495

RESULT 37
LOCUS BF537535
DEFINITION 602053182F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4192100 5',
 mRNA sequence.
ACCESSION BF537535
VERSION BF537535.1
KEYWORDS GI:11624903
SOURCE EST.
ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarhontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 938)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-re@mail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: Incyte Genomics, Inc.
 Found through the I.M.A.G.E. Consortium information can be
 <http://image.llnl.gov>
 Plate: LHAM9522 row: d column: 21
 High quality sequence stop: 418.
 Location/Qualifiers
 1..938
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4192100"

FEATURES source

/lab host="DH10B (T1 phage-resistant)" /clone.lib="NCI_CGAP_SG2" /note=Organ: salivary gland; vector: pCMV-SPORT6; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."	
ORIGIN	
Query Match	72.0%; Score 18; DB 7; Length 938;
Best Local Similarity	100.0%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 GCAAGTCGAACGGAAGG 18
Db	648 GCAAGTCGAACGGAAGG 665
RESULT 38	
BX342644	994 bp mRNA linear EST 07-APR-2004
LOCUS	BX342644 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
DEFINITION	Homo sapiens cDNA clone CS0DL004YB13 5-PRIME, mRNA sequence.
ACCESSION	BX342644
VERSION	BX342644.2 GI:46275066
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	On May 2, 2003 this sequence version replaced gi:30342105. Contact: Genoscope Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6269.F For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS0DL004CA07QP1&c=6269.F.
FEATURES	source 1..994 Location/Qualifiers /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0DL004YB13" /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED" /cell_line="RAMOS CELL LINE" /clone.lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED" /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN	
Query Match	72.0%; Score 18; DB 4; Length 994;
Best Local Similarity	75.0%; Pred. No. 1.7e+03;
Matches 18; Conservative 3; Mismatches 3; Indels 0; Gaps 0;	
Qy	2 CAAGTCGAACGGAAGGCTTCG 25
Db	928 CAATCGAATTGAAGGCTTCG 951
RESULT 39	
BX342644	273 bp mRNA linear EST 13-FEB-1998
LOCUS	vt03c06.r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone
DEFINITION	IMAG8:1161994 5', mRNA sequence.
ACCESSION	AA815626
VERSION	AA815626.1 GI:2885222
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	The WashU-HMI Mouse EST Project Unpublished (1996) Contact: Marra M/Mouse EST Project WashU-HMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the IMAG Consortium (info@image.llnl.gov) for further information. MGI: 204085 Seq primer: mob.REGA+ET High quality sequence stop: 213. Location/Qualifiers 1..223 /organism="Mus musculus" /mol_type="mRNA" /db_xref="taxon:10090" /clone="IMAG8:313469" /dev_stage="19.5 dpc total fetus" /lab_host="DH10B (ampicillin resistant)" /clone.lib="Soares mouse p3NMF19.5" /notes=Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCATCTGAAGTGGAGCGCGGCAATTTTATTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."
ORIGIN	
Query Match	71.2%; Score 17.8; DB 10; Length 223;
Best Local Similarity	90.5%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Qy	2 CAAGTCGAACGGAAGGCTTT 22
Db	42 CAAGTCGAACGGAAGGACTT 62
RESULT 40	
AA815626	273 bp mRNA linear EST 13-FEB-1998
LOCUS	vt03c06.r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone
DEFINITION	IMAG8:1161994 5', mRNA sequence.
ACCESSION	AA815626
VERSION	AA815626.1 GI:2885222
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus

fraction > 1 kb"

ORIGIN

Query Match 71.2%; Score 17.8; DB 4; Length 347;
 Best Local Similarity 90.5%; Pred. No. 1.8e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22
 |||||
 Db 95 CAAGTCGAACGGAAGGCCTT 115
 |||||

RESULT 43

W65078 357 bp mRNA linear EST 10-JUN-1996
 LOCUS me01d06.r1 Soares mouse embryo NM013.5 14.5 Mus musculus cDNA
 clone IMAGE:386219 5', mRNA sequence.

ACCESSION W65078
 VERSION W65078.1 GI:1372728
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 357)
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Streptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of MedicineP
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:238051

Seq primer: mob.REGA+ET

High quality sequence stop: 327.

FEATURES

source
 Location/Qualifiers
 1..357
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:386219"
 /sex="unknown"
 /tissue_type="embryo"
 /dev_stage="13.5-14.5dpc total fetus"
 /lab_host="DH10B"
 /clone_lib="Soares mouse embryo NM013.5 14.5"
 /note="Vector: pT7T3D-Paci; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5].

TGTTACCAACTGAGTGGGAGCGCGCGAAATTTTTTTTTTTTTTTTTTTT
 T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
 State Univ., from 2]; double-stranded cDNA was ligated to
 Eco RI adaptors (Pharmacia), digested with Not I and
 cloned into the Not I and Eco RI sites of the modified
 pT7T3 vector. Library went through one round of
 normalization, and was constructed by Bento Soares and
 M. Fatima Bonaldo.

ORIGIN

Query Match 71.2%; Score 17.8; DB 10; Length 357;
 Best Local Similarity 90.5%; Pred. No. 1.8e+03;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22
 |||||
 Db 183 CAAGTCGAACGGAAGGCCTT 203
 |||||

RESULT 44
 CF425395/c
 LOCUS

DEFINITION CF425395 384 bp mRNA linear EST 03-SEP-2003
 lad53e02.y1 Gastric Epithelial Progenitor Mus musculus cDNA 5',
 similar to TR:088546 088546 COP9 COMPLEX SUBUNIT 7A. ;, mRNA
 sequence.

ACCESSION CF425395
 VERSION CF425395.1 GI:34438096
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 384)

AUTHORS Tidwell,R., Clifton,S., Marra,M., Hillier,L., Pape,D., Martin,J.,
 Wylie,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennet,J.,
 Ronko,I., Tsagareishvili,R., Belaygorod,L., Grow,A., Maguire,L.,
 Waterston,R. and Wilson,R.

TITLE WashU Stem cell EST Project
 JOURNAL Unpublished (2002)

COMMENT Contact: Jeff Gordon and Mike Lovett
 WashU, Human Genetics Division

Washington University School of Medicine
 1st strand of cDNA was synthesized with reverse transcriptase and
 oligo(dT) beads, then cDNA was amplified by PCR using modified
 SMART primers. The final cDNA was cloned in pAMP1 vector in
 annealing reaction with Uracil DNA Glycosylase (UDG). Library
 constructed by Y.Korshunova and M. Lovett. Library materials
 provided by Mills JC & Gordon JI.
 Putative full length read
 vector to vector length is

Possible reversed clone: similarity on wrong strand

Seq primer: -4ORP from Gibco.

FEATURES
 source
 Location/Qualifiers
 1..384

/organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /tissue_type="Gastric Epithelial Progenitor"
 /dev_stage="adult"
 /lab_host="DH5alpha"
 /clone_lib="Gastric Epithelial Progenitor"
 /note="Vector: pAMP1; This library was created from
 laser-captured isthmal cells from tox176 transgenic mice.
 1st strand of cDNA was synthesized with reverse
 transcriptase and oligo(dT) beads, then cDNA was amplified
 by PCR using modified SMART primers. The final cDNA was
 cloned in pAMP1 vector in annealing reaction with Uracil
 DNA Glycosylase (UDG). Library constructed by Y.Korshunova
 and M. Lovett. Library materials provided by Mills JC &
 Gordon JI."

ORIGIN

Query Match 71.2%; Score 17.8; DB 5; Length 384;

Best Local Similarity 90.5%; Pred. No. 1.9e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22
 |||||
 Db 90 CAAGTCGAACGGAAGGCCTT 70
 |||||

RESULT 45

AL363886 400 bp mRNA linear EST 04-AUG-2000
 LOCUS

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:901645
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 418.

FEATURES
source
Location/Qualifiers
1..419
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:137917"
 /sex="male"
 /tissue_type="Thymus"
 /dev_stage="4 weeks"
 /lab_host="DH10B"
 /clone_lib="Soares thymus 2NBMT"
 /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCGAAGTGGAGCGCCGCTTTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M.Fatima Bonaudo."

ORIGIN

Query Match 71.2%; Score 17.8; DB 1; Length 419;
Best Local Similarity 90.5%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAAGGCCTT 22
 |||||
DB 367 CAAGTCGAACGGAAAGGCATT 387
 |||||

RESULT 47
AI1713707
LOCUS
DEFINITION
UI-R-AG1-aao-b-08-0-UI.s1 UI-R-AG1 Rattus norvegicus cDNA clone
AI1713707
AI1713707.1 GI:5017507
EST.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 420)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
8889548
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEERF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Oligo-dr track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: Clones will be available through
Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLA=No. Location/Qualifiers
1..420
 /organism="Rattus norvegicus"

FEATURES
source
Location/Qualifiers

```

/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clones="UI-R-AGI-aao-b-08-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-AGI"
/notes="Vector: pT73D-PacI; Site 1: Not I; Site 2: Eco RI;
The UI-R-AGI library is a normalized library constructed
from 13 dpc rat ventricle. The tag is a string of 6
nucleotides present between the Not I site and the
oligo-dt track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6:
791-806, 1996. Tissue provided by Jim Lin, Department of
Biology, University of Iowa.
TAG_TISSUE=atrium at 16.5 dpc
TAG_LIB=UI-R-AGI
TAG_SEQ=GATTC"

```

ORIGIN

```

Query Match      71.2%; Score 17.8; DB 1; Length 420;
Best Local Similarity 90.5%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      2 CAAGTCGAACGGAAGGCCTT 22
        ||||| ||||| ||||| |||||
Db      143 CAAGTCGAACGGAAGGCATT 163

```

```

RESULT 48
AA818546
LOCUS

```

```

DEFINITION UI-R-A0-aw-f-05-0-UI.s1 UI-R-A0 Rattus norvegicus cDNA clone
UI-R-A0-aw-f-05-0-UI 3' similar to gb|02529|RATPRZ2H Rattus
norvegicus Drosophila polarity gene (frizzled) homologous mRNA,
complete cds, mRNA sequence.

```

```

ACCESSION AA818546
VERSION AA818546.1 GI:4228339
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)

```

```

ORGANISM Rattus norvegicus

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
1 (bases 1 to 424)

```

```

Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery

```

```

Genome Res. 6 (9), 791-806 (1996)

```

```

8889548

```

```

On Feb 17, 1998 this sequence version replaced gi:2889285.

```

```

Contact: Soares, MB

```

```

Coordinated Laboratory for Computational Genomics

```

```

University of Iowa

```

```

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

```

```

Tel: 319 335 8250

```

```

Fax: 319 335 9565

```

```

Email: bento-soares@uiowa.edu

```

```

Oligo-dt track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.
Fatima Bonaldo, Ph.D. Clone distribution: clones will be available
through Research Genetics This clone is also available through the
I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE

```

```

ID=1776549

```

```

Seq primer: M13 Forward

```

```

POLYA=No.

```

FEATURES

```

source

```

```

1. .424
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clones="UI-R-A0-aw-f-05-0-UI"

```

```

/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-A0"
/notes="Vector: pT73D-PacI; Site 1: Not I; Site 2: Eco RI;
This library consists of a mixture of individually tagged
normalized libraries constructed from rat placenta, adult
lung, brain, liver, kidney, heart, spleen, ovary, and
muscle. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dt track which allows
identification of the library of origin of a clone within
the mixture."

```

ORIGIN

```

Query Match      71.2%; Score 17.8; DB 1; Length 424;
Best Local Similarity 90.5%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      2 CAAGTCGAACGGAAGGCCTT 22
        ||||| ||||| ||||| |||||
Db      143 CAAGTCGAACGGAAGGCATT 163

```

```

RESULT 49
BU743860
LOCUS

```

```

DEFINITION BU743860 444 bp mRNA linear EST 21-APR-2003
mai49f01.y1 McCarrey Eddy round spermatid Mus musculus cDNA clone
IMAGE:6449520 5', mRNA sequence.

```

```

ACCESSION BU743860
VERSION BU743860.1 GI:23691980
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

```

```

ORGANISM Mus musculus

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 444)

```

```

REFERENCE
AUTHORS

```

```

McCarrey, J., Eddy, M., Marra, M., Hillier, L., Clifton, S., Pape, D.,
Martin, J., Wylie, T., Dantes, M., Bowers, Y., Theising, B., Gibbons, M.,
Ritter, E., Tsagaris, R., Ronko, I., Maguire, L., Kennedy, S.,
Bennett, J., Waterston, R. and Wilson, R.

```

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NIEHS Mouse

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Unpublished (2002)

```

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Contact: McCarrey/Eddy NIEHS Mouse

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NIEHS Mouse

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Washington University School of Medicine

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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

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Tel: 314 286 1800

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Fax: 314 286 1810

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Email: est@watson.wustl.edu

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```

This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

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MGI:2093832

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Seq primer: -40RP from Gibco

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High quality sequence stop: 422.

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Location/Qualifiers

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source

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1. .444
/organism="Mus musculus"
/mol_type="mRNA"

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/db_xref="CD-1"
/clone_xref="taxon:10090"

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/clones="IMAGE:6449520"

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/sex="male"

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/tissue_type="round spermatids, pooled from multiple mice"

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/dev_stage="60 day"
/lab_host="DH10B (phage-resistant)"
/clone_lib="McCarrey Eddy round spermatid"
/notes="Organ: testis; Vector: pBluescript SK+
(Stratagene); Site 1: XhoII; Site 2: EcoRI; cDNA oligo
dt-primed [5'-(GA)10-ACTAGTCGAGTTTTTTTTTT-3'] and
directionally cloned using 5' linkers 5'-BATTGCGACGAG-3'
and 5'-CTCGTCCG-3'. Size selection of >400bp material
gives average insert size ranging from 1-2 kb. Library was
mass excised (from lambda-UnizAP-XR) and resulting

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single-stranded phagemids were prepped and transformed into DH10B. Library contains 98.5% recombinants.
References: J. Androl. 20:635-639 and Gene 25:263-269.
Library constructed and donated by J. McCarrey, Ph.D. (Southwest Foundation for Biomedical Research, Dept. of Genetics); excision done by E.M. Eddy, Ph.D. (National Institutes of Health, National Institute of Environmental Health Sciences). Original lambda-based library is available through ATCC, catalog #63423."

ORIGIN

Query Match 71.2%; Score 17.8; DB 3; Length 444;
Best Local Similarity 90.5%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCGCTT 22
|||||
Db 12 CAAGTCGAACGGAAGGACTT 32

RESULT 50

W47680

LOCUS mc89h02.r1 Soares mouse embryo NM013.5 14.5 Mus musculus cDNA
DEFINITION clone IMAGE:355731 5', mRNA sequence.

ACCESSION

W47680

VERSION

W47680.1

KEYWORDS

EST.

SOURCE

ORGANISM

Mus musculus

(house mouse)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1332776.
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:227531

Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 400.

Location/Qualifiers
1..446

FEATURES

source

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:355731"
/sex="unknown"
/tissue_type="embryo"
/dev_stages="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/clone_lib="Soares mouse embryo NM013.5 14.5"
/note="Vector: pT73D-Pac1; Site1: Not I; Site2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5',
TGTTACCAATCTGAAGTCGAGCGCGCGAAATTTTTTTTTTTTTTTTTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2]; double-stranded cDNA was ligated to

Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT73 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo. "

ORIGIN

Query Match 71.2%; Score 17.8; DB 10; Length 446;
Best Local Similarity 90.5%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCGCTT 22
|||||
Db 80 CAAGTCGAACGGAAGGACTT 100

RESULT 51

A1593186

LOCUS

DEFINITION

A1593186

ACCESSION

VERSION

A1593186.1

KEYWORDS

EST.

SOURCE

ORGANISM

Mus musculus

(house mouse)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)

Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:627906

This read is a RESEQUENCE of a previously sequenced mouse clone

This read has been verified (found to hit its original self in the

correct orientation)

Seq primer: -40RP from Gibco

High quality sequence stop: 466.

Location/Qualifiers

1..473

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C3H"

/db_xref="taxon:10090"

/clone="IMAGE:1161994"

/cell_line="C2C12"

/lab_host="DH10B"

/clone_lib="Barstead mouse myotubes MPLRB5"

/note="Vector: pT73D-Pac1; Site1: EcoRI; Site2: NotI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5',
TGTTACCAATCTGAAGTCGAGCGCGCGCTTTTTTTTTTTTTTTTTTTTTT
3']"; double-stranded cDNA was ligated to Eco RI adaptors
[AAATCGAGCTTGG], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pT73 vector.
Library constructed by Bob Barstead. The C2C12 cell line
(available from ATCC, catalog # CRL-1772) differentiates
rapidly, forming contractile myotubes and producing
characteristic muscle proteins. "

ORIGIN

Query Match 71.2%; Score 17.8; DB 1; Length 473;
 Best Local Similarity 90.5%; Pred. No. 1.9e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCCTT 22
 |||||
 Db 293 CAAGTCGAACGGAAGGCATT 313

RESULT 52
 CN692701
 LOCUS
 DEFINITION E0326F01-5 NIA Mouse E10.5 whole embryo cDNA library (Long) Mus linear EST 18-MAY-2004
 musculus cDNA clone NTA:E0326F01 IMAGE:30861468 5', mRNA sequence.

ACCESSION CN692701
 VERSION
 KEYWORDS EST.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 492)
 AUTHORS Sharov, A.A., Piao, Y., Matoba, R., Dudekula, D.B., Qian, Y.,
 VanBuren, V., Falco, G., Martin, P.R., Stagg, C.A., Bassey, U.C.,
 Wang, Y., Carter, M.G., Hamatani, T., Aiba, K., Akutsu, H., Sharova, L.,
 Tanaka, T.S., Kimber, W.L., Yoshikawa, T., Jaradat, S.A., Pantano, S.,
 Nagaraja, R., Boheler, K.R., Taub, D., Hodes, R.J., Longo, D.L.,
 Schlesinger, D., Keller, J., Klutz, E., Kelsoe, G., Umezawa, A.,
 Vescovi, A.L., Rossant, J., Kunath, T., Hogan, B.L., Curci, A.,
 D'Urso, M., Kelsoe, J., Hide, M. and Ko, M.S.

TITLE Transcriptional analysis of mouse stem cells and early embryos
 JOURNAL PLoS Biol. 1 (3), 410-419 (2003)
 COMMENT Contact: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@lgsun.grc.nia.nih.gov
 Plate: E0326 row: F column: 01
 Seq primer: M13 Reverse
 High quality sequence stop: 492
 POLYA=No.

FEATURES source
 1..492 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="niaEST:E0326F01-5"
 /clones="NIA:E0326F01 IMAGE:30861468"
 /tissue_type="whole embryo including extraembryonic
 tissues at 10.5-days postcoitum"
 /dev_stage="E10.5"
 /lab_host="DH10B"
 /clone_lib="NIA Mouse E10.5 whole embryo cDNA library
 (Long)"
 /note="vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI;
 Site 2: NotI; Mouse cDNA project by the Laboratory of
 Genetics, National Institute on Aging (NIA), Intramural
 Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
 This is a long-transcript enriched cDNA library (Ref.
 Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total
 RNAs were extracted from a pool of 8 embryos at 10.5-days
 postcoitum. Double-stranded cDNAs were synthesized with an
 oligo(dT) primer [Invitrogen]:
 5'-pGACTAGTTCGAGCGCGCCGCCCTTTT-3' from
 2ug of total RNA, treated with T4 DNA polymerase, and
 purified by ethanol-precipitation. The cDNAs were ligated
 to lone-linker Li-Sal4, purified by phenol/chloroform, and
 separated from free linkers by Centricon 100. Then, the
 cDNAs were amplified by long-range high fidelity PCR using
 Ex Taq polymerase (Takara) with a primer Sal4-S. The

products were purified by phenol/chloroform and Centricon
 100. The cDNAs were digested with SalI and NotI enzymes
 and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
 vector. The DH10B E. coli host was transformed with the
 ligation mixture by the standard chemical method. The
 average insert size is about 3.4Kb. The library was
 constructed by Yulan Piao."

ORIGIN

Query Match 71.2%; Score 17.8; DB 8; Length 492;
 Best Local Similarity 90.5%; Pred. No. 1.9e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCCTT 22
 |||||
 Db 107 CAAGTCGAACGGAAGGCATT 127

RESULT 53
 AA014214/c

LOCUS
 DEFINITION AA014214 500 bp mRNA linear EST 21-JAN-1997
 clone IMAGE:442914 5', mRNA sequence.

ACCESSION AA014214
 VERSION
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 500)
 AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.

TITLE The WashU-HHMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HHMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:268250

Seq primer: mob.REGA+ET
 High quality sequence stop: 477.
 Location/Qualifiers

1..500
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:442914"
 /sex="unknown"
 /tissue_type="placenta"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="Soares mouse placenta 4NbMPI3.5 14.5"
 /note="Organ: placenta; Vector: pT73D-PacI; Site 1: Not
 I; Site 2: EcoRI; 1st strand cDNA was primed with a Not I
 -oligo(dT) primer [5,
 TGTACCAATCTGAAGTGGGCGCGCGGAATTTTTTTTTTTTTTTTTTTT
 T 3']; double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Qy 2 CAAGTCGAACGGAAGGCCCTT 22

6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890

Email: mst@mail.nih.gov

cDNA Library Preparation: M.B. Soares Lab Clone distribution:
Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It
should be noted that Bento Soares is generating a small number of
additional specialized non-redundant arrays of BMAP cDNAs whose
availability will be considered under appropriate and limited
collaborative arrangements

Seq primer: M13 Reverse.

FEATURES

source

Location/Qualifiers

1..527

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clones="UI-M-BH0-ake-d-02-0-UI"

/dev_stage="27-32 days"

/lab_hosts="DH10B (Life Technologies)"

/clone_lib="NIH BMAP_M_S1"

/notes="Vector: pRT3D-Pac1; Site_1: Not I; Site_2: Eco RI;
The NIH BMAP_M_S1 library is a subtracted library derived
from a mixture of normalized libraries from ten regions of
the mouse brain (cerebellum, brain stems, olfactory bulbs,
hypothalamus, cortex, amygdala, basal ganglia, pineal
gland, striatum, hippocampus). The driver used for
subtraction consisted of a pool of 20,000 cDNA clones
obtained from non-normalized and normalized libraries of
these ten regions of the mouse brain."

ORIGIN

Query Match 71.2%; Score 17.8; DB 7; Length 527;

Best Local Similarity 90.5%; Pred. No. 1.9e+03;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22

Db 83 CAAGTCGAACGGAAGGACTT 103

RESULT 57

BQ569727

LOCUS

DEFINITION BQ569727 532 bp mRNA linear EST 19-JUN-2002

clone gi135c11.y1 Mouse Organ of Corti cDNA pbluescript Mus musculus cDNA

clone gi135c11.5', mRNA sequence.

ACCESSION BQ569727

VERSION BQ569727.1

KEYWORDS GI:21473044

SOURCE EST.

ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 532)

REFERENCE

AUTHORS Kachar,B

TITLE EST analysis of gene expression in the mouse Organ of Corti at the

onset of hearing

Unpublished (2002)

Contact: Kachar,B

Structural Cell Biology

National Institute of Deafness and other Communication Disorders

50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Tel: 301-402-1599

Fax: 301-402-1765

Email: kachar@nidcd.nih.gov

Plate: 135 row: C column: 11

Seq primer: M13RP1 reverse primer (ABI).

Location/Qualifiers

1..532

/organism="Mus musculus"

/mol_type="mRNA"

/strain="BALB/c"

/db_xref="taxon:10090"

/clone="gi135c11"

/sex="male and female"

/dev_stage="Post natal day 5 to 13"

/notes="Organ: Mouse Organ of Corti; Vector: pbluescript; The
organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
epithelium was carefully dissected out of the modiolus.
Total RNA was extracted using the Micro Fasttrack kit
(catalog # KI593-02; Invitrogen, Carlsbad, CA), according
to manufacturer's instructions. Reverse transcription and
library construction were carried out with the Uni-Zap XR
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
Gigapack III Gold Cloning kit (catalog # 237612), both
from Stratagene (La Jolla, CA, USA), according to
manufacturer's instructions. Briefly: 1.5 ug mRNA was
reverse transcribed using a hybrid oligo(dT) linker-primer
that contains an Xho I site. First strand synthesis was
primed with the linker- primer and transcribed using
Mooney murine leukemia virus reverse transcriptase
(MMLV-RT) and 5-methyl dCTP. The second strand was
synthesized with DNA polymerase and RNase H. Complementary
DNA was blunt ended with Pfu DNA polymerase, ligated with
EcoR I adapters in the presence of ligase and digested
with Xho I. The cDNA was sequentially size fractionated
over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)
and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)
columns to enrich for cDNAs greater than 400bp and 1000
bp, respectively. The cDNA was then directionally ligated
to the Uni-Zap XR vector, which had been predigested with
EcoR I and Xho I. The phagemid was packaged with Gigapack
III Gold and, upon titration on Xl1 Blue MRF' cells, the
yield of the phage library was estimated to be 11,100,000
recombinants. Stratagene's ExAssist Interference
resistance helper phage (catalogue # 211203) was adopted
to rescue plasmid DNA from the phages. Upon plating of the
rescued library, individual cDNA clones were selected and
grown in 96-well, 2 ml growth plate. Plasmid DNA was
purified from 200 ul of saturated culture with the
Concert96(TM) plasmid purification kit (Invitrogen,
Carlsbad, CA) as instructed by the manufacturer. ESTs from
the 5' end of the cDNA clones were generated with the
universal M13 reverse primer (CAGGAAACAGCTATGACC) and 25'
strength BigDye terminator sequencing chemistry (Applied
Biosystems, Foster City, CA). Sequencing reactions were
performed on MJ Tetrad thermal cyclers (MJ Research,
Waltham, MA), and analyzed on 3700 automated capillary
sequencers using POP5 polymer (Applied Biosystems, Foster
City, CA). The frequency distribution of the library is
as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10;
1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of
genes are present in GenBank and have know function; 23%
have hits in GenBank, but do not have assigned function;
12% are uncharacterized ESTs and 20% are unidentified."

ORIGIN

Query Match 71.2%; Score 17.8; DB 3; Length 532;

Best Local Similarity 90.5%; Pred. No. 1.9e+03;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22

Db 334 CAAGTCGAACGGAAGGACTT 354

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RESULT 58
BF022607/c
LOCUS          542 bp      mRNA      linear      EST 29-DEC-2000
DEFINITION     uys1d11.v1 NCI CGAP Lu30 Mus musculus cDNA clone IMAGE:3663093 5',
                similar to TR:088546 O88546 COP9 COMPLEX SUBUNIT 7A. ;, mRNA
                sequence.
ACCESSION      BF022607
VERSION        BF022607.1
KEYWORDS       EST.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus

REFERENCE      1 (bases 1 to 542)
AUTHORS        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                Tumor Gene Index
JOURNAL        Unpublished (1997)
COMMENT        Contact: Robert Strausberg, Ph.D.
                Email: cgapbs-remail.nih.gov
                Tissue Procurement: Gilbert Smith, Ph.D.
                CNA Library Preparation: Life Technologies, Inc.
                CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Washington University Genome Sequencing Center
                Clone distribution: NCI-CGAP clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                image.llnl.gov/image/html/iresources.shtml

FEATURES       source
                MGI:1423861
                Possible reversed clone: similarity on wrong strand
                Seq primer: -40RP from Gibco
                High quality sequence stop: 461.
                Location/Qualifiers
                1..542
                /organism="Mus musculus"
                /mol_type="mRNA"
                /strain="Czech II"
                /db_xref="taxon:10090"
                /clone="IMAGE:3663093"
                /tissue_type="tumor, metastatic to mammary"
                /lab_host="DH10B"
                /clone_lib="NCI CGAP Lu30"
                /note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
                Site 2: SalI; transgenic model WNT-1, expression driven by
                MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
                dT. Library constructed by Life Technologies.
                Investigator providing samples: Gilbert Smith, NIH"

ORIGIN
Query Match          71.2%; Score 17.8; DB 7; Length 542;
Best Local Similarity 90.5%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAAGGCCTT 22
    |||||
Db 135 CAAGTCGAACGAAAGGACTT 115

RESULT 59
A1603423
LOCUS          543 bp      mRNA      linear      EST 21-APR-1999
DEFINITION     UI-R-AC1-XU-b-09-0-UI.s1 UI-R-AC1 Rattus norvegicus cDNA clone
                UI-R-AC1-XU-b-09-0-UI 3', mRNA sequence.
ACCESSION      A1603423
VERSION        A1603423.1
KEYWORDS       EST.
SOURCE         Rattus norvegicus (Norway rat)
ORGANISM       Rattus norvegicus

REFERENCE      1 (bases 1 to 543)
AUTHORS        Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
                Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

AUTHORS        Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE          Normalization and subtraction: two approaches to facilitate gene
                discovery
JOURNAL        Genome Res. 6 (9), 791-806 (1996)
PUBMED         889548
COMMENT        Contact: Soares, MB
                Coordinated Laboratory for Computational Genomics
                University of Iowa
                375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
                Tel: 319 335 8250
                Fax: 319 335 9585
                Email: bento-soares@uiowa.edu
                Oligo-dT track not found, Not I site shown in beginning of sequence
                is likely internal to the message. cDNA Library Preparation: M.B.
                Soares Lab Clone distribution: Clones will be available through
                Research Genetics (www.resgen.com)
                Seq primer: M13 Forward.
                Location/Qualifiers
                1..543
                /organism="Rattus norvegicus"
                /mol_type="mRNA"
                /strain="Sprague-Dawley"
                /db_xref="taxon:10116"
                /clone="UI-R-AC1-XU-b-09-0-UI"
                /dev_stage="adult"
                /lab_host="DH10B (Life Technologies)"
                /clone_lib="UI-R-AC1"
                /note="Vector: pT73D-PacI; Site 1: Not I; Site 2: Eco RI;
                The UI-R-AC1 library is a normalized library constructed
                from 16.5 dpc rat atrioventricular (AV) canal. The tag
                is a string of 5 nucleotides present between the Not I
                site and the oligo-dT track. The library was constructed
                as described by Bonaldo, Lennon and Soares, Genome
                Research 6: 791-806, 1996. Tissue provided by Jim Lin,
                Department of Biology, University of Iowa."

ORIGIN
Query Match          71.2%; Score 17.8; DB 1; Length 543;
Best Local Similarity 90.5%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAAGGCCTT 22
    |||||
Db 143 CAAGTCGAACGAAAGGACTT 163

RESULT 60
AZ024985/c
LOCUS          566 bp      DNA      linear      GSS 25-FEB-2000
DEFINITION     RPCI-23-386J13.TJ RPCI-23 Mus musculus genomic clone
                RPCI-23-386J13, genomic survey sequence.
ACCESSION      AZ024985
VERSION        AZ024985.1
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus

REFERENCE      1 (bases 1 to 566)
AUTHORS        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE      1 (bases 1 to 566)
AUTHORS        Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
                Akinret,B., Levins,M., McGann,S., Teegaye,G., Geer,K., Krol,M., de
                Jong,P. and Fraser,C.M.
                Mouse BAC End Sequences from Library RPCI-23
                Unpublished (1999)
                Other GSSs: RPCI-23-386J13.TV
                Contact: Shaying Zhao
                Department of Eukaryotic Genomics
                The Institute for Genomic Research
                9712 Medical Center Dr., Rockville, MD 20850, USA
                Tel: 301 838 0200
                Fax: 301 838 0208
                Email: szhao@tigr.org

```

Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
 Plate: 386 row: J column: 13
 Seq primer: SP6
 Class: BAC ends.

FEATURES

```

source
1. .566
  /location/Qualifiers
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="RPCI-23-386J13"
    /sex="Female"
    /lab_host="DH10B"
    /clone_lib="RPCI-23"
    /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

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ORIGIN

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Query Match      71.2%; Score 17.8; DB 11; Length 566;
Best Local Similarity 90.5%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 CAAGTCGAACGGAAGGCCTT 22
    ||||| ||||| ||||| |||||
Db  417 CAAGTCGACGGAAGGCCTT 397

```

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RESULT 61
CN692527
LOCUS      CN692527      571 bp      mRNA      linear      EST 18-MAY-2004
DEFINITION E0324C02-5 NTA Mouse E10.5 whole embryo cDNA library (Long) Mus
            musculus cDNA clone NTA:E0324C02 IMAGE:30861241 5', mRNA sequence.
ACCESSION  CN692527
VERSION     CN692527.1 GI:47461275
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 571)
Sharov,A.A., Piao,Y., Matoba,R., Dudekula,D.B., Qian,Y.,
VanBuren,V., Falco,G., Martin,P.R., Stagg,C.A., Bassey,D.C.,
Wang,Y., Carter,M.G., Hamatani,T., Aiba,K., Akutsu,H., Sharova,L.,
Tanaka,T.S., Kimber,W.L., Yoshikawa,T., Jaradat,S.A., Pantano,S.,
Nagaraja,R., Boheler,K.R., Taub,D., Hodes,R.J., Longo,D.L.,
Schlessinger,D., Keller,J., Klotz,E., Kelsoe,G., Umezawa,A.,
Vecovici,A.L., Rossant,J., Kunath,F., Hogan,B.W., Curcio,A.,
D'Urso,M., Kelsoe,J., Hide,W. and Ko,M.S.
Transcriptome analysis of mouse stem cells and early embryos
PLOS Biol. 1 (3), 410-419 (2003)
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: E0324 row: C column: 02
Seq primer: M13 Reverse
High quality sequence stop: 571
POLYA-No.

```

FEATURES

```

source
1. .571
  /location/Qualifiers
    /organism="Mus musculus"

```

```

/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="niaEST:E0324C02-5"
/db_xref="taxon:10090"
/clone="NTA:E0324C02 IMAGE:30861241"
/tissue_type="whole embryo including extraembryonic
tissues_at 10.5-days postcoitum"
/dev_stage="E10.5"
/lab_host="DH10B"
/clone_lib="NTA Mouse E10.5 whole embryo cDNA library
(Long)"
/note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI;
Site 2: NotI; Mouse cDNA project by the Laboratory of
Genetics' National Institute on Aging (NTA), Intramural
Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total
RNAs were extracted from a pool of 8 embryos at 10.5-days
postcoitum. Double-stranded cDNAs were synthesized with an
Oligo(dT) primer [Invitrogen:
5'-PGACTAGTCTTAGATCCGAGCGGCCCTTTTCTTTT-3'] from
2ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to Lona-linker LL-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by the standard chemical method. The
average insert size is about 3.4Kb. The library was
constructed by Yulan Piao."

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ORIGIN

```

Query Match      71.2%; Score 17.8; DB 8; Length 571;
Best Local Similarity 90.5%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 CAAGTCGAACGGAAGGCCTT 22
    ||||| ||||| ||||| |||||
Db  107 CAAGTCGAACGGAAGGCCTT 127

RESULT 62
BE288370/c
LOCUS      BE288370      577 bp      mRNA      linear      EST 26-OCT-2000
DEFINITION 601094841F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3489299 5',
            mRNA sequence.
ACCESSION  BE288370
VERSION     BE288370.1 GI:9168018
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 577)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8530 row: a column: 12
High quality sequence stop: 577.

```

FEATURES
source

Location/Qualifiers
1. .577
/organism="Mus musculus"
/mol_type="mRNA"
/strain="mix FVB/N, C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3489299"
/tissue_type="tumor, gross tissue"
/dev_stages="7 months"
/lab_host="DH10B"
/clone_lib="NCI CCAP Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

ORIGIN

Query Match 71.2%; Score 17.8; DB 7; Length 577;
Best Local Similarity 90.5%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 CAAGTCGAACGGAAGGCCTT 22

Db 202 CAAGTCGAACGGAAGGCCTT 182

RESULT 63

DN215604/c DN215604 600 bp mRNA linear EST 28-FEB-2005
LOCUS MEST971.D01.77-1 UGA-ZmSAM-X22 Zea mays cDNA, mRNA sequence.

DEFINITION DN215604

ACCESSION DN215604.1

VERSION DN215604.1 GI:60348631

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 600)

Chen, H.D., Zhang, X., Zhou, R.L., Arias, L.A.C., Shendelman, J.M., Zazubovits, N., Borsuk, L.A., Emrich, S.J., Ashlock, D.A., Scanlon, M.J. and Schnable, P.S.

Expressed Sequence Tags from B73 Maize Shoot Apical Meristems

Unpublished (2004)

Contact: Patrick S. Schnable

Schnable Laboratory

Iowa State University

2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA

Tel: 515-294-0975

Fax: 515-294-5256

Email: schnable@iastate.edu.

Location/Qualifiers

FEATURES

source

1. .600
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="inbred B73"
/db_xref="taxon:4577"
/tissue_type="vegetative Shoot Apical Meristem (SAM) and leaf primordia staged P1-P4"
/lab_host="XLI-Blue"
/clone_lib="UGA-ZmSAM-X22"
/note="Organ: Shoot apex; Vector: Uni-Zap XR; Site 1: EcoRI; Site 2: XhoI; This library was constructed by Xiaolan Zhang. Vegetative Shoot Apical Meristem (SAM) and leaf primordia staged P1-P4 from 14-17 day-after germination seedlings were quickly dissected into dry ice under a light microscope. Total RNA was isolated using Trizol and mRNA was purified with Dynal Oligo-DT25. ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with an XhoI oligo-dT primer (5'-GAGAGAGAGAGAGAGACTAGTCTCGAGTGTGTTTTTTTTTTTTT).

The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with XhoI and size-selected to be >600 bp. The resulting molecules were directionally cloned into the EcoRI and XhoI sites of the Uni-Zap XR vector.

The lambda library was packaged with Gigapack III Gold packaging extract and was mass excised by XLI-Blue cells and ExSist helper phage. Excised phagemids were titered in SOLR cells and plated onto LB-ampicillin agar plates.

Base calling was conducted using Phred. Trimming was performed using Lucy with the following criteria:

(-minimum 200 -error 0.01 0.01 -bracket 10 0.01). A low complexity filter was applied and additional trimming was conducted to remove E. coli, vector, and organelle contamination. After processing ~30% of the sequences contained a minimum of 10 Ts at the beginning of the sequence. For reasons that are not understood many of the clones in this library lack an XhoI site at their 3' ends."

ORIGIN

Query Match 71.2%; Score 17.8; DB 9; Length 600;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 CAAGTCGAACGGAAGGCCTT 22

Db 550 CAAGTCGAACGGAAGGCCTT 530

RESULT 64

DR968997/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 602)

Rao, K., Collura, K., Wissotski, M., Smart, D., Kudrna, D., Muller, C., Rac, K., Haller, K., Wing, R., Soderlund, C., Walbot, V. and Yu, Y.

Maize Full-length cDNA Project

Unpublished (2005)

Contact: Yeisoo Yu

Arizona Genomics Institute

The University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9585

Fax: 520 621 1259

Email: yeisoo@genome.arizona.edu

Plate: 0090 row: I column: 18.

Location/Qualifiers

1. .602

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="B73"

/db_xref="taxon:4577"

/tissue_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"

/dev_stages="varies by tissue"

/lab_host="DH10B T1 phage resistant"

/clone_lib="ZM_BFB"

/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for

expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (<http://www.genome.arizona.edu/orders/>).

ORIGIN

Query Match 71.2%; Score 17.8; DB 10; Length 602;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAACTCGAACGGAAGGCCTT 22
||||| ||||| ||||| ||||| |||||
Db 583 CAACTGGAACGAAAGGCCTT 563

RESULT 65

AW914801 613 bp mRNA linear EST 25-MAY-2000
LOCUS EST346105 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
DEFINITION RGIH48 5' end, mRNA sequence.

ACCESSION AW914801
VERSION AW914801.1 GI:8080481
KEYWORDS EST.
SOURCE Rattus sp.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

REFERENCE

1 (bases 1 to 613)
Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (RESt) Catalog & Rat Gene Index

JOURNAL

Unpublished (1998)

COMMENT

Contact: Lee, NH

The Institute for Genomic Research

9712, Medical Center Drive, Rockville, MD 20850, USA

Tel: (301)-838-3529

Fax: (301)-838-0208

Email: nhlee@tigr.org

This clone is available through the ATCC, contact the ATCC

tel#703-365-2700 for further information

Seq primer: M13 Reverse.

FEATURES

Location/Qualifiers
1..613
/organism="Rattus sp."
/mol_type="mRNA"
/db_xref="taxon:10118"
/clone_lib="RGIH48"
/note="Organ: ovary; Vector: pT73pac; Site_1: EcoRI; Site_2: NotI"

ORIGIN

Query Match 71.2%; Score 17.8; DB 7; Length 613;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAACTCGAACGGAAGGCCTT 22
||||| ||||| ||||| ||||| |||||
Db 61 CAACTCGAAGTGAAGGACTT 81

RESULT 66

BI648126 622 bp mRNA linear EST 12-SEP-2001
LOCUS 603278444F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5318818 5',
DEFINITION mRNA sequence.

ACCESSION BI648126
VERSION BI648126.1 GI:15562362

KEYWORDS

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 622)
NIH-MGC <http://mgc.nci.nih.gov/>.

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-x@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM1808 row: g column: 11

High quality sequence stop: 605.

FEATURES

source

Location/Qualifiers
1..622
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5318818"
/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam3"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999)."

ORIGIN

Query Match 71.2%; Score 17.8; DB 2; Length 622;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAACTCGAACGGAAGGCCTT 22
||||| ||||| ||||| ||||| |||||
Db 433 CAACTCGAAGTGAAGGACTT 453

RESULT 67

CX734384/c 635 bp mRNA linear EST 24-JAN-2005
LOCUS jB01e11.y1 Mouse Whole eye, equalized: ja/jb/jc Mus musculus cDNA
DEFINITION clone jB01e11 5', mRNA sequence.

ACCESSION CX734384

VERSION CX734384.1 GI:58061220

KEYWORDS

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 635)

AUTHORS

Wisow G. and Tonarev, S.

TITLE

Expressed sequence tag analysis of mouse whole eye

JOURNAL

Unpublished (2004)

COMMENT

Contact: Wisow G

Section on Molecular Structure and Function

National Eye Institute

6/31, NIH, Bethesda, MD 20892-2740, USA

Tel: 301 402 3452

Fax: 301 496 0078

Email: graeme@helix.nih.gov

Plate: 01 row: e column: 11

Seq primer: M13RP1 reverse primer (ABI).

FEATURES

Location/Qualifiers

source

1..635

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57Bl6J"

/db_xref="taxon:10090"

/clone="jb01e11"

/tissue_type="whole eye"

/dev_stage="Adult"

/lab_host="EMDH10B"

/note="Organ: Eye; Vector: pSPORT1; Approximately 1mg

total RNA was extracted from 100 adult mouse whole eyes. A

directionally cloned cDNA library in the pSPORT1 vector

(Invitrogen) was constructed at Bioserve Biotechnology

(laurel MD) essentially following the protocols of the

SuperScript Plasmid System full details of which are

contained in the manufacturer's instruction manual

(http://www.lifetech.com/). First strand synthesis was

carried out using a Not I primer-adaptor

[5'-pGATCTAGTTCTAGTCGCGAGCGCCCTT)15-3']. cDNA was

cloned in Not I/Sal I sites. EST analysis was performed on

the unamplified library at the NIH Intramural Sequencing

Center (NISC)."

ORIGIN

Query Match 71.2%; Score 17.8; DB 9; Length 635;

Best Local Similarity 90.5%; Pred. No. 2e+03;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22

|||||

Db 403 CAAGTCGAACGGAAGGCCTT 383

RESULT 68

BI331633

LOCUS

DEFINITION 602983168F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5136040 5',

mRNA sequence.

ACCESSION BI331633

VERSION BI331633.1

KEYWORDS GI:15016290

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 641)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

JOURNAL

Contact: Robert Strausberg, Ph.D.

COMMENT

Email: cgapbs@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: L1AM11334 row: g column: 17

High quality sequence stop: 640.

FEATURES

Location/Qualifiers

source

1..641

/organism="Mus musculus"

/mol_type="mRNA"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:5136040"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NCI CGAP Li9"

/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.9 kb. Constructed by Life

Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Query Match 71.2%; Score 17.8; DB 2; Length 641;

Best Local Similarity 90.5%; Pred. No. 2e+03;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22

|||||

Db 206 CAAGTCGAACGGAAGGCCTT 226

RESULT 69

CF897511

LOCUS

DEFINITION

A0226805-5 NIA Mouse Embryonic Germ Cell cDNA Library (Long,

subtracted) Mus musculus cDNA clone NIA:A0226805 IMAGE:30730864 5',

mRNA sequence.

ACCESSION CF897511

VERSION CF897511.1

KEYWORDS GI:38164560

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.

Construction of long-transcript enriched cDNA libraries from

submicrogram amounts of total RNAs by a universal PCR amplification

method

Genome Res. 11 (9), 1553-1558 (2001)

1154199

Contact: Dawood B. Dudekula

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

Email: cdna@igsun.grc.nia.nih.gov

Plate: A0226 row: B column: 05

Seq primer: M13 Reverse

High quality sequence stop: 641

POLYA-No. Location/Qualifiers

1..641

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL6"

/db_xref="niaEST:A0226805-5"

/db_xref="taxon:10090"

/clone="NIA:A0226805 IMAGE:30730864"

/sex="male"

/dev_stage="embryonic day 8"

/lab_host="DH10B"

/clone_lib="NIA Mouse Embryonic Germ Cell cDNA Library

(Long, subtracted)"

/note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI;


```

/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4160215"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Lig"
/notes="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."

ORIGIN
Query Match      71.2%; Score 17.8; DB 7; Length 647;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2 CAAGTCGAACGGAAGGCGCTT 22
    |||||
Db   530 CAAGTCGAACGGAAGGACTT 550

RESULT 72
CF898433
LOCUS      CF898433                651 bp      mRNA      linear      EST 04-NOV-2003
DEFINITION A0239B05-5 NIA Mouse Embryonic Germ Cell cDNA Library (Long,
            substracted) Mus musculus cDNA clone NIA:A0239B05 IMAGE:30732112 5',
            mRNA sequence.
ACCESSION  CF898433
VERSION     CF898433.1 GI:38165482
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
            1 (bases 1 to 651)
REFERENCE  1 (bases 1 to 651)
AUTHORS   Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
TITLE     Construction of long-transcript enriched cDNA libraries from
            submicrogram amounts of total RNAs by a universal PCR amplification
            method
JOURNAL    Genome Res. 11 (9), 1553-1558 (2001)
PUBMED    11541199
COMMENT    Contact: Dawood B. Dudekula
            Laboratory of Genetics
            National Institute on Aging/National Institutes of Health
            333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
            Email: cdna@igsun.grc.nia.nih.gov
            Plate: A0239 row: B Column: 05
            Seq primer: M13 Reverse
            High quality sequence stop: 651
            POLYA=No.

FEATURES             Location/Qualifiers
     source           1..651
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                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL6"
                     /db_xref="niaEST:A0239B05-5"
                     /db_xref="taxon:10090"
                     /clone="NIA:A0239B05 IMAGE:30732112"
                     /sex="male"
                     /dev_stages="embryonic day 8"
                     /lab_host="DH10B"
                     /clone_lib="NIA Mouse Embryonic Germ Cell cDNA Library
                     (Long, substracted)"
                     /note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI;
                     Site 2: NotI; Mouse cDNA project by the Laboratory of
                     Genetics, National Institute on Aging (NIA), Intramural
                     Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA).
                     This is a long-transcript enriched cDNA library (Ref.
                     Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). EG
                     cells were obtained from Dr. Brigid L.M. Hogan and RNA was
                     prepared by Dr. Mark G. Carter (NIH/NIA-IRP). EG cells
                     were cultured at 37. C, 5% CO2 in DMEM supplemented with
                     15% ES cell-qualified FBS, 0.1mM non-essential amino
                     acids, 2 mM glutamine, penicillin/streptomycin, 1 mM
                     sodium pyruvate, 0.1 mM beta-mercaptoethanol, and 10~7
                     units of LIF per liter. Double-stranded cDNAs were
                     synthesized with an Oligo(dt) primer [Invitrogen:
                     5'-pGACTAGTTCTAGATCGGAGCGCGCCCTTTT-3'] from
                     2.5 ug of total RNA, treated with T4 DNA polymerase, and
                     purified by ethanol-precipitation. The cDNAs were ligated
                     to lone-linker LL-Sal4, purified by phenol/chloroform, and
                     separated from free linkers by Centricon 100. Then, the
                     cDNAs were amplified by long-range high fidelity PCR using
                     Ex Taq polymerase (Takara) with a primer Sal4-S. The
                     products were double digested with NotI and SalI enzymes,
                     then purified by phenol/chloroform and Centricon 100. The
                     cDNA mixture was subjected to a special subtraction
                     procedure by Dr.Kazuhiro Kondo at AIGIN Cosmos. Then the
                     subtracted cDNAs were cloned into SalI/NotI site of
                     pCMV-SPORT6 plasmid vector. The DH10B E. coli host was
                     transformed with the ligation mixture by the standard
                     chemical method. The average insert size is about 2.2kb.
                     The library was constructed by Yulan Piao and Kazuhiro
                     Kondo."

```

Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAATCTGAAT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH).

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Query Match      71.2%; Score 17.8; DB 8; Length 682;
Best Local Similarity 90.5%; Pred. NO. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 CAAGTCGAACGGAAAGCCTT 22
        |||||
Db      148 CAAGTCGAACGAAAGGACTT 168

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RESULT	75
DT945027/c	
LOCUS	DT945027 685 bp mRNA linear EST 21-SEP-2005
DEFINITION	ZM BFD0132B03.f ZM BFD Zea mays cDNA 3', mRNA sequence.

TITLE
Maize Full-length cDNA Project
JOURNAL
Unpublished (2005)
COMMENT
Contact: Yeisoo Yu
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9585
Fax: 520 621 1259
Email: yeisoo@genome.arizona.edu
Plate: 0132 row: B column: 03.

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/organism="zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="mixed (silks, husks, ears, pollen, shoot
tips, leaf, root tips, whole seed, embryo)"
/dev_stage="varies by tissue"
/lab_host="PH10B T1 phage resistant"
/clone_lib="ZM BfB"

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Notes: Vector: pCMV-Sport 6.1; Site: EcoRV; Size: 2.8 kb; Library: Maize Full length cDNA library (3530 library).
 1. Tissues: silk, husk, ear, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A) + mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 day aleurone; 4.

immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona
(<http://www.genome.arizona.edu/orders/>).

ORIGIN

Query Match 71.2%; Score 17.8; DB 10; Length 685;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAACTCGAACGGAAGGCCTT 22
||||| ||||| ||||| ||||| |||||

Db 506 CAACTGGAACGGAAGGCCTT 486

RESULT 76

CO429338
LOCUS UI-M-HW0-crq-b-13-0-UI_r1 NIH_BMAP_HW0 Mus musculus cDNA clone
DEFINITION IMAGE:30681540 5', mRNA sequence.

ACCESSION CO429338
VERSION CO429338.1 GI:49675632
KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 695)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5.

FEATURES

source

1. 695
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30681540"
/tissue_type="whole eye"
/dev_stage="newborn (1, 5, 15 days)"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_HW0"
/note="Organ: Eye; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AATAATTACG. This library was created for the University

ORIGIN

Query Match 71.2%; Score 17.8; DB 8; Length 695;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAACTCGAACGGAAGGCCTT 22
||||| ||||| ||||| ||||| |||||

Db 355 CAACTCGAACTGAAAGGACTT 375

RESULT 77

BI649774
LOCUS 603279966F1_NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5319904 5',
DEFINITION mRNA sequence.

ACCESSION BI649774

VERSION BI649774.1 GI:15564010

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 700)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM1811 Row: d Column: 17
High quality sequence start: 62
High quality sequence stop: 684.

FEATURES

source

1. 700
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5319904"
/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam3"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."

ORIGIN

Query Match 71.2%; Score 17.8; DB 2; Length 700;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAACTCGAACGGAAGGCCTT 22
||||| ||||| ||||| ||||| |||||

Db 363 CAACTCGAACTGAAAGGACTT 383

RESULT 78

DV541234/c

LOCUS DV541234 710 bp mRNA linear EST 25-OCT-2005
 DEFINITION ZM_BFb0235018.f ZM_BFb Zea mays cDNA 3', mRNA sequence.
 ACCESSION DV541234
 VERSION DV541234.1 GI:78122850
 KEYWORDS EST.
 SOURCE Zea mays

ORGANISM

Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

AUTHORS 1 (bases 1 to 710)
 Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
 Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.

TITLE

Maize Full-length cDNA Project

JOURNAL

Unpublished (2005)

COMMENT

Contact: Yeisoo Yu
 Arizona Genomics Institute
 The University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA
 Tel: 520 626 9585
 Fax: 520 621 1259
 Email: yeisoo@genome.arizona.edu

Plate: 0235 row: O column: 18.

Location/Qualifiers

1. 710

FEATURES

source

1. 710

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="B73"

/db_xref="taxon:4577"

/tissue_type="mixed (silks, husks, ears, pollen, shoot

tips, leaf, root tips, whole seed, embryo)"

/dev_stage="varies by tissue"

/lab_host="DH10B T1 phage resistant"

/clone_lib="ZM_BFb"

/note="Vector: pCMV-SPORT 6.1; Site_1: EcoRV; Site 2:

NotI; Maize Full length cDNA library (3530 library)

created by Invitrogen from multiple tissues; Organ: silks,

husks, ears, pollen, shoot tips, leaf, root tips, whole

seed, embryo. This is a Gateway compatible vector.

permitting clone movement to new vector backbones for

expression in diverse host cells using recombination

rather than restriction enzymes. poly(A)+ mRNA was

prepared by Invitrogen, and equimolar amounts of RNA from

each of the 12 tissue samples were mixed together for

a normalization step was conducted against the mixture of

RNA sources. Tissues prepared: 1. just emerging silks; 2.

inner husks from ears of sample #1; 3. 20 dap aleurone; 4.

immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to

2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from

15 day old seedlings; all leaves with an expanded or

partially expanded sheath were removed; 8. mature leaf

tissue; 9. 0.5 cm long root tips from 15 day old

seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and

embryo; 12. 17 dap endosperm and embryo. All of the

sequenced clones in Maize Full-length cDNA Project will be

archived at the University of Arizona. Clones, high

density filters and amplified library can be ordered from

the University of Arizona

(http://www.genome.arizona.edu/orders/).

ORIGIN

Query Match 71.2%; Score 17.8; DB 10; Length 710;
 Best Local Similarity 90.5%; Pred. No. 2e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGACGAAAGGCCTT 22

|||||

Db 565 CAAGTCGACGAAAGGCCTT 545

RESULT 79

DT654257/c

LOCUS

DT654257 711 bp mRNA linear EST 07-SEP-2005
 DEFINITION ZM_BFb0127110.f ZM_BFb Zea mays cDNA 3', mRNA sequence.
 ACCESSION DT654257

VERSION DT654257.1 GI:74246343

KEYWORDS EST.

SOURCE Zea mays

ORGANISM

Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

AUTHORS 1 (bases 1 to 711)
 Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
 Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.

TITLE

Maize Full-length cDNA Project

JOURNAL

Unpublished (2005)

COMMENT

Contact: Yeisoo Yu
 Arizona Genomics Institute
 The University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA
 Tel: 520 626 9585
 Fax: 520 621 1259
 Email: yeisoo@genome.arizona.edu

Plate: 0127 row: I column: 10.

Location/Qualifiers

1. 711

FEATURES

source

1. 711

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="B73"

/db_xref="taxon:4577"

/tissue_type="mixed (silks, husks, ears, pollen, shoot

tips, leaf, root tips, whole seed, embryo)"

/dev_stage="varies by tissue"

/lab_host="DH10B T1 phage resistant"

/clone_lib="ZM_BFb"

/note="Vector: pCMV-SPORT 6.1; Site_1: EcoRV; Site 2:

NotI; Maize Full length cDNA library (3530 library)

created by Invitrogen from multiple tissues; Organ: silks,

husks, ears, pollen, shoot tips, leaf, root tips, whole

seed, embryo. This is a Gateway compatible vector.

permitting clone movement to new vector backbones for

expression in diverse host cells using recombination

rather than restriction enzymes. poly(A)+ mRNA was

prepared by Invitrogen, and equimolar amounts of RNA from

each of the 12 tissue samples were mixed together for

a normalization step was conducted against the mixture of

RNA sources. Tissues prepared: 1. just emerging silks; 2.

inner husks from ears of sample #1; 3. 20 dap aleurone; 4.

immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to

2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from

15 day old seedlings; all leaves with an expanded or

partially expanded sheath were removed; 8. mature leaf

tissue; 9. 0.5 cm long root tips from 15 day old

seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and

embryo; 12. 17 dap endosperm and embryo. All of the

sequenced clones in Maize Full-length cDNA Project will be

archived at the University of Arizona. Clones, high

density filters and amplified library can be ordered from

the University of Arizona

(http://www.genome.arizona.edu/orders/).

ORIGIN

Query Match 71.2%; Score 17.8; DB 10; Length 711;
 Best Local Similarity 90.5%; Pred. No. 2e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGACGAAAGGCCTT 22

|||||

Db 510 CAAGTCGACGAAAGGCCTT 490

RESULT 80

DT945215/c

LOCUS DT945215 714 bp mRNA linear EST 21-SEP-2005
DEFINITION ZM_BF0132F09.f ZM_BFB Zea mays cDNA 3', mRNA sequence.
ACCESSION DT945215
VERSION DT945215.1 GI:76018045
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 714)
AUTHORS Kim, H., Collura, K., Wisotzki, M., Smart, D., Kudrna, D., Muller, C.,
 Rao, K., Haller, K., Wing, K., Soderlund, C., Walbot, V. and Yu, Y.
TITLE Maize Full-length cDNA Project
JOURNAL Unpublished (2005)
COMMENT Contact: Yeisoo Yu
 Arizona Genomics Institute
 The University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA
 Tel: 520 626 9585
 Fax: 520 621 1259
 Email: yeisoo@genome.arizona.edu
 Plate: 0132 row: F column: 09.
FEATURES Location/Qualifiers
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 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="B73"
 /db_xref="taxon:4577"
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 tips, leaf, root tips, whole seed, embryo)"
 /dev_stages="varies by tissue"
 /lab_host="DH10B T1 phage resistant"
 /clone_lib="ZM BPb"
 /note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV, Site 2:
 NotI; Maize Full length cDNA library (3530 library)
 created by invitrogen from multiple tissues; Organ: silks,
 husks, ears, pollen, shoot tips, leaf, root tips, whole
 seed, embryo. This is a Gateway compatible vector,
 permitting clone movement to new vector backbones for
 expression in diverse host cells using recombination
 rather than restriction enzymes. poly(A)+ mRNA was
 prepared by invitrogen, and equimolar amounts of RNA from
 each of the 12 tissue samples were mixed together for
 selection of mRNA with a 5' cap. After synthesis of cDNA,
 a normalization step was conducted against the mixture of
 RNA sources. Tissues prepared: 1. just emerging silks; 2.
 inner husks from ears of sample #1; 3. 20 dap aleurone; 4.
 immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to
 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from
 15 day old seedlings; all leaves with an expanded or
 partially expanded sheath were removed; 8. mature leaf
 tissue; 9. 0.5 cm long root tips from 15 day old
 seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and
 embryo; 12. 17 dap endosperm and embryo. All of the
 sequenced clones in Maize Full-length cDNA Project will be
 archived at the University of Arizona. Clones, high
 density filters and amplified library can be ordered from
 the University of Arizona
 (http://www.genome.arizona.edu/orders/)."
ORIGIN
 Query Match 71.2%; Score 17.8; DB 10; Length 714;
 Best Local Similarity 90.5%; Pred. No. 2e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 2 CAAGTCGAACGGAAGGCCTT 22
 ||||| ||||| ||||| ||||| |||||
 Db 513 CAAGTGAACGGAAGGCCTT 493
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RESULT 81
BF099995
 Query Match 71.2%; Score 17.8; DB 7; Length 716;
 Best Local Similarity 90.5%; Pred. No. 2e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 2 CAAGTCGAACGGAAGGCCTT 22
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 Db 513 CAAGTGAACGGAAGGCCTT 533
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RESULT 82
BQ445033
LOCUS BQ445033 729 bp mRNA linear EST 29-MAY-2002
DEFINITION UI-M-ERO-bxp-o-13-0-UI.r1 NIH_BMAP_ERO Mus musculus cDNA clone
 IMAGE:5711460 5', mRNA sequence.
ACCESSION BQ445033
VERSION BQ445033.1 GI:21248145
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 729)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: csapbs@mail.nih.gov
 Tissue Procurement: Dr. James Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

LOCUS BF099995 716 bp mRNA linear EST 19-OCT-2000
DEFINITION 601752156F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3980005 5',
 mRNA sequence.
ACCESSION BF099995
VERSION BF099995.1 GI:10882521
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 716)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: csapbs@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM9174 row: o column: 14
 High quality sequence stop: 670.
FEATURES Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone_image="IMAGE:3980005"
 /tissue_type="tumor, biopsy sample"
 /dev_stage="3 months, virgin"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP Mam1"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies. Investigator
 providing samples: Gilbert Smith, NIH"
ORIGIN
 Query Match 71.2%; Score 17.8; DB 7; Length 716;
 Best Local Similarity 90.5%; Pred. No. 2e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 2 CAAGTCGAACGGAAGGCCTT 22
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 Db 513 CAAGTCGAACGGAAGGCCTT 533
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RESULT 82
BQ445033
LOCUS BQ445033 729 bp mRNA linear EST 29-MAY-2002
DEFINITION UI-M-ERO-bxp-o-13-0-UI.r1 NIH_BMAP_ERO Mus musculus cDNA clone
 IMAGE:5711460 5', mRNA sequence.
ACCESSION BQ445033
VERSION BQ445033.1 GI:21248145
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 729)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: csapbs@mail.nih.gov
 Tissue Procurement: Dr. James Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

FEATURES

source
Location/Qualifiers
1. .729
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:5711460"
/tissue_type="whole brain"
/dev_stage="embryo 15.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_ER0"
/note="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA
tail, is GTGCGTGGAA. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institutes of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 71.2%; Score 17.8; DB 3; Length 729;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22

Db 142 CAAGTCGAACGGAAGGACTT 162

RESULT 83

CO383984
LOCUS
DEFINITION
AGENCOURT 26623469 NIH MGC 253 Rattus norvegicus cDNA clone
IMAGE:7304949 5', mRNA sequence.

CO383984

CO383984

CO383984.1 GI:49489807

EST.

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Muridae; Murinae; Rattus.

1 (bases 1 to 738)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical

College of Wisconsin

cdna Library Preparation: Express Genomics

cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LHAM15342 row: f column: 19

High quality sequence stop: 612.

Location/Qualifiers

1. .738

/organism="Rattus norvegicus"

/mol_type="mRNA"

/db_xref="taxon:10116"

/clone="IMAGE:7304949"

/tissue_type="Ovary - Brown Norway Line 3 Age 8 weeks.

Tissues were snap-frozen and transferred in -70C. RNase

free the entire procedure."

/lab_host="DH10B Tona"

/clone_lib="NIH_MGC_253"

/note="Organ: ovary; Vector: pExpress-1; Site 1: EcoRV;

Site 2: NotI; RNA obtained from female animals at 8 wk

old. Tissues were snap-frozen and kept at -80C for two

days before RNA extraction and purification (Tri-reagent

method). cDNA was primed using oligo-dT primer:

5'-pGACTAGTTTGTAGTCGAGCGCCGCCCTT-3' and cloned into

the EcoRV/NotI sites of pExpress-1. Size-selection >1.25Kb

resulted in an average insert size of 1.5 kb. This primary

library is normalized (non-normalized primary library is

NIH MGC 252) and was constructed by Express Genomics

(Frederick, MD). Note: this is a NIH_MGC library."

ORIGIN

Query Match 71.2%; Score 17.8; DB 8; Length 738;

Best Local Similarity 90.5%; Pred. No. 2e+03;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22

Db 202 CAAGTCGAACGGAAGGACTT 222

RESULT 84

BI414831/c

LOCUS

DEFINITION

602990771F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5146936 5',

mRNA sequence.

BI414831

BI414831

BI414831.1 GI:15175754

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Muridae; Murinae; Mus.

1 (bases 1 to 739)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cdna Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LHAM11362 row: m column: 17

High quality sequence start: 23

High quality sequence stop: 739.

Location/Qualifiers

1. .739

/organism="Mus musculus"

/mol_type="mRNA"

/strain="Czech II"

/db_xref="taxon:10090"

FEATURES

source


```

/clone="IMAGE:5145936"
/tissue_type="pooled lung tumors"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NCI CGAP Lu33"
/note="Organ: lung; Vector: pT7T3D-PacI; Site 1: NotI;
Site 2: EcoRI; 1st strand cDNA was prepared from mRNA
obtained from pooled lung tumors with a Not I - oligo(dT)
primer [5']
TGTTACCAATCTGAAGTGGAGCGCGCCTCTGTTTTTTTTTTTTTTT 3'}.
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN
Query Match 71.2%; Score 17.8; DB 2; Length 739;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAACTCGAAGCGAAGGCCTT 22
|||||
Db 708 CAACTCGAAGCGAAGGCCTT 688

RESULT 85
BX855983/c
LOCUS 740 bp mRNA linear EST 20-MAY-2004
DEFINITION BX855983 tcay Oncorhynchus mykiss cDNA clone tcay0040b.g.16 5prim,
mRNA sequence.
BX855983
BX855983.2 GI:42752904
EST.
Oncorhynchus mykiss (rainbow trout)
Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 740)
Govoroun,M., Guiguen,Y. and Le Gac,F.
Construction and primary characterization of normalized cDNA
libraries in rainbow trout, Oncorhynchus mykiss
Unpublished (2003)
On Dec 16, 2003 this sequence version replaced gi:39952993.
Contact: Guiguen Y
INRA - SCRIBE
Campus de beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenassupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0040 row: 9 column: 16
Seq primer: M13R.
Location/Qualifiers
1. .740
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="tcay0040b.g.16"
/tissue_type="adipose tissue, blood, brain,
differentiating gonads, gills, interrenal, intestine,
kidney, liver, muscle, ovary, pituitary, testis"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/clone_lib="tcay"
/note="Vector: pT7T3D-PacI; Rainbow trout multi-tissues -
normalized + 1 subraction (tcay); Clone distribution :
AGENAE Resource centre. Francois PIUMI,
Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, France, +33 (0) 1.34.65.28.02, +33

FEATURES
source

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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

source
 1. 745
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="E860117P18"
 /cell_type="8 cells"
 /dev_stage="8 cells embryo"
 /clone_lib="RIKEN full-length enriched, 8 cells embryo"

ORIGIN

Query Match 71.2%; Score 17.8; DB 4; Length 745;
 Best Local Similarity 90.5%; Pred. No. 2e+03; Length 745;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 CAAGTCGAACGGAAGGCCTT 22
 Db 368 CAAGTCGAACGGAAGGACTT 388

RESULT 87

DV942547/c
 LOCUS 1000137-E05.T7-1 UGI-Reseq Zea mays cDNA, mRNA linear EST 05-DEC-2005
 DEFINITION DV942547
 ACCESSION DV942547
 VERSION DV942547.1 GI:83278539
 KEYWORDS EST.
 SOURCE Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1. (bases 1 to 746)
 Zhou, R.L., Shendelman, J.M., Borsuk, L.A., Chen, H.D., Chen, Y.R. and Schnable, P.S.

REFERENCE

Authors Zhou, R.L., Shendelman, J.M., Borsuk, L.A., Chen, H.D., Chen, Y.R. and Schnable, P.S.
 Title Resequencing Unigene I EST set
 Journal Unpublished (2005)
 Comment Contact: Patrick S. Schnable
 Schnable Laboratory
 Iowa State University
 2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA
 Tel: 515-294-0975
 Fax: 515-294-5256
 Email: schnable@iastate.edu

FEATURES

source
 1. 746
 Location/Qualifiers
 Insert Length: 746 Std Error: 0.00.
 /organism="Zea mays"
 /mol_type="mRNA"
 /db_xref="taxon:4577"
 /clone_lib="UGI-Reseq"

ORIGIN

Query Match 71.2%; Score 17.8; DB 10; Length 746;

Best Local Similarity 90.5%; Pred. No. 2e+03; Length 752 bp
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 CAAGTCGAACGGAAGGCCTT 22
 Db 613 CAAGTCGAACGGAAGGCCTT 593

RESULT 88

DR794419/c
 LOCUS 1000137-E05.f ZM_BFB Zea mays cDNA 3', mRNA linear EST 27-JUL-2005
 DEFINITION DR794419
 ACCESSION DR794419
 VERSION DR794419.1 GI:71315610
 KEYWORDS EST.
 SOURCE Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; PACCAD clade; Panicoideae; Andropogoneae; Zea.
 1. (bases 1 to 752)
 Kim, H., Collura, K., Wissotski, M., Smart, D., Kudrna, D., Muller, C., Rao, K., Haller, K., Wing, R., Soderlund, C., Walbot, V. and Yu, Y.
 Maize Full-length cDNA Project
 Unpublished (2005)
 Contact: Yeisoo Yu
 Arizona Genomics Institute
 The University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA
 Tel: 520 626 9585
 Fax: 520 621 1259
 Email: yeisoo@genome.arizona.edu
 Plate: 0015 row: C column: 05.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source
 1. 752
 Location/Qualifiers
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /tissue_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"
 /dev_stage="varies by tissue"
 /lab_host="DH10B T1 phage resistant"
 /clone_lib="ZM BFB"
 /note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (<http://www.genome.arizona.edu/orders/>)."

ORIGIN

Query Match 71.2%; Score 17.0; DB 10; Length 752;

Best Local Similarity 90.5%; Pred. No. 2e+03; Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		Best Local Similarity 90.5%; Pred. No. 2e+03; Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	2 CAAGTCGAACGGAAGGCCTT 22 	QY	2 CAAGTCGAACGGAAGGCCTT 22
DB	583 CAAGTGGAAACGAAAGGCCTT 563	DB	510 CAAGTGGAAACGAAAGGCCTT 490
RESULT 89		RESULT 90	
DVI64476/c		DR786717/c	
LOCUS	DVI64476 753 bp mRNA linear EST 04-OCT-2005	LOCUS	DR786717 777 bp mRNA linear EST 27-JUL-2005
DEFINITION	ZM_BF60160P07.f ZM_BFB Zea mays cDNA 3', mRNA sequence.	DEFINITION	ZM_BF50003M10.f ZM_BFB Zea mays cDNA 3', mRNA sequence.
ACCESSION	DVI64476	ACCESSION	DR786717
VERSION	DVI64476.1 GI:76911873	VERSION	DR786717.1 GI:71301364
KEYWORDS	EST.	KEYWORDS	EST.
SOURCE	Zea mays	SOURCE	Zea mays
ORGANISM	Zea mays	ORGANISM	Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.	
REFERENCE	1 (bases 1 to 753)	REFERENCE	1 (bases 1 to 777)
AUTHORS	Kim,H., Collura,K., Wisotski,M., Smart,D., Kudrna,D., Muller,C., Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.	AUTHORS	Kim,H., Collura,K., Wisotski,M., Smart,D., Kudrna,D., Muller,C., Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
TITLE	Maize Full-length cDNA Project	TITLE	Maize Full-length cDNA Project
JOURNAL	Unpublished (2005)	JOURNAL	Unpublished (2005)
COMMENT	Contact: Yeisoo Yu Arizona Genomics Institute The University of Arizona Forbes Building Room 303, Tucson, AZ 85721-0036, USA Tel: 520 626 9585 Fax: 520 621 1259 Email: yeisoo@genome.arizona.edu Plate: 0160 row: P column: 07.	COMMENT	Contact: Yeisoo Yu Arizona Genomics Institute The University of Arizona Forbes Building Room 303, Tucson, AZ 85721-0036, USA Tel: 520 626 9585 Fax: 520 621 1259 Email: yeisoo@genome.arizona.edu Plate: 0003 row: M column: 18.
FEATURES	Location/Qualifiers	FEATURES	Location/Qualifiers
source	1..753	source	1..777
/organism="Zea mays"		/organism="Zea mays"	
/mol_type="mRNA"		/mol_type="mRNA"	
/cultivar="B73"		/cultivar="B73"	
/db_xref="taxon:4577"		/db_xref="taxon:4577"	
/tissue_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"		/tissue_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"	
/dev_stage="varies by tissue"		/dev_stage="varies by tissue"	
/lab_host="DH10B T1 phage resistant"		/lab_host="DH10B T1 phage resistant"	
/clone_lib="ZM BFB"		/clone_lib="ZM BFB"	
/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (http://www.genome.arizona.edu/orders/)."		/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (http://www.genome.arizona.edu/orders/)."	
ORIGIN		ORIGIN	
Query Match	71.2%; Score 17.8; DB 10; Length 753;	Query Match	71.2%; Score 17.8; DB 10; Length 777;

Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGAAAGGCCTT 22
|||||
Db 535 CAAGTCGAACGAAAGGCCTT 515

RESULT 91
DR954333/c
LOCUS ZM BFB0046F03.f 777 bp mRNA linear EST 03-AUG-2005
DEFINITION ZM BFB0046F03.f ZM_BFB Zea mays cDNA 3', mRNA sequence.
ACCESSION DR954333
VERSION DR954333.1 GI:71756396
KEYWORDS EST.
SOURCE Zea mays

ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 777)

AUTHORS Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.

TITLE Maize Full-length cDNA Project

JOURNAL Unpublished (2005)

COMMENT

Contact: Yeisoo Yu

Arizona Genomics Institute

The University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9585

Fax: 520 621 1259

Email: yeisoo@genome.arizona.edu

Plate: 0046 row: F column: 03.

Location/Qualifiers

1. .777

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="B73"

/db_xref="taxon:4577"

/tissue_type="mixed (silks, husks, ears, pollen, shoot

tips, leaf, root tips, whole seed, embryo)"

/dev_stage="varies by tissue"

/lab_hosts="DH10B T1 phage resistant"

/clone_lib="ZM BFB"

/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2:

NotI; Maize Full length cDNA library (3530 library)

created by Invitrogen from multiple tissues; Organ: silks,

husks, ears, pollen, shoot tips, leaf, root tips, whole

seed, embryo. This is a Gateway compatible vector,

permitting clone movement to new vector backbones for

expression in diverse host cells using recombination

rather than restriction enzymes. poly(A)+ mRNA was

prepared by Invitrogen, and equimolar amounts of RNA from

each of the 12 tissue samples were mixed together for

selection of mRNA with a 5' cap. After synthesis of cDNA,

a normalization step was conducted against the mixture of

RNA sources. Tissues prepared: 1. just emerging silks; 2.

inner husks from ears of sample #1; 3. 20 dap aleurone; 4.

immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to

15 day old seedlings; all leaves with an expanded or

partially expanded sheath were removed; 8. mature leaf

tissue; 9. 0.5 cm long root tips from 15 day old

seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and

embryo; 12. 17 dap endosperm and embryo. All of the

sequenced clones in Maize Full-length cDNA Project will be

archived at the University of Arizona. Clones, high

density filters and amplified library can be ordered from

the University of Arizona

(http://www.genome.arizona.edu/orders/).

ORIGIN

Query Match 71.2%; Score 17.8; DB 10; Length 777;

Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGAAAGGCCTT 22
|||||
Db 535 CAAGTCGAACGAAAGGCCTT 515

RESULT 92
DV164117/c

LOCUS ZM BFB0160H01.f 780 bp mRNA linear EST 04-OCT-2005

DEFINITION ZM BFB0160H01.f ZM_BFB Zea mays cDNA 3', mRNA sequence.

ACCESSION DV164117

VERSION DV164117.1 GI:76910962

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 780)

AUTHORS Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,

Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.

TITLE Maize Full-length cDNA Project

JOURNAL Unpublished (2005)

COMMENT

Contact: Yeisoo Yu

Arizona Genomics Institute

The University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9585

Fax: 520 621 1259

Email: yeisoo@genome.arizona.edu

Plate: 0160 row: H column: 01.

Location/Qualifiers

1. .780

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="B73"

/db_xref="taxon:4577"

/tissue_type="mixed (silks, husks, ears, pollen, shoot

tips, leaf, root tips, whole seed, embryo)"

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/lab_hosts="DH10B T1 phage resistant"

/clone_lib="ZM BFB"

/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2:

NotI; Maize Full length cDNA library (3530 library)

created by Invitrogen from multiple tissues; Organ: silks,

husks, ears, pollen, shoot tips, leaf, root tips, whole

seed, embryo. This is a Gateway compatible vector,

permitting clone movement to new vector backbones for

expression in diverse host cells using recombination

rather than restriction enzymes. poly(A)+ mRNA was

prepared by Invitrogen, and equimolar amounts of RNA from

each of the 12 tissue samples were mixed together for

selection of mRNA with a 5' cap. After synthesis of cDNA,

a normalization step was conducted against the mixture of

RNA sources. Tissues prepared: 1. just emerging silks; 2.

inner husks from ears of sample #1; 3. 20 dap aleurone; 4.

immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to

15 day old seedlings; all leaves with an expanded or

partially expanded sheath were removed; 8. mature leaf

tissue; 9. 0.5 cm long root tips from 15 day old

seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and

embryo; 12. 17 dap endosperm and embryo. All of the

sequenced clones in Maize Full-length cDNA Project will be

archived at the University of Arizona. Clones, high

density filters and amplified library can be ordered from

the University of Arizona

(http://www.genome.arizona.edu/orders/).

ORIGIN

Query Match 71.2%; Score 17.8; DB 10; Length 780;

Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22
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Db 510 CAAGTCGAACGGAAGGCCTT 490

RESULT 93
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LOCUS
DEFINITION AGNCOURT_13687210 NIH_MGC_176 Mus musculus cDNA clone
IMAGE:30304304 5', mRNA sequence.
CB953248
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 808)
NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Michael Brownstein Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILLNL at:
<http://image.llnl.gov>

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Location/Qualifiers
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/clone="IMAGE:30304304"
/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH_MGC_176"
/note="Organ: kidney; Vector: pDNR-LIB; Site 1: SfiI
(ggcattatggcc); Site 2: SfiI (ggcgctcggcc); cDNA made
by oligo-dT priming and directionally cloned. 5' and 3'
adaptors were used in cloning as follows:
5'-AAGCAGTGTATCAACGAGATGGCCATTACGCCGG-3' and
5'-ATTCTAGAGCGCGCGCCCATG-dt(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.5 kb
size fraction. Library created in the laboratory of M.
Brownstein (NIH, NIH). Note: this is a NIH_MGC Library."

FEATURES
source

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/clone_lib="ZM_BFB"
/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2:
NotI; Maize Full length cDNA library (3530 library)
created by Invitrogen from multiple tissues; Organ: silks,
husks, ears, pollen, shoot tips, leaf, root tips, whole
seed, embryo. This is a Gateway compatible vector,
permitting clone movement to new vector backbones for
expression in diverse host cells using recombination
rather than restriction enzymes. poly(A) + mRNA was
prepared by Invitrogen, and equimolar amounts of RNA from
each of the 12 tissue samples were mixed together for
selection of mRNA with a 5' cap. After synthesis of cDNA,
a normalization step was conducted against the mixture of
RNA sources. Tissues prepared: 1 just emerging silks; 2.
inner husks from ears of sample #1; 3. 20 dap aleurone; 4.
immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to
2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from
15 day old seedlings; all leaves with an expanded or
partially expanded sheath were removed; 8. mature leaf
tissue; 9. 0.5 cm long root tips from 15 day old
seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and
embryo; 12. 17 dap endosperm and embryo. All of the
sequenced clones in Maize Full-length cDNA Project will be
archived at the University of Arizona. Clones, high
density filters and amplified library can be ordered from
the University of Arizona
(<http://www.genome.arizona.edu/orders/>) .

ORIGIN

Query Match 71.2%; Score 17.8; DB 4; Length 808;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22
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Db 394 CAAGTCGAACGGAAGGCCTT 414

RESULT 94
DR794420
LOCUS
DEFINITION ZM_BFB0015C05.r ZM_BFB Zea mays cDNA 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
Zea mays

ORGANISM

Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 816)
Kim, H., Collura, K., Wissotski, M., Smart, D., Kudrna, D., Muller, C.,
Rao, K., Haller, K., Wing, R., Soderlund, C., Walbot, V. and Yu, Y.
Maize Full-length cDNA Project
Unpublished (2005)
Contact: Veisoo Yu
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9585
Fax: 520 621 1259
Email: veisoo@genome.arizona.edu
Plate: 0015 row: C column: 05.
Location/Qualifiers
1. 816
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="mixed (silks, husks, ears, pollen, shoot
tips, leaf, root tips, whole seed, embryo)"
/dev_stage="varies by tissue"
/lab_host="DH10B T1 phage resistant"
/clone_lib="ZM_BFB"
/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2:
NotI; Maize Full length cDNA library (3530 library)
created by Invitrogen from multiple tissues; Organ: silks,
husks, ears, pollen, shoot tips, leaf, root tips, whole
seed, embryo. This is a Gateway compatible vector,
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expression in diverse host cells using recombination
rather than restriction enzymes. poly(A) + mRNA was
prepared by Invitrogen, and equimolar amounts of RNA from
each of the 12 tissue samples were mixed together for
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a normalization step was conducted against the mixture of
RNA sources. Tissues prepared: 1 just emerging silks; 2.
inner husks from ears of sample #1; 3. 20 dap aleurone; 4.
immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to
2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from
15 day old seedlings; all leaves with an expanded or
partially expanded sheath were removed; 8. mature leaf
tissue; 9. 0.5 cm long root tips from 15 day old
seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and
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(<http://www.genome.arizona.edu/orders/>) .

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

ORIGIN

Query Match 71.2%; Score 17.8; DB 10; Length 816;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22
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Db 776 CAAGTCGAACGGAAGGCCTT 796

RESULT 95
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LOCUS
DEFINITION ZM_BFB0160P07.r ZM_BFB Zea mays cDNA 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
Zea mays

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ORGANISM      Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS      Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
              Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
TITLE        Maize Full-length cDNA Project
JOURNAL      Unpublished (2005)
COMMENT      Contact: Yeisoo Yu
              Arizona Genomics Institute
              The University of Arizona
              Forbes Building Room 303, Tucson, AZ 85721-0036, USA
              Tel: 520 626 9585
              Fax: 520 621 1259
              Email: yeisoo@genome.arizona.edu
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                 /cultivar="B73"
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                 NotI; Maize Full length cDNA library (3530 library)
                 created by Invitrogen from multiple tissues; Organ: silks,
                 husks, ears, pollen, shoot tips, leaf, root tips, whole
                 seed, embryo. This is a Gateway compatible vector,
                 permitting clone movement to new vector backbones for
                 expression in diverse host cells using recombination
                 rather than restriction enzymes. poly(A) + mRNA was
                 prepared by Invitrogen, and equimolar amounts of RNA from
                 each of the 12 tissue samples were mixed together for
                 selection of mRNA with a 5' cap. After synthesis of cDNA,
                 a normalization step was conducted against the mixture of
                 RNA sources. Tissues prepared: 1. just emerging silks; 2.
                 inner husks from ears of sample #1; 3. 20 dap aleurone; 4.
                 immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to
                 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from
                 15 day old seedlings; all leaves with an expanded or
                 partially expanded sheath were removed; 8. mature leaf
                 tissue; 9. 0.5 cm long root tips from 15 day old
                 seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and
                 embryo; 12. 17 dap endosperm and embryo. All of the
                 sequenced clones in Maize Full-length cDNA Project will be
                 archived at the University of Arizona. Clones, high
                 density filters and amplified library can be ordered from
                 the University of Arizona
                 (http://www.genome.arizona.edu/orders/)."

ORIGIN
Query Match      71.2%; Score 17.8; DB 10; Length 820;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 96
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LOCUS      DY361640      824 bp      mRNA      linear      EST 09-FEB-2006
DEFINITION      ZO_Ed0007M16.r ZO_Ed Zingiber officinale cDNA clone ZO_Ed0007M16
3', mRNA sequence.
ACCESSION      DY361640
VERSION      DY361640.1 GI:87094856
KEYWORDS      EST.

ORGANISM      Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS      Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
              Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
TITLE        Maize Full-length cDNA Project
JOURNAL      Unpublished (2005)
COMMENT      Contact: Yeisoo Yu
              Arizona Genomics Institute
              The University of Arizona
              Forbes Building Room 303, Tucson, AZ 85721-0036, USA
              Tel: 520 626 9585
              Fax: 520 621 1259
              Email: yeisoo@genome.arizona.edu
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ORIGIN
Query Match      71.2%; Score 17.8; DB 10; Length 824;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4  AGTCGAACGGAAGGCCCTTTC 24
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DEFINITION      ZM_BFB003M18.r ZM_BFB Zea mays cDNA 5', mRNA sequence.
ACCESSION      DR786718
VERSION      DR786718.1 GI:71301367
KEYWORDS      EST.
SOURCE      Zea mays
ORGANISM      Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS      Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
              Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
TITLE        Maize Full-length cDNA Project
JOURNAL      Unpublished (2005)
COMMENT      Contact: Yeisoo Yu
              Arizona Genomics Institute
              The University of Arizona
              Forbes Building Room 303, Tucson, AZ 85721-0036, USA
              Tel: 520 626 9585
              Fax: 520 621 1259
              Email: yeisoo@genome.arizona.edu
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SOURCE      Zingiber officinale
ORGANISM      Zingiber officinale
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Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales;
Zingiberaceae; Zingiber.
REFERENCE
AUTHORS      Ma,X.Q., Koo,H.J., Haller,K.P., Soderlund,C.A. and Gang,D.R.
TITLE        Comparative Analysis of Expressed Sequence Tags from Different
              Organs of Ginger and Turmeric. Insights into Specialized Metabolism
              in Traditional Medicinal Plants
JOURNAL      Unpublished (2006)
COMMENT      Contact: David R. Gang
              Department of Plant Sciences
              The University of Arizona
              Forbes Building Room 303, Tucson, AZ 85721-0036, USA
              Tel: 520 621 7154
              Fax: 520 621 7186
              Email: gang@ag.arizona.edu
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ORIGIN
Query Match      71.2%; Score 17.8; DB 10; Length 824;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4  AGTCGAACGGAAGGCCCTTTC 24
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Db      337 337 AGACGAACGGAAGGCCCTTTC 357

RESULT 97
DR786718
LOCUS      DR786718      827 bp      mRNA      linear      EST 27-JUL-2005
DEFINITION      ZM_BFB003M18.r ZM_BFB Zea mays cDNA 5', mRNA sequence.
ACCESSION      DR786718
VERSION      DR786718.1 GI:71301367
KEYWORDS      EST.
SOURCE      Zea mays
ORGANISM      Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS      Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
              Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
TITLE        Maize Full-length cDNA Project
JOURNAL      Unpublished (2005)
COMMENT      Contact: Yeisoo Yu
              Arizona Genomics Institute
              The University of Arizona
              Forbes Building Room 303, Tucson, AZ 85721-0036, USA
              Tel: 520 626 9585
              Fax: 520 621 1259
              Email: yeisoo@genome.arizona.edu
              Plate: 0003 row: M column: 18.
              Location/Qualifiers
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                 /organism="Zea mays"
                 /mol_type="mRNA"
                 /cultivar="B73"
                 /db_xref="taxon:4577"

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/tissue_type="mixed (silks, husks, ears, pollen, shoot
tips, leaf, root tips, whole seed, embryo)"
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NotI; Maize Full length cDNA library (3530 library)
created by Invitrogen from multiple tissues; Organ: silks,
husks, ears, pollen, shoot tips, leaf, root tips, whole
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RNA sources. Tissues prepared: 1. just emerging silks; 2.
inner husks from ears of sample #1; 3. 20 dap aleurone; 4.
immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to
2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from
15 day old seedlings; all leaves with an expanded or
partially expanded sheath were removed; 8. mature leaf
tissue; 9. 0.5 cm long root tips from 15 day old
seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and
embryo; 12. 17 dap endosperm and embryo. All of the
sequenced clones in Maize Full-length cDNA Project will be
archived at the University of Arizona. Clones, high
density filters and amplified library can be ordered from
the University of Arizona
(http://www.genome.arizona.edu/orders/)."

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ORIGIN

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Query Match 71.2%; Score 17.8; DB 10; Length 827;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 774 CAAGTGAACGGAAGGCCTT 794
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RESULT 98
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DEFINITION DR966931
ACCESSION DR966931.1 GI:71768994
VERSION EST.
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1. (Bases 1 to 848)
Kim,H., Collura,K., Wissorski,M., Smart,D., Kudrna,D., Muller,C.,
Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
Maize Full-length cDNA Project
Unpublished (2005)
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Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9585
Fax: 520 621 1259
Email: yeisoo@genome.arizona.edu
Plate: 0087 row: 1 column: 16.
Location/Qualifiers
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/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4579"
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FEATURES

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source
/tissue_type="mixed (silks, husks, ears, pollen, shoot
tips, leaf, root tips, whole seed, embryo)"
/dev_stage="varies by tissue"
/lab_hosts="DH10B T1 phage resistant"
/clone_lib="ZM_BFb"
/notes="Vector: pCMV-SPORT 6.1; Site_1: EcoRV; Site_2:
NotI; Maize Full length cDNA library (3530 library)
created by Invitrogen from multiple tissues; Organ: silks,
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seed, embryo. This is a Gateway compatible vector,
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each of the 12 tissue samples were mixed together for
selection of mRNA with a 5' cap. After synthesis of cDNA,
a normalization step was conducted against the mixture of
RNA sources. Tissues prepared: 1. just emerging silks; 2.
inner husks from ears of sample #1; 3. 20 dap aleurone; 4.
immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to
2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from
15 day old seedlings; all leaves with an expanded or
partially expanded sheath were removed; 8. mature leaf
tissue; 9. 0.5 cm long root tips from 15 day old
seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and
embryo; 12. 17 dap endosperm and embryo. All of the
sequenced clones in Maize Full-length cDNA Project will be
archived at the University of Arizona. Clones, high
density filters and amplified library can be ordered from
the University of Arizona
(http://www.genome.arizona.edu/orders/)."

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ORIGIN

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Query Match 71.2%; Score 17.8; DB 10; Length 848;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 2 CAAGTCGAACGGAAGGCCTT 22
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Db 777 CAAGTGAACGGAAGGCCTT 797
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RESULT 99
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LOCUS DT876921
DEFINITION DT876921 851 bp mRNA linear EST 18-SEP-2005
AGENCOURT 58666791 NIH_ZGC_9 Danio rerio cDNA clone IMAGE:8131516
5', mRNA sequence.
DT876921
DT876921.1 GI:75846661
VERSION EST.
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1. (Bases 1 to 851)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Chi-Bin Chien
cDNA Library Preparation: Dr. Sumio Sugano
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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FEATURES

source

Location/Qualifiers

1. 851

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/clones="IMAGE:8131516"

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/lab_host="DH10B Tona"

/clone_lib="NIH_ZGC_9"

/note="Organ: eye; Vector: pME18S-FL3; Site 1: DraIII; Site 2: DraIII; 1st strand cDNA was primed with an oligo(dT) primer

[GGGCTGAGAGCGCCTATGTGGCTTTTITTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [GGCCUACUG], digested and directionally cloned into distinct DraIII sites of the pME18S-FL3. Library was size selected for 1.0 kb, with a average insert size of ~1.2kb, and is not amplified. Library constructed by Yutaka Suzuki (University of Tokyo Institute of Medical Science). Custom primers recommended for sequencing: 5' end primer 5'-GGATGTGCTCTTACTTCTA-3' and 3' end primer 5'-CGACTCGAGTCGACACA-3'. Note: This is a Zebrafish Gene Collection (ZGC) library"

ORIGIN

Query Match 71.2%; Score 17.8; DB 10; Length 851;

Best Local Similarity 90.5%; Pred. No. 2e+03; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 2;

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RESULT 100

BI664538

LOCUS

DEFINITION 603290164F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5324391 5', 856 bp mRNA linear EST 12-SEP-2001

ACCESSION BI664538

VERSION BI664538.1 GI:15578771

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 856)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: Jeffrey Green M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

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FEATURES

source

Location/Qualifiers

1. 851

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[GGGCTGAGAGCGCCTATGTGGCTTTTITTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [GGCCUACUG], digested and directionally cloned into distinct DraIII sites of the pME18S-FL3. Library was size selected for 1.0 kb, with a average insert size of ~1.2kb, and is not amplified. Library constructed by Yutaka Suzuki (University of Tokyo Institute of Medical Science). Custom primers recommended for sequencing: 5' end primer 5'-GGATGTGCTCTTACTTCTA-3' and 3' end primer 5'-CGACTCGAGTCGACACA-3'. Note: This is a Zebrafish Gene Collection (ZGC) library"

ORIGIN

Query Match 71.2%; Score 17.8; DB 2; Length 856;

Best Local Similarity 90.5%; Pred. No. 2e+03; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 2;

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Db 530 CAAGTCGAACTGAAAGGACTT 550

Search completed: May 19, 2006, 07:05:41

Job time : 1696.99 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2006, 23:59:38 ; Search time 76.506 Seconds
(without alignments)
611.425 Million cell updates/sec

Title: US-10-665-708-21

Perfect score: 25

Sequence: 1 gcaagtcgaacgaaaggcttctg 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	21	84.0	22	US-09-738-274-23	Sequence 23, Appl
7	21	84.0	1475	US-08-641-291A-92	Sequence 92, Appl
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15	19.8	79.2	1464	US-09-726-774-7	Sequence 134, App
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145	15.6	62.4	1869	3	US-09-328-352-650	Sequence 650, App	c 218	15.4	61.6	37711	3	US-09-949-016-12832	Sequence 12832, A
c 146	15.6	62.4	2014	3	US-09-270-767-13561	Sequence 13561, A	c 219	15.4	61.6	37712	3	US-09-949-016-16704	Sequence 16704, A
c 147	15.6	62.4	2409	3	US-09-252-991A-1259	Sequence 1259, App	c 220	15.4	61.6	72455	3	US-09-949-016-13793	Sequence 13793, A
c 148	15.6	62.4	4009	3	US-08-902-540-341	Sequence 341, App	221	15.4	61.6	103792	3	US-09-949-016-13553	Sequence 13553, A
149	15.6	62.4	12759	3	US-09-949-016-16299	Sequence 16299, App	222	15.4	61.6	103993	3	US-09-949-016-12317	Sequence 12317, A
150	15.6	62.4	12759	3	US-09-949-016-16300	Sequence 16300, A	223	15.4	61.6	104475	3	US-09-949-016-12115	Sequence 12115, A
151	15.6	62.4	12759	3	US-09-949-016-16301	Sequence 16301, A	224	15.4	61.6	111282	3	US-09-754-250-3	Sequence 3, Appl
152	15.6	62.4	12759	3	US-09-949-016-16302	Sequence 16302, A	225	15.4	61.6	111282	3	US-10-094-989-3	Sequence 3, Appl
153	15.6	62.4	12759	3	US-09-949-016-16303	Sequence 16303, A	226	15.4	61.6	157822	3	US-09-949-016-16723	Sequence 16723, A
154	15.6	62.4	12759	3	US-09-949-016-16304	Sequence 16304, A	c 227	15.4	61.6	267482	3	US-09-949-002-659	Sequence 659, App
155	15.6	62.4	12759	3	US-09-949-016-16305	Sequence 16305, A	c 228	15.4	61.6	267505	3	US-09-949-002-783	Sequence 783, App
156	15.6	62.4	12768	3	US-09-949-016-14302	Sequence 14302, A	c 229	15.2	60.8	403	2	US-08-133-179-1	Sequence 1, Appl
157	15.6	62.4	12768	3	US-09-949-016-14303	Sequence 14303, A	230	15.2	60.8	507	3	US-09-902-540-4995	Sequence 4995, App
158	15.6	62.4	12768	3	US-09-949-016-14304	Sequence 14304, A	231	15.2	60.8	601	3	US-09-949-016-28465	Sequence 28465, A
159	15.6	62.4	12768	3	US-09-949-016-14305	Sequence 14305, A	232	15.2	60.8	601	3	US-09-949-016-169844	Sequence 169844, A
160	15.6	62.4	12768	3	US-08-949-016-14306	Sequence 14306, A	c 233	15.2	60.8	906	3	US-08-957-351-2	Sequence 2, Appl
161	15.6	62.4	12768	3	US-09-949-016-14307	Sequence 14307, A	c 234	15.2	60.8	906	3	US-08-957-351-6	Sequence 6, Appl
162	15.6	62.4	12768	3	US-09-949-016-14308	Sequence 14308, A	c 235	15.2	60.8	1017	3	US-08-957-351-5	Sequence 5, Appl
163	15.6	62.4	12768	3	US-09-949-016-14309	Sequence 14309, A	236	15.2	60.8	1023	3	US-09-543-681A-3911	Sequence 3911, App
164	15.6	62.4	12768	3	US-09-949-016-14310	Sequence 14310, A	c 237	15.2	60.8	1223	3	US-08-957-351-4	Sequence 4, Appl
165	15.6	62.4	12768	3	US-09-949-016-14311	Sequence 14311, A	c 238	15.2	60.8	1223	3	US-08-957-351-29	Sequence 29, Appl
166	15.6	62.4	12768	3	US-09-949-016-14312	Sequence 14312, A	c 239	15.2	60.8	1240	3	US-08-957-351-8	Sequence 8, Appl
167	15.6	62.4	12768	3	US-09-949-016-14313	Sequence 14313, A	240	15.2	60.8	1275	3	US-09-894-844-112	Sequence 112, App
168	15.6	62.4	12768	3	US-09-949-016-14314	Sequence 14314, A	c 241	15.2	60.8	1392	3	US-08-957-351-1	Sequence 1, Appl
169	15.6	62.4	12768	3	US-09-949-016-14315	Sequence 14315, A	242	15.2	60.8	1477	3	US-09-606-401B-1	Sequence 1, Appl

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243 15.2 60.8 1542 3 US-09-134-000C-2261 Sequence 2261, Ap
c 244 15.2 60.8 3405 4 US-10-154-419-35 Sequence 35, Appl
c 245 15.2 60.8 4064 3 US-10-209-792-1 Sequence 1, Appl
c 246 15.2 60.8 4614 3 US-09-364-707A-17 Sequence 17, Appl
c 247 15.2 60.8 4614 3 US-09-912-165-17 Sequence 17, Appl
c 248 15.2 60.8 4657 3 US-09-364-707A-18 Sequence 18, Appl
c 249 15.2 60.8 4657 3 US-09-912-165-18 Sequence 18, Appl
c 250 15.2 60.8 5916 3 US-09-826-630-9 Sequence 9, Appl
c 251 15.2 60.8 7507 4 US-08-975-763-1 Sequence 1, Appl
c 252 15.2 60.8 7745 4 US-10-154-419-33 Sequence 33, Appl
c 253 15.2 60.8 23951 3 US-09-902-540-1245 Sequence 1245, Ap
c 254 15.2 60.8 32155 3 US-08-311-731A-1 Sequence 1, Appl
c 255 15.2 60.8 35828 3 US-09-449-218D-17 Sequence 17, Appl
c 256 15.2 60.8 35828 3 US-09-668-529A-17 Sequence 17, Appl
c 257 15.2 60.8 35828 3 US-09-668-037A-17 Sequence 17, Appl
c 258 15.2 60.8 35828 3 US-09-668-021-17 Sequence 17, Appl
c 259 15.2 60.8 45819 3 US-09-453-702B-72 Sequence 72, Appl
c 260 15.2 60.8 46819 3 US-10-114-170-72 Sequence 72, Appl
c 261 15.2 60.8 47115 3 US-09-949-016-12278 Sequence 12278, A
c 262 15.2 60.8 47122 3 US-09-949-016-16520 Sequence 16520, A
c 263 15.2 60.8 50341 2 US-08-247-901C-1 Sequence 1, Appl
c 264 15.2 60.8 50341 2 US-09-075-904-1 Sequence 1, Appl
c 265 15.2 60.8 63860 3 US-09-949-016-15825 Sequence 15825, A
c 266 15.2 60.8 66933 3 US-09-544-398B-11 Sequence 11, Appl
c 267 15.2 60.8 66933 3 US-09-543-771B-11 Sequence 11, Appl
c 268 15.2 60.8 67088 4 US-09-531-120-186 Sequence 186, App
c 269 15.2 60.8 95223 4 US-09-531-120-188 Sequence 188, App
c 270 15.2 60.8 152132 3 US-09-949-016-13845 Sequence 13845, A
c 271 15.2 60.8 152145 3 US-09-949-016-12371 Sequence 12371, A
c 272 15.2 60.8 166698 3 US-09-949-016-16038 Sequence 16038, A
c 273 15.2 60.8 611587 4 US-09-531-120-209 Sequence 209, App
c 274 15 60.0 38 3 US-09-735-271-1390 Sequence 1390, App
c 275 15 60.0 208 3 US-09-513-999C-12870 Sequence 12870, A
c 276 15 60.0 335 3 US-09-270-767-9387 Sequence 9387, Ap
c 277 15 60.0 335 3 US-09-270-767-24669 Sequence 24669, A
c 278 15 60.0 564 3 US-09-533-559-1038 Sequence 1038, Ap
c 279 15 60.0 601 3 US-09-949-016-19418 Sequence 19418, A
c 280 15 60.0 601 3 US-09-949-016-19419 Sequence 19419, A
c 281 15 60.0 601 3 US-09-949-016-37443 Sequence 37443, A
c 282 15 60.0 601 3 US-09-949-016-49599 Sequence 49599, A
c 283 15 60.0 601 3 US-09-949-016-49600 Sequence 49600, A
c 284 15 60.0 601 3 US-09-949-016-145228 Sequence 145228,
c 285 15 60.0 601 3 US-09-949-016-163729 Sequence 163729,
c 286 15 60.0 601 3 US-09-949-016-167311 Sequence 167311,
c 287 15 60.0 601 3 US-09-949-016-195627 Sequence 195627,
c 288 15 60.0 601 3 US-09-949-016-200123 Sequence 200123,
c 289 15 60.0 678 3 US-08-998-416-1053 Sequence 1053, Ap
c 290 15 60.0 689 3 US-09-270-767-2314 Sequence 2314, Ap
c 291 15 60.0 689 3 US-09-270-767-17596 Sequence 17596, A
c 292 15 60.0 700 3 US-09-735-271-34 Sequence 34, Appl
c 293 15 60.0 700 3 US-09-735-271-35 Sequence 35, Appl
c 294 15 60.0 702 3 US-09-533-559-4619 Sequence 4619, Ap
c 295 15 60.0 762 4 US-09-297-648-5063 Sequence 5063, Ap
c 296 15 60.0 762 4 US-09-297-648-5065 Sequence 5065, Ap
c 297 15 60.0 765 3 US-09-620-312D-1089 Sequence 1089, Ap
c 298 15 60.0 770 3 US-09-303-518D-385 Sequence 385, App
c 299 15 60.0 852 3 US-09-222-939-3 Sequence 3, Appl
c 300 15 60.0 921 3 US-09-902-540-6272 Sequence 6272, Ap

ALIGNMENTS

RESULT 1
US-09-738-274-21
; Sequence 21, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc

RESULT 2
US-09-738-274-22
; Sequence 22, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc

TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
FILE REFERENCE: GP107-02, UT
CURRENT APPLICATION NUMBER: US/09/738,274
CURRENT FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: 60/172,190
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
OTHER INFORMATION: oligonucleotide
US-09-738-274-21

Query Match 100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTCG 25
Db 1 GCAAGTCGAACGGAAGGCCTTTCG 25

RESULT 3
US-09-738-274-23
; Sequence 23, Application US/09949230A
; Patent No. 6551591
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc

TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
FILE REFERENCE: GP107-02, UT
CURRENT APPLICATION NUMBER: US/09/738,274
CURRENT FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: 60/172,190
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
OTHER INFORMATION: oligonucleotide
US-09-738-274-22

Query Match 96.0%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTTTCG 25
Db 1 CAAGTCGAACGGAAGGCCTTTCG 24

RESULT 3
US-09-949-230A-1
; Sequence 1, Application US/09949230A
; Patent No. 6551591
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc

TITLE OF INVENTION: New Antibiotics for Microbispora
FILE REFERENCE: 262/095
CURRENT APPLICATION NUMBER: US/09/949,230A
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; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1584
; TYPE: DNA
; ORGANISM: Microbispora corallina
; FEATURE:
; NAME/KEY: n
; LOCATION: (1350)..(1584)
; OTHER INFORMATION: Unsure
; NAME/KEY: misc feature
; LOCATION: (1350)..(1584)
; OTHER INFORMATION: Unsure
US-09-949-230A-1

Query Match 87.2%; Score 21.8; DB 3; Length 1584;
Best Local Similarity 92.0%; Pred. No. 0.4;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTCG 25
Db 124 GCAAGTCGAGCGGAAGGCCTTCG 148
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RESULT 4

US-09-738-972-7
; Sequence 7, Application US/09738972
; Patent No. 6747141

; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; TITLE OF INVENTION: AVIUM COMPLEX SPECIES
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738.972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7

; LENGTH: 32
; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: primer
US-09-738-972-7

Query Match 85.6%; Score 21.4; DB 3; Length 32;
Best Local Similarity 95.7%; Pred. No. 0.27;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTCG 23
Db 1 GCAAGTCGAACGGAAGGCCTTCT 23
|||||

RESULT 5

US-09-738-972-14/c

; Sequence 14, Application US/09738972
; Patent No. 6747141

; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; TITLE OF INVENTION: AVIUM COMPLEX SPECIES
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738.972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15

; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: probe
US-09-738-972-14

Query Match 85.6%; Score 21.4; DB 3; Length 32;
Best Local Similarity 95.7%; Pred. No. 0.27;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTCG 23
Db 32 GCAAGTCGAACGGAAGGCCTCT 10
|||||

RESULT 6

US-09-738-274-23

; Sequence 23, Application US/09738274
; Patent No. 6664081

; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738.274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23

; LENGTH: 22
; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-23

Query Match 84.0%; Score 21; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GTCGAACGGAAGGCCTTTCG 25
Db 1 GTCGAACGGAAGGCCTTTCG 21
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RESULT 7

US-08-641-291A-92

; Sequence 92, Application US/08641291A
; Patent No. 6037122

; GENERAL INFORMATION:

; APPLICANT: MABILAT Claude
; APPLICANT: RUINY Raymond
; TITLE OF INVENTION: NUCLEOTIDE FRAGMENT OF THE 16S RIBOSOMAL RNA OF CORYNEBACTERIUM
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release # 1.0, version # 1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/641,291A
FILING DATE: 30-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bertrige, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 38273
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 1475 base pairs
TYPE: nucleotide
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: rRNA
US-08-641-291A-92

Query Match 84.0%; Score 21; DB 3; Length 1475;
Best Local Similarity 90.5%; Pred. No. 1;
Matches 19; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCT 21
|||||
Db 24 GCAAGUCGACGGAAGGCCU 44

RESULT 8

US-10-085-871C-1
Sequence 1, Application US/10085871C
Patent No. 6716615
GENERAL INFORMATION:
APPLICANT: Lee, Fang-Yu
APPLICANT: Lee, Ming-Liang
APPLICANT: Anderson, Hong C.
APPLICANT: Chiu, Chung-Ching
TITLE OF INVENTION: New Strains of Saccharothrix, Process for Producing Pravastatin U
FILE REFERENCE: 004135.P005
CURRENT APPLICATION NUMBER: US/10/085,871C
CURRENT FILING DATE: 2002-02-27
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1437
TYPE: DNA
ORGANISM: Saccharothrix 44442
US-10-085-871C-1

Query Match 80.8%; Score 20.2; DB 3; Length 1437;
Best Local Similarity 88.0%; Pred. No. 2.5;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCTTTCG 25
|||||
Db 30 GCAAGTCGACGGTAAGGCCCTTCG 54

RESULT 9

US-10-085-871C-2
Sequence 2, Application US/10085871C
Patent No. 6716615
GENERAL INFORMATION:
APPLICANT: Lee, Fang-Yu
APPLICANT: Lee, Ming-Liang
APPLICANT: Anderson, Hong C.

APPLICANT: Chiu, Chung-Ching
TITLE OF INVENTION: New Strains of Saccharothrix, Process for Producing Pravastatin U
FILE REFERENCE: 004135.P005
CURRENT APPLICATION NUMBER: US/10/085,871C
CURRENT FILING DATE: 2002-02-27
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 1471
TYPE: DNA
ORGANISM: Saccharothrix 45494
US-10-085-871C-2

Query Match 80.8%; Score 20.2; DB 3; Length 1471;
Best Local Similarity 88.0%; Pred. No. 2.5;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCTTTCG 25
|||||
Db 30 GCAAGTCGACGGTAAGGCCCTTCG 54

RESULT 10

US-10-756-683B-1
Sequence 1, Application US/10756683B
Patent No. 7022875
GENERAL INFORMATION:
APPLICANT: Hwang, Byung Kook
APPLICANT: Lee, Jung Yeop
TITLE OF INVENTION: THIOTRACIN AND ANTIFUNGAL AND ANTIOOMYCETE COMPOSITION FOR
FILE REFERENCE: 4228-102
CURRENT APPLICATION NUMBER: US/10/756,683B
CURRENT FILING DATE: 2004-01-13
PRIOR APPLICATION NUMBER: KR 10-2003-0015628
PRIOR FILING DATE: 2003-03-13
PRIOR APPLICATION NUMBER: KR 10-2003-0015629
PRIOR FILING DATE: 2003-03-13
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 1488
TYPE: DNA
ORGANISM: Lechevalieria aerocolonigenes
US-10-756-683B-1

Query Match 80.8%; Score 20.2; DB 5; Length 1488;
Best Local Similarity 88.0%; Pred. No. 2.5;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCTTTCG 25
|||||
Db 42 GCAAGTCGACGGTAAGGCCCTTCG 66

RESULT 11

US-09-463-618A-1
Sequence 1, Application US/09463618A
Patent No. 6368835
GENERAL INFORMATION:
APPLICANT: KYOWA HAKKO KOGYO CO., LTD
TITLE OF INVENTION: A PROCESS FOR PRODUCING A BRAN PICKLES FLAVORING SOLUTION
FILE REFERENCE: 11142WO
CURRENT APPLICATION NUMBER: US/09/463,618A
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: H10-166226
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1460
TYPE: DNA

US-09-463-618A-1
Sequence 1, Application US/09463618A
Patent No. 6368835
GENERAL INFORMATION:
APPLICANT: KYOWA HAKKO KOGYO CO., LTD
TITLE OF INVENTION: A PROCESS FOR PRODUCING A BRAN PICKLES FLAVORING SOLUTION
FILE REFERENCE: 11142WO
CURRENT APPLICATION NUMBER: US/09/463,618A
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: H10-166226
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1460
TYPE: DNA

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; ORGANISM: Corynebacterium sp.NK-1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (166)
; OTHER INFORMATION: n is "a" or "g" or "c" or "t".
US-09-463-618A-1

Query Match      80.0%; Score 20; DB 3; Length 1460;
Best Local Similarity 100.0%; Pred. No. 3.2; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 GCAAGTCGAACGGAAGGCC 20
    |||||
Db 38 GCAAGTCGAACGGAAGGCC 57

RESULT 12
US-10-062-777-1
; Sequence 1, Application US/10062777
; Patent No. 6589774
; GENERAL INFORMATION:
; APPLICANT: KYOKA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: A PROCESS FOR PRODUCING A BRAN PICKLES FLAVORING SOLUTION
; FILE REFERENCE: 11142W0
; CURRENT APPLICATION NUMBER: US/10/062,777
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/463,618
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Corynebacterium sp.NK-1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (166)
; OTHER INFORMATION: n is "a" or "g" or "c" or "t".
US-10-062-777-1

Query Match      80.0%; Score 20; DB 3; Length 1460;
Best Local Similarity 100.0%; Pred. No. 3.2; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 GCAAGTCGAACGGAAGGCC 20
    |||||
Db 38 GCAAGTCGAACGGAAGGCC 57

RESULT 13
US-09-738-274-14
; Sequence 14, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.U7
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-14

Query Match      79.2%; Score 19.8; DB 3; Length 32;
Best Local Similarity 91.3%; Pred. No. 1.7; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 2;

Qy 1 GCAAGTCGAACGGAAGGCCCTTT 23
    |||||
Db 1 GCAAGTCGAACGGAAGGTCCTCT 23

RESULT 14
US-08-938-858-1
; Sequence 1, Application US/08938858
; Patent No. 5985569
; GENERAL INFORMATION:
; APPLICANT: Foxall, Paul A.
; APPLICANT: Kumar, Harish
; TITLE OF INVENTION: Primers for Amplification of a Genus
; TITLE OF INVENTION: Specific Sequence of the Mycobacterium 16S rRNA Gene
; Patent No. 5985569
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Becton Dickinson and Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07417-6800
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,858
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fugit, Donna R.
; REGISTRATION NUMBER: 32,135
; REFERENCE/DOCKET NUMBER: P-3490/5510-12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-847-7166
; TELEFAX: 201-848-9228
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1464 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
US-08-938-858-1

Query Match      79.2%; Score 19.8; DB 2; Length 1464;
Best Local Similarity 91.3%; Pred. No. 4; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 2;

Qy 1 GCAAGTCGAACGGAAGGCCCTTT 23
    |||||
Db 20 GCAAGTCGAACGGAAGGTCCTCT 42

RESULT 15
US-09-726-774-7
; Sequence 7, Application US/09726774
; Patent No. 6677153
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
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; TITLE OF INVENTION: Antisense Antibacterial Method and
; FILE REFERENCE: Composition
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/09/726,774
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-726-774-7

Query Match          79.2%; Score 19.8; DB 3; Length 1464;
Best Local Similarity 91.3%; Pred. No. 4;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGAAAGGCCTTT 23
    |||||
Db 20 GCAAGTCGAACGAAAGGTCTCT 42
    |||||

RESULT 16
US-08-311-731A-134/c
; Sequence 134, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36241 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium leprae
US-08-311-731A-134

Query Match          79.2%; Score 19.8; DB 3; Length 36241;
Best Local Similarity 91.3%; Pred. No. 8.2;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGAAAGGCCTTT 23
    |||||
Db 36188 GCAAGTCGAACGAAAGGTCTCT 36166
    |||||

RESULT 18
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
```

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; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match      79.2%; Score 19.8; DB 3; Length 4403765;
Best Local Similarity 91.3%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GCAAGTCGACGGAAGGCCTTT 23
Db      1471427 GCAAGTCGACGGAAGGTCCT 1471449

RESULT 19
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match      79.2%; Score 19.8; DB 3; Length 4411529;
Best Local Similarity 91.3%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GCAAGTCGACGGAAGGCCTTT 23
Db      1471903 GCAAGTCGACGGAAGGTCCT 1471925

RESULT 20
US-09-738-274-27
; Sequence 27, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-24

Query Match      72.0%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 GAACGGAAAGCCTTTTCG 25
Db      1 GAACGGAAAGCCTTTTCG 18

RESULT 22
US-07-915-922-1
; Sequence 1, Application US/07915922
; Patent No. 5422242
; GENERAL INFORMATION:
; APPLICANT: Young, Karen K.Y.
; TITLE OF INVENTION: Mycobacterium Primers and Probes
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110-1199
```

```
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-27

Query Match      76.0%; Score 19; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 CAAGTCGAACGGAAAGGCC 20
Db      1 CAAGTCGAACGGAAAGGCC 19

RESULT 21
US-09-738-274-24
; Sequence 24, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-24

Query Match      72.0%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 GAACGGAAAGCCTTTTCG 25
Db      1 GAACGGAAAGCCTTTTCG 18

RESULT 22
US-07-915-922-1
; Sequence 1, Application US/07915922
; Patent No. 5422242
; GENERAL INFORMATION:
; APPLICANT: Young, Karen K.Y.
; TITLE OF INVENTION: Mycobacterium Primers and Probes
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110-1199
```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/915,922
FILING DATE: 19920717
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sias, Stacey R.
REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER: 8616
TELEPHONE: (510) 814-2863
TELEFAX: (510) 522-1285
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-915-922-1

Query Match 72.0%; Score 18; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGG 18
|||||
DB 6 GCAAGTCGAACGGAAGG 23

RESULT 23
US-08-039-866-5
Sequence 5, Application US/09039866
Patent No. 6001611
GENERAL INFORMATION:
APPLICANT: Will, Stephen G.
TITLE OF INVENTION: MODIFIED NUCLEIC ACID AMPLIFICATION
TITLE OF INVENTION: PRIMERS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Roche Molecular Systems
STREET: 1080 U.S. Highway 202
CITY: Branchburg
STATE: New Jersey
COUNTRY: United States
ZIP: 08876
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,866
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 1023P
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-039-866-5

Query Match 72.0%; Score 18; DB 3; Length 23;

Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAAGTCGAACGGAAGG 18
|||||
DB 6 GCAAGTCGAACGGAAGG 23
RESULT 24
US-09-149-476-59
Sequence 59, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,597
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,502
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,633
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,583
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,617
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,618
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,503
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,592
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,581
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,584
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,500
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,587
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,492
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,598
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,613
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,582
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,596
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,612

RESULT 25
US-09-149-476-226
; Sequence 226, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; EARLIER FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595

; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 68.8%; Score 17.2; DB 3; Length 1791;
Best Local Similarity 79.2%; Pred. No. 84;
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCTTTTCG 25
Db 973 CAAGTCGAATGAAGACTGTCG 996
|||||

RESULT 26
US-09-252-991A-2715/c
; Sequence 2715, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 2715
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2715

Query Match 68.0%; Score 17; DB 3; Length 417;
Best Local Similarity 80.0%; Pred. No. 76;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCTTTTCG 25
Db 181 GCAAGTCGAAGAGAGAGGCTTTCG 157
|||||

RESULT 27

US-09-252-991A-6717
; Sequence 6717, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6717
; LENGTH: 2106
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6717

Query Match 68.0%; Score 17; DB 3; Length 2106;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCTTTTCG 25
Db 127 GCAAGCGGTACGGAAGGCTTCG 151
|||||

RESULT 28

US-09-252-991A-2899/c
; Sequence 2899, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 2899

```

; NAME: BERRIDGE, WILLIAM P
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 38238
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)-836-6400
; TELEFAX: (703)-836-2787
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1569 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-632-470-47

Query Match 66.4%; Score 16.6; DB 2; Length 1569;
Best Local Similarity 82.6%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTTG 23
Db 119 GCAAGTCGAACGGAAGGCGCTTTG 141

RESULT 31
US-09-949-016-13974/c
; Sequence 13974, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13974
; LENGTH: 106418
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(106418)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13974

Query Match 66.4%; Score 16.6; DB 3; Length 106418;
Best Local Similarity 82.6%; Pred. No. 4.1e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 AAGTCGAACGGAAGGCGCTTTG 25
Db 10377 AAGTCGAACGGAAGGCGCTTTG 10355

RESULT 32
US-09-949-016-16621/c
; Sequence 16621, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14

```

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; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16621
; LENGTH: 108341
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16621

Query Match          66.4%; Score 16.6; DB 3; Length 108341;
Best Local Similarity 82.6%; Pred. No. 4.1e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2 CAAGTCGAACGGAAGGCGCTTTC 24
        ||||| ||||| ||||| |||||
Db      94196 CAAGTCGAAGGAAGGCGATTTC 94174

RESULT 33
US-09-949-016-13781/c
; Sequence 13781, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13781
; LENGTH: 228851
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(228851)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13781

Query Match          66.4%; Score 16.6; DB 3; Length 228851;
Best Local Similarity 82.6%; Pred. No. 4.8e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      3 AAGTCGAACGGAAGGCGCTTTCG 25
        ||||| ||||| ||||| |||||
Db      132603 AAGTCCTACGGAAGGCGCTTTTG 132581

RESULT 34
US-08-485-602-61
; Sequence 61, Application US/08485602
; Patent No. 5712095
; GENERAL INFORMATION:
; APPLICANT: Britschgi, Theresa B.
; APPLICANT: Cangelosi, Gerard A.
; TITLE OF INVENTION: Rapid and Sensitive Detection of
; Antibiotic-Resistant Mycobacteria Using Oligonucleotide
; PROBES SPECIFIC FOR RIBOSOMAL RNA PRECURSORS
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; APPLICATION NUMBER: US 08/261,068
```

```
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,602
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,068
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 11652-79-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: rRNA
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium habana
US-08-485-602-61

Query Match          65.6%; Score 16.4; DB 2; Length 25;
Best Local Similarity 78.9%; Pred. No. 82;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      7 CGAACGGAAGGCGCTTTCG 25
        ||||| ||||| ||||| |||||
Db      1 CGAACGGAAGGCGCCUUCG 19

RESULT 35
US-08-757-180-60
; Sequence 60, Application US/08757180
; Patent No. 5726021
; GENERAL INFORMATION:
; APPLICANT: Britschgi, Theresa B
; APPLICANT: Cangelosi, Gerard A
; TITLE OF INVENTION: RAPID LYSIS METHODS FOR RELEASING INTACT
; RIBOSOMAL RNA PRECURSORS FROM MYCOBACTERIUM
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,180
; FILING DATE: 27-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,068
```

```
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hsi, Petrina S
; REGISTRATION NUMBER: 38,496
; REFERENCE/DOCKET NUMBER: BD3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: rRNA
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium simiae
;
US-08-757-180-60

Query Match 65.6%; Score 16.4; DB 2; Length 25;
Best Local Similarity 78.9%; Pred. No. 82;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 7 CGAACGGAAGCCTTCG 25
Db 1 CGAACGGAAGNCCCUUG 19

RESULT 36
US-08-745-638-61
; Sequence 61, Application US/08745638
; Patent No. 5770373
; GENERAL INFORMATION:
; APPLICANT: Britschgi, Theresa B.
; APPLICANT: Cangelosi, Gerard A.
; TITLE OF INVENTION: Rapid and Sensitive Detection of
; TITLE OF INVENTION: Antibiotic-Resistant Mycobacteria Using Oligonucleotide
; TITLE OF INVENTION: Probes Specific for Ribosomal RNA Precursors
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/745,638
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,602
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/261,068
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 11652-79-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
```

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; MOLECULE TYPE: rRNA
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium habana
;
US-08-745-638-61

Query Match 65.6%; Score 16.4; DB 2; Length 25;
Best Local Similarity 78.9%; Pred. No. 82;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 7 CGAACGGAAGCCTTCG 25
Db 1 CGAACGGAAGNCCCUUG 19

RESULT 37
US-09-191-099-5
; Sequence 5, Application US/09191099
; Patent No. 6096323
; GENERAL INFORMATION:
; APPLICANT: Walker, Richard L.
; APPLICANT: Read, Deryck H.
; APPLICANT: Hird, David W.
; APPLICANT: LeFebvre, Rance B.
; APPLICANT: Berry, Steven L.
; APPLICANT: Cullor, James S.
; APPLICANT: Lefler, Hank M.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Vaccine Against Papillomatous Digital Dermatitis (PDD)
; FILE REFERENCE: 023070-081110US
; CURRENT APPLICATION NUMBER: US/09/191,099
; CURRENT FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: US 08/943,571
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1405
; TYPE: DNA
; ORGANISM: Treponema sp.
; FEATURE:
; OTHER INFORMATION: 16S rRNA for spirochete 9-3143
; NAME/KEY: modified_base
; LOCATION: (42)
; OTHER INFORMATION: n = unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (414)
; OTHER INFORMATION: n = unknown
;
US-09-191-099-5

Query Match 65.6%; Score 16.4; DB 3; Length 1405;
Best Local Similarity 94.4%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGG 18
Db 21 GCAAGTCGAACGGAAGG 38

RESULT 38
US-09-191-099-1
; Sequence 1, Application US/09191099
; Patent No. 6096323
; GENERAL INFORMATION:
; APPLICANT: Walker, Richard L.
; APPLICANT: Read, Deryck H.
; APPLICANT: Hird, David W.
; APPLICANT: LeFebvre, Rance B.
; APPLICANT: Berry, Steven L.
; APPLICANT: Cullor, James S.
; APPLICANT: Lefler, Hank M.
; APPLICANT: The Regents of the University of California
```

; TITLE OF INVENTION: Vaccine Against Papillomatous Digital Dermatitis (PDD)
; FILE REFERENCE: 023070-081110US
; CURRENT APPLICATION NUMBER: US/09/191,099
; CURRENT FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: US 08/943,571
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1413
; TYPE: DNA
; ORGANISM: Treponema sp.
; FEATURE:
; OTHER INFORMATION: 16S rRNA for spirochete 2-1498
; NAME/KEY: modified_base
; LOCATION: (43)
; OTHER INFORMATION: n = unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (270)
; OTHER INFORMATION: n = unknown
; OTHER INFORMATION: n = unknown
; US-09-191-099-1

Query Match 65.6%; Score 16.4; DB 3; Length 1413;
Best Local Similarity 94.4%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAAGG 18
|||||
Db 25 GCAAGTCGAACGGCAAGG 42

RESULT 39

US-09-191-099-3
; Sequence 3, Application US/09191099
; Patent No. 6096323

GENERAL INFORMATION:

APPLICANT: Walker, Richard L.
APPLICANT: Read, Deryck H.
APPLICANT: Hird, David W.
APPLICANT: Lefebvre, Rance B.
APPLICANT: Berry, Steven L.
APPLICANT: Cullor, James S.
APPLICANT: Lefler, Hank M.

APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Vaccine Against Papillomatous Digital Dermatitis (PDD)

; FILE REFERENCE: 023070-081110US

; CURRENT APPLICATION NUMBER: US/09/191,099

; CURRENT FILING DATE: 1998-11-12

; EARLIER APPLICATION NUMBER: US 08/943,571

; EARLIER FILING DATE: 1997-10-03

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 1462

; TYPE: DNA

; ORGANISM: Treponema sp.

; FEATURE:

; OTHER INFORMATION: 16S rRNA for spirochete 7-2009

; FEATURE:

; NAME/KEY: modified_base

; LOCATION: (274)

; OTHER INFORMATION: n = unknown

; FEATURE:

; NAME/KEY: modified_base

; LOCATION: (1115)

; OTHER INFORMATION: n = unknown

; US-09-191-099-3

Query Match 65.6%; Score 16.4; DB 3; Length 1462;
Best Local Similarity 94.4%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAAGG 18
|||||
Db 29 GCAAGTCGAACGGCAAGG 46

RESULT 40

US-08-943-571-2
; Sequence 2, Application US/08943571
; Patent No. 6287575

GENERAL INFORMATION:

APPLICANT: Walker, Richard L.
APPLICANT: Read, Deryck H.
APPLICANT: Hird, David W.
APPLICANT: Lefebvre, Rance B.
APPLICANT: Berry, Steven L.
APPLICANT: Cullor, James S.
APPLICANT: Lefler, Hank M.

; TITLE OF INVENTION: Vaccine Against Papillomatous Digital

; TITLE OF INVENTION: Dermatitis (PDD)

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/943,571

; FILING DATE: 03-OCT-1997

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Parent, Annette S.

; REGISTRATION NUMBER: 42,058

; REFERENCE/DOCKET NUMBER: 023070-081100US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1490 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: rRNA

; LOCATION: 1..1490

; OTHER INFORMATION: /product= "16S rRNA"

; OTHER INFORMATION: /note= "bovine Treponema spirochete

; OTHER INFORMATION: strain 1-9185MED"

; US-08-943-571-2

Query Match 65.6%; Score 16.4; DB 3; Length 1490;
Best Local Similarity 94.4%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAAGG 18
|||||
Db 51 GCAAGTCGAACGGCAAGG 68

RESULT 41

US-08-943-571-1

; Sequence 1, Application US/08943571

; Patent No. 6287575

; GENERAL INFORMATION:

APPLICANT: Walker, Richard L.
APPLICANT: Read, Deryck H.
APPLICANT: Hird, David W.
APPLICANT: Lefebvre, Rance B.
APPLICANT: Berry, Steven L.
APPLICANT: Cullor, James S.
APPLICANT: Lefler, Hank M.
TITLE OF INVENTION: Vaccine Against Pappillomatous Digital
TITLE OF INVENTION: Dermatitis (PDD)
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,571
FILING DATE: 03-OCT-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 023070-081100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1503 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: rRNA
LOCATION: 1..1503
OTHER INFORMATION: /product= "16S rRNA"
OTHER INFORMATION: /note= "bovine Treponema spirochete
strain 2-1498"
US-08-943-571-1

Query Match 65.6%; Score 16.4; DB 3; Length 1503;
Best Local Similarity 94.4%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGG 18
Db 51 GCAAGTCGACGGAAGG 68

RESULT 42
US-09-949-016-69524
; Sequence 69524, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69524
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-69524

Query Match 64.8%; Score 16.2; DB 3; Length 601;
Best Local Similarity 78.3%; Pred. No. 2.1e+02;
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 3 AAGTCGAACGGAAGGCTTTTCG 25
Db 293 AAGTCCTAYGGAAGGCTTTTG 315

RESULT 43
US-09-949-016-76807
; Sequence 76807, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76807
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-76807

Query Match 64.8%; Score 16.2; DB 3; Length 601;
Best Local Similarity 78.3%; Pred. No. 2.1e+02;
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 3 AAGTCGAACGGAAGGCTTTTCG 25
Db 285 AAGTCCTAYGGAAGGCTTTTG 307

RESULT 44
US-09-533-559-7113
; Sequence 7113, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 5849.200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7113


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; LENGTH: 637
; TYPE: DNA
; ORGANISM: Aspergillus oryzae
US-09-533-559-7113

Query Match      64.8%; Score 16.2; DB 3; Length 637;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 CAAGTCGAACGGAAGGCCTT 22
Db      29 CATGTCGAACGGAAGGCCTT 49

RESULT 45
US-09-974-300-4677/c
; Sequence 4677, Application US/09974300
; Patent No. 7018794
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4677
; LENGTH: 972
; TYPE: DNA
; ORGANISM: Bacillus clausii
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(972)
; OTHER INFORMATION: n = A,T,C or G
US-09-974-300-4677

Query Match      64.8%; Score 16.2; DB 5; Length 972;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 CAAGTCGAACGGAAGGCCTT 22
Db      384 CAAGTCGAACGGAAGGCCTT 364

RESULT 46
US-09-608-285A-45/c
; Sequence 45, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180

Query Match      64.8%; Score 16.2; DB 3; Length 1498;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 AAGTCGAACGGAAGGCCTTT 23
Db      512 AAGTCGAACGGAATGCTCTGT 492

RESULT 47
US-09-557-800C-45/c
; Sequence 45, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 28110/38457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 1498
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-557-800C-45

Query Match      64.8%; Score 16.2; DB 3; Length 1498;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 AAGTCGAACGGAAGGCCTTT 23
Db      512 AAGTCGAACGGAATGCTCTGT 492
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RESULT 48
US-09-608-285A-53/c
; Sequence 53, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-608-285A-53

Query Match      64.8%; Score 16.2; DB 3; Length 1588;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 AAGTCGAACGGAAGGCCTTT 23
      |||||
Db      659 AAGTCGAACGGAATGCTCTGT 639

RESULT 49
US-09-608-285A-53/c
; Sequence 53, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447

Query Match      64.8%; Score 16.2; DB 3; Length 1588;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 AAGTCGAACGGAAGGCCTTT 23
      |||||
Db      659 AAGTCGAACGGAATGCTCTGT 639

RESULT 50
US-09-608-285A-49/c
; Sequence 49, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 2294
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-608-285A-49

Query Match      64.8%; Score 16.2; DB 3; Length 2294;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 AAGTCGAACGGAAGGCCTTT 23
      |||||
Db      191 AAGTCGAACGGAATGCTCTGT 171
```

```
RESULT 51
US-09-557-800C-49/c
; Sequence 49, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 2294
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-557-800C-49

Query Match      64.8%; Score 16.2; DB 3; Length 2294;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 AAGTCGAACGGAAGGCCTTT 23
Db      191 AAGTCGAACGGAATGCTCTGT 171

RESULT 52
US-09-495-050A-215
; Sequence 215, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guegler, Karl, J.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED P
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495,050A
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/118,318
; PRIOR FILING DATE: February 1, 1999
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 215
; LENGTH: 2340
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6492505 2488060CT1
; NAME/KEY: unsure
; LOCATION: 2094
; OTHER INFORMATION: a, t, c, g, or other
```

```
US-09-495-050A-215

Query Match      64.8%; Score 16.2; DB 3; Length 2340;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GCAAGTCGAACGGAAGGCCTT 21
Db      53 GCAAGTTCAAAGGAAGGCCTT 73

RESULT 53
US-09-608-285A-46/c
; Sequence 46, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 2371
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-608-285A-46

Query Match      64.8%; Score 16.2; DB 3; Length 2371;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 AAGTCGAACGGAAGGCCTTT 23
Db      268 AAGTCGAACGGAATGCTCTGT 248

RESULT 54
US-09-557-800C-46/c
; Sequence 46, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
```

US-09-608-285A-51/c
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 2371
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-557-800C-46

Query Match 64.8%; Score 16.2; DB 3; Length 2371;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGTCGAACGGAAGGCGCTTT 23
|||||
DB 268 AAGTCGAACGGAATGCTCTGT 248

RESULT 55
US-09-608-285A-51/c
; Sequence 51, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 2497
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-608-285A-51
Query Match 64.8%; Score 16.2; DB 3; Length 2497;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 AAGTCGAACGGAAGGCGCTTT 23
|||||
DB 394 AAGTCGAACGGAATGCTCTGT 374
RESULT 56
US-09-557-800C-51/c
; Sequence 51, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 2497
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-557-800C-51
Query Match 64.8%; Score 16.2; DB 3; Length 2497;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 AAGTCGAACGGAAGGCGCTTT 23
|||||
DB 394 AAGTCGAACGGAATGCTCTGT 374
RESULT 57
US-09-608-285A-48/c
; Sequence 48, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800

; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 2693
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-608-285A-48

Query Match 64.8%; Score 16.2; DB 3; Length 2693;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGTCGAACGGAAGGCGCTTT 23
|||||
Db 590 AAGTCGAACGGAATGCTCTGT 570

RESULT 58
US-09-557-800C-48/c
; Sequence 48, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 2693
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-557-800C-48

Query Match 64.8%; Score 16.2; DB 3; Length 2693;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 3 AAGTCGAACGGAAGGCGCTTT 23
|||||
Db 590 AAGTCGAACGGAATGCTCTGT 570

RESULT 59
US-09-608-285A-26/c
; Sequence 26, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (148)..(1599)
US-09-608-285A-26

Query Match 64.8%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGTCGAACGGAAGGCGCTTT 23
|||||
Db 659 AAGTCGAACGGAATGCTCTGT 639

RESULT 60
US-09-608-285A-52/c
; Sequence 52, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-608-285A-52

Query Match 64.8%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGTCGAACGGAAGGCCTTT 23
|||||
DB 659 AAGTCGAACGGAATGTCCTGT 639

RESULT 61
US-09-240-639-1/c
; Sequence 1, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240,639
; CURRENT FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1599)
US-09-240-639-1

Query Match 64.8%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGTCGAACGGAAGGCCTTT 23
|||||
DB 659 AAGTCGAACGGAATGTCCTGT 639

RESULT 62
US-09-370-265-26/c
; Sequence 26, Application US/09370265
; Patent No. 6447771

; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 2811/35908
; CURRENT APPLICATION NUMBER: US/09/370,265
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: PCT/US99/16180
; EARLIER FILING DATE: 1999-07-16
; EARLIER APPLICATION NUMBER: 09/350,836
; EARLIER FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: 09/273,447
; EARLIER FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: 09/244,444
; EARLIER FILING DATE: 1999-02-04
; EARLIER APPLICATION NUMBER: 09/122,449
; EARLIER FILING DATE: 1998-07-24
; EARLIER APPLICATION NUMBER: 09/118,205
; EARLIER FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (148)..(1599)
US-09-370-265-26

Query Match 64.8%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGTCGAACGGAAGGCCTTT 23
|||||
DB 659 AAGTCGAACGGAATGTCCTGT 639

RESULT 63
US-09-557-800C-26/c
; Sequence 26, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 2762

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (148)..(1599)
US-09-557-800C-26

Query Match      64.8%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 AAGTCGAACGGAAGGCCTTT 23
Db      659 AAGTCGAACGGAATGCTCTGT 639

RESULT 64
US-09-557-800C-52/c
; Sequence 52, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/124449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-557-800C-52

Query Match      64.8%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 AAGTCGAACGGAAGGCCTTT 23
Db      659 AAGTCGAACGGAATGCTCTGT 639

RESULT 65
US-09-370-625A-26/c
; Sequence 26, Application US/09370625A
; Patent No. 6600032
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; TITLE OF INVENTION: ACIDS
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/09/370,625A
; CURRENT FILING DATE: 1999-08-09
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; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (148)..(1599)
US-09-370-625A-26

Query Match      64.8%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 AAGTCGAACGGAAGGCCTTT 23
Db      659 AAGTCGAACGGAATGCTCTGT 639

RESULT 66
US-09-908-510A-1/c
; Sequence 1, Application US/09908510A
; Patent No. 6759214
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; TITLE OF INVENTION: ACIDS
; FILE REFERENCE: 28110/36120E
; CURRENT APPLICATION NUMBER: US/09/908,510A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1599)
; OTHER INFORMATION:
US-09-908-510A-1

Query Match      64.8%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 AAGTCGAACGGAAGGCCTTT 23
Db      659 AAGTCGAACGGAATGCTCTGT 639

RESULT 67
US-09-905-744B-1/c
; Sequence 1, Application US/09905744B
; Patent No. 6780410
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; TITLE OF INVENTION: ACIDS
; FILE REFERENCE: 28110/36120A
; CURRENT APPLICATION NUMBER: US/09/905,744B
; CURRENT FILING DATE: 2001-07-13
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; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1599)
; OTHER INFORMATION:
US-10-905-744B-1

Query Match 64.8%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGTCGAACGGAAGGCCTTT 23
|||||
Db 659 AAGTCGAACGGAATGCTCTGT 639

RESULT 68

US-10-107-660-1/c
; Sequence 1, Application US/10107660
; Patent No. 6780977
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/10/107,660
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US/09/240,639
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1599)
US-10-107-660-1

Query Match 64.8%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGTCGAACGGAAGGCCTTT 23
|||||
Db 659 AAGTCGAACGGAATGCTCTGT 639

RESULT 69

US-10-107-576-1/c
; Sequence 1, Application US/10107576
; Patent No. 6783959
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; TITLE OF INVENTION: ACIDS
; FILE REFERENCE: 28110/36120H
; CURRENT APPLICATION NUMBER: US/10/107,576
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1599)
; OTHER INFORMATION:
US-10-107-576-1

Query Match 64.8%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGTCGAACGGAAGGCCTTT 23
|||||
Db 659 AAGTCGAACGGAATGCTCTGT 639

RESULT 70

US-09-905-732B-1/c
; Sequence 1, Application US/09905732B
; Patent No. 6787328
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; FILE REFERENCE: 28110/36120B
; CURRENT APPLICATION NUMBER: US/09/905,732B
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1599)
; OTHER INFORMATION:
US-09-905-732B-1

Query Match 64.8%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGTCGAACGGAAGGCCTTT 23
|||||
Db 659 AAGTCGAACGGAATGCTCTGT 639

RESULT 71

US-09-905-743B-1/c
; Sequence 1, Application US/09905743B
; Patent No. 6828423
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; FILE REFERENCE: 28110/36120C
; CURRENT APPLICATION NUMBER: US/09/905,743B
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo Sapiens


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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1599)
; OTHER INFORMATION:
US-09-905-743B-1

Query Match      64.8%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGTCGAACGGAAGGCGCTTT 23
Db 659 AAGTCGAACGGAATGCTCCTGT 639

RESULT 72
US-09-905-589-1/c
; Sequence 1, Application US/09905589
; Patent No. 6884872
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/905.589
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US/09/240.639
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1599)
US-09-905-589-1

Query Match      64.8%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGTCGAACGGAAGGCGCTTT 23
Db 659 AAGTCGAACGGAATGCTCCTGT 639

RESULT 73
US-10-108-171A-1/c
; Sequence 1, Application US/10108171A
; Patent No. 6899875
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; TITLE OF INVENTION: ACIDS
; FILE REFERENCE: 28110/36120F
; CURRENT APPLICATION NUMBER: US/10/108.171A
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 09/240.639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1599)
; OTHER INFORMATION:
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```
US-10-108-171A-1

Query Match      64.8%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGTCGAACGGAAGGCGCTTT 23
Db 659 AAGTCGAACGGAATGCTCCTGT 639

RESULT 74
US-09-608-285A-50/c
; Sequence 50, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608.285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583.231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557.800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481.238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370.265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350.836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273.447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244.444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122.449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118.205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 2805
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-608-285A-50

Query Match      64.8%; Score 16.2; DB 3; Length 2805;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGTCGAACGGAAGGCGCTTT 23
Db 659 AAGTCGAACGGAATGCTCCTGT 639

RESULT 75
US-09-557-800C-50/c
; Sequence 50, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557.800C
```

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/ CURRENT FILING DATE: 2000-04-25
/ PRIOR APPLICATION NUMBER: 09/481,238
/ PRIOR FILING DATE: 2000-01-11
/ PRIOR APPLICATION NUMBER: 09/370,265
/ PRIOR FILING DATE: 1998-08-09
/ PRIOR APPLICATION NUMBER: PCT/US99/16180
/ PRIOR FILING DATE: 1999-07-16
/ PRIOR APPLICATION NUMBER: 09/350836
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: 09/273447
/ PRIOR FILING DATE: 1999-03-19
/ PRIOR APPLICATION NUMBER: 09/122449
/ PRIOR FILING DATE: 1998-07-24
/ PRIOR APPLICATION NUMBER: 09/244444
/ PRIOR FILING DATE: 1999-02-04
/ PRIOR APPLICATION NUMBER: 09/118,205
/ PRIOR FILING DATE: 1998-07-16
/ NUMBER OF SEQ ID NOS: 56
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 50
/ LENGTH: 2805
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/
US-09-557-800C-50

Query Match      64.8%; Score 16.2; DB 3; Length 2805;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGTCGAACGGAAGGCCTTT 23
   |||||
Db 659 AAGTCGAACGGAATGCTCTGT 639

RESULT 76
US-09-608-285A-54/c
; Sequence 54, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 2882
; TYPE: DNA
; ORGANISM: Homo sapiens
/
```

```
US-09-608-285A-54

Query Match      64.8%; Score 16.2; DB 3; Length 2882;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGTCGAACGGAAGGCCTTT 23
   |||||
Db 659 AAGTCGAACGGAATGCTCTGT 639

RESULT 77
US-09-557-800C-54/c
; Sequence 54, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 2882
; TYPE: DNA
; ORGANISM: Homo sapiens
/
US-09-557-800C-54

Query Match      64.8%; Score 16.2; DB 3; Length 2882;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGTCGAACGGAAGGCCTTT 23
   |||||
Db 659 AAGTCGAACGGAATGCTCTGT 639

RESULT 78
US-09-039-866-6
; Sequence 6, Application US/09039866
; Patent No. 6001611
; GENERAL INFORMATION:
; APPLICANT: Will, Stephen G.
; TITLE OF INVENTION: MODIFIED NUCLEIC ACID AMPLIFICATION
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/039,866
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 2882
; TYPE: DNA
; ORGANISM: Homo sapiens
/
```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/039,866
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 1023P
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-039-866-6

Query Match          64.0%; Score 16; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAA 16
Db 9 GCAAGTCGACGGAAA 24

RESULT 79
US-09-738-274-28
; Sequence 28, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-28

Query Match          64.0%; Score 16; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GTCGACGCGAAGGCC 20
Db 1 GTCGACGCGAAGGCC 16

RESULT 80
US-09-974-300-6612/c
; Sequence 6612, Application US/09974300
; Patent No. 7018794
; GENERAL INFORMATION:
```

```
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6612
; LENGTH: 161
; TYPE: DNA
; ORGANISM: Bacillus clausii
US-09-974-300-6612

Query Match          64.0%; Score 16; DB 5; Length 161;
Best Local Similarity 79.2%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CAAGTCGACGGAAAGGCCTTTTCG 25
Db 81 CAAGGCAACGGCAATGCCTTTTCG 58

RESULT 81
US-09-621-976-17351/c
; Sequence 17351, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 17351
; LENGTH: 248
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-17351

Query Match          64.0%; Score 16; DB 3; Length 248;
Best Local Similarity 79.2%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAAGGCCTTTTC 24
Db 203 GCAAGCCGGACAGAAAGCCTTTTC 180

RESULT 82
US-09-621-976-17350/c
; Sequence 17350, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 17350
; LENGTH: 257
```

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-17350

Query Match          64.0%; Score 16; DB 3; Length 257;
Best Local Similarity 79.2%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTC 24
    ||||| ||| ||| ||| ||| ||| |||
Db 203 GCAAGCGGACACAGAAAGCGCTTTC 180

RESULT 83
US-09-640-211A-60
; Sequence 60, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-60

Query Match          64.0%; Score 16; DB 3; Length 455;
Best Local Similarity 79.2%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTC 24
    ||| ||| ||| ||| ||| ||| ||| |||
Db 20 GGAAGAGACCGGAAGGCGCTTTC 43

RESULT 84
US-09-640-211A-1958
; Sequence 1958, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1958
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-1958

Query Match          64.0%; Score 16; DB 3; Length 455;
Best Local Similarity 79.2%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTC 24
    ||| ||| ||| ||| ||| ||| ||| |||
Db 20 GGAAGAGACCGGAAGGCGCTTTC 43

RESULT 85
US-09-252-991A-13661
; Sequence 13661, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13661
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13661

Query Match          64.0%; Score 16; DB 3; Length 465;
Best Local Similarity 79.2%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTC 24
    ||| ||| ||| ||| ||| ||| ||| |||
Db 399 GCAGTTGATCGAAGGCGCTTTC 422

RESULT 86
US-09-270-767-13570
; Sequence 13570, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13570
; LENGTH: 470
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13570

Query Match          64.0%; Score 16; DB 3; Length 470;
Best Local Similarity 79.2%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTC 24
    ||||| ||| ||| ||| ||| ||| |||
Db 260 GCAGCCCATCGGCAAGGCCATTC 283

RESULT 87
US-09-252-991A-6201
; Sequence 6201, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
```

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; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6201
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6201

Query Match          64.0%; Score 16; DB 3; Length 552;
Best Local Similarity 79.2%; Pred. No. 2.6e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  2 CAAGTCGAACGGAAGGCCTTTCG 25
Db  44 CAGGCCGTCGGAAGAGCGCGTTCG 67

RESULT 88
US-09-949-016-79652
; Sequence 79652, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79652
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-79652

Query Match          64.0%; Score 16; DB 3; Length 601;
Best Local Similarity 79.2%; Pred. No. 2.6e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  2 CAAGTCGAACGGAAGGCCTTTCG 25
Db  328 CAAAACGACCGGAATGCGCTTTTG 351

RESULT 89
US-09-949-016-201683/c
; Sequence 201683, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201683
; LENGTH: 601
```

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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-201683

Query Match          64.0%; Score 16; DB 3; Length 601;
Best Local Similarity 79.2%; Pred. No. 2.6e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  2 CAAGTCGAACGGAAGGCCTTTCG 25
Db  228 CAAGTCGAATCGAAATTCCTTTGG 205

RESULT 90
US-09-134-001C-1552
; Sequence 1552, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1552
; LENGTH: 834
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1552

Query Match          64.0%; Score 16; DB 3; Length 834;
Best Local Similarity 79.2%; Pred. No. 2.8e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  1 GCAAGTCGAACGGAAGGCCTTTC 24
Db  601 GTRACTCGAAGGAAAAAGCCTTTC 624

RESULT 91
US-09-252-991A-13763/c
; Sequence 13763, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13763
; LENGTH: 855
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13763

Query Match          64.0%; Score 16; DB 3; Length 855;
Best Local Similarity 79.2%; Pred. No. 2.8e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  1 GCAAGTCGAACGGAAGGCCTTTC 24
Db  271 GCACGTTGATCGAAGAGGCCTTTC 248
```

Query Match 64.0%; Score 16; DB 3; Length 1269;
Best Local Similarity 79.2%; Pred. No. 3.1e+02;
Matches 19; Conservative 0; Mismatches 5; Indels

RESULT 96
US-09-118-324-1/c
; Sequence 1, Application US/09118324

```
; Patent No. 6110720
; GENERAL INFORMATION:
; APPLICANT: Li, Xin-Liang
; APPLICANT: Ljungdahl, Lars G.
; APPLICANT: Chen, Huizhong
; TITLE OF INVENTION: Orpinomyces Cellulase CelE Protein and Coding Sequences
; FILE REFERENCE: 32-98sequence listing
; CURRENT APPLICATION NUMBER: US/09/118.324
; CURRENT FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1532
; TYPE: DNA
; ORGANISM: Orpinomyces sp. PC-2
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (39)..(1472)
US-09-118-324-1

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Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db      860  GCTAGTGGACGGAAGTCTTTTC 837

RESULT 97
US-09-252-991A-887
; Sequence 887, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 887
; LENGTH: 1698
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-887

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RESULT 98
US-09-533-559-5520
; Sequence 5520, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjørke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 5849.200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
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; LENGTH: 1710
; TYPE: DNA
; ORGANISM: Aspergillus oryzae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1710)
; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-5520

Query Match          64.0%; Score 16; DB 3; Length 1710;
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RESULT 99
US-09-799-451-258
; Sequence 258, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Duanrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 258
; LENGTH: 2103
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1184)..(1303)
US-09-799-451-258

Query Match          64.0%; Score 16; DB 3; Length 2103;
Best Local Similarity 79.2%; Pred. No. 3.5e+02;
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RESULT 100

US-09-543-679A-2542
; Sequence 2542, Application US/09543679A
; Patent No 7034007
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
; COMPOSITIONS, KIT & METHOD FOR TREATMENT
; OF AIRWAY DISORDERS ASSOCIATED WITH
; BRONCHOCOCONSTRICTION, LUNG INFLAMMATION,
; NUMBER OF SEQUENCES: 3111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: NJ
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-R
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: N/A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/543,679A
; FILING DATE: 13-Apr-2000
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/127,958
; FILING DATE: 1998-08-03
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-0067191b
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2542:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9900 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2542:
US-09-543-679A-2542

Query Match 64.0%; Score 16; DB 5; Length 9900;
Best Local Similarity 79.2%; Pred. No. 4.9e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 4598 GCAAGTAAACGTTAAGGCTTGC 4621

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7	23.4	93.6	1482	10	US-10-697-802A-5				
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93	17.2	68.8	1776	16	US-11-144-347-59	Sequence 59, Appl	166	16.4	65.6	25	8	US-10-220-212A-31	Sequence 31, Appl
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107	17	68.0	60	6	US-10-149-187-8	Sequence 4, Appl	c 180	16.2	64.8	464	12	US-10-301-480-50320	Sequence 50320, A
108	17	68.0	60	6	US-10-149-187-8	Sequence 4, Appl	c 181	16.2	64.8	464	12	US-10-301-480-50320	Sequence 50320, A
c 109	17	68.0	200	16	US-11-098-686-4821	Sequence 4821, Ap	c 182	16.2	64.8	484	6	US-10-027-632-194226	Sequence 194226, A
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c 112	17	68.0	920	8	US-10-437-963-34505	Sequence 34505, A	c 185	16.2	64.8	512	6	US-10-027-632-194226	Sequence 194226, A
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114	17	68.0	1468	16	US-11-093-805-14	Sequence 14, Appl	c 187	16.2	64.8	513	4	US-09-925-065A-544396	Sequence 544396, A
c 115	17	68.0	2199	8	US-10-282-122A-31703	Sequence 31703, A	c 188	16.2	64.8	513	5	US-09-925-065A-544396	Sequence 544396, A
c 116	17	68.0	2325	3	US-09-815-242-4026	Sequence 4026, Ap	c 189	16.2	64.8	513	5	US-09-925-065A-544396	Sequence 544396, A
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c 119	17	68.0	5163	8	US-10-437-963-11723	Sequence 19204, A	c 192	16.2	64.8	565	12	US-10-301-480-304063	Sequence 304063, A
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c 122	17	68.0	5501	16	US-11-136-527-3427	Sequence 66272, A	c 195	16.2	64.8	590	9	US-10-115-278-16	Sequence 16, Appl
c 123	17	68.0	35058	13	US-11-097-143-5575	Sequence 3427, Ap	c 196	16.2	64.8	590	9	US-10-115-278-16	Sequence 16, Appl
c 124	17	68.0	1457619	16	US-11-098-686-8739	Sequence 5575, Ap	c 197	16.2	64.8	635	16	US-11-096-568A-8058	Sequence 8058, Ap
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c 126	17	68.0	9025608	7	US-10-156-761-1	Sequence 1, Appl	c 199	16.2	64.8	637	9	US-10-653-047-7113	Sequence 7113, Ap
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c 128	17	68.0	9025608	7	US-10-156-761-1	Sequence 1, Appl	c 201	16.2	64.8	638	6	US-10-027-632-292604	Sequence 292604, A
c 129	16.6	66.4	25	10	US-10-956-157-105928	Sequence 105928,	c 202	16.2	64.8	638	6	US-10-027-632-292604	Sequence 292604, A
c 130	16.6	66.4	25	10	US-10-956-157-105928	Sequence 105928,	c 203	16.2	64.8	638	6	US-10-027-632-292604	Sequence 292604, A
c 131	16.6	66.4	338	3	US-09-867-550-1961	Sequence 1961, Ap	c 204	16.2	64.8	638	6	US-10-286-926-45	Sequence 45, Appl
c 132	16.6	66.4	381	10	US-10-450-763-13678	Sequence 13678, A	c 205	16.2	64.8	1588	7	US-10-286-926-45	Sequence 45, Appl
c 133	16.6	66.4	537	12	US-10-301-480-228090	Sequence 228090,	c 206	16.2	64.8	1588	7	US-10-286-926-45	Sequence 45, Appl
c 134	16.6	66.4	537	12	US-10-301-480-841499	Sequence 228090,	c 207	16.2	64.8	1902	7	US-10-369-493-46887	Sequence 46887, A
c 135	16.6	66.4	537	12	US-10-301-480-841499	Sequence 841499,	c 208	16.2	64.8	2239	13	US-11-097-143-383	Sequence 383, App
c 136	16.6	66.4	552	4	US-09-925-065A-738727	Sequence 738727,	c 209	16.2	64.8	2239	13	US-11-097-143-383	Sequence 383, App
c 137	16.6	66.4	552	4	US-09-925-065A-738727	Sequence 738727,	c 210	16.2	64.8	2239	13	US-11-097-143-383	Sequence 383, App
c 138	16.6	66.4	558	4	US-09-925-065A-131770	Sequence 131770,	c 211	16.2	64.8	2239	13	US-11-097-143-383	Sequence 383, App
c 139	16.6	66.4	572	4	US-09-925-065A-131770	Sequence 131770,	c 212	16.2	64.8	2239	13	US-11-097-143-383	Sequence 383, App
c 140	16.6	66.4	572	4	US-09-925-065A-131770	Sequence 131770,	c 213	16.2	64.8	2239	13	US-11-097-143-383	Sequence 383, App
c 141	16.6	66.4	572	4	US-09-925-065A-131770	Sequence 131770,	c 214	16.2	64.8	2239	13	US-11-097-143-383	Sequence 383, App
c 142	16.6	66.4	572	4	US-09-925-065A-131770	Sequence 131770,	c 215	16.2	64.8	2239	13	US-11-097-143-383	Sequence 383, App
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c 158	16.6	66.4	572	4	US-09-925-065A-131770	Sequence 131770,	c 231	16.2	64.8	2239	13	US-11-097-143-383	Sequence 383, App
c 159	16.6	66.4	572	4	US-09-925-065A-131770	Sequence 131770,	c 232	16.2	64.8	2239	13	US-11-097-143-383	Sequence 383, App
c 160	16.6	66.4	572	4	US-09-925-065A-131770	Sequence 131770,	c 233	16.2	64.8	2239	13	US-11-097-143-383	Sequence 383, App
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c 237 16 64.0 201 9 US-10-741-600-71827
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c 240 16 64.0 330 3 US-09-764-860-71
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c 263 16 64.0 635 9 US-10-425-115-59269
c 264 16 64.0 714 4 US-09-925-065A-563474
c 265 16 64.0 714 5 US-09-925-065A-563474
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c 270 16 64.0 790 5 US-09-925-065A-5109
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c 299 16 64.0 1326 11 US-10-932-182A-80747
c 300 16 64.0 1430 3 US-09-927-904-6

ALIGNMENTS

RESULT 1
US-09-738-274-21
; Sequence 21, Application US/09738274
; Publication No. US20030165824A1

Sequence 71827, A
Sequence 42379, A
Sequence 30479, A
Sequence 71, Appl
Sequence 71, Appl
Sequence 71, Appl
Sequence 60, Appl
Sequence 1958, Ap
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Sequence 244880,
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Sequence 11110, A
Sequence 6018, Ap
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Sequence 719755,
Sequence 1014, Ap
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Sequence 1189987,
Sequence 171, App
Sequence 171, App
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Sequence 776915,
Sequence 776916,
Sequence 776917,
Sequence 776918,
Sequence 80747, A
Sequence 6, Appl

GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAN, Philippe
; APPLICANT: ROBRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-21

Query Match 100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred.No. 0.091;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGAAAGCCCTTCG 25
Db 1 GCAAGTCGACGAAAGCCCTTCG 25

RESULT 2
US-10-665-708-21
; Sequence 21, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAN, Philippe
; APPLICANT: ROBRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-10-665-708-21

Query Match 100.0%; Score 25; DB 10; Length 25;
Best Local Similarity 100.0%; Pred.No. 0.091;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGAAAGCCCTTCG 25
Db 1 GCAAGTCGACGAAAGCCCTTCG 25

RESULT 3

US-09-738-274-22
; Sequence 22, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-22

Query Match 96.0%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCGCTTTCG 25
Db 1 CAAGTCGAACGGAAGGCGCTTTCG 24

RESULT 4
US-10-665-708-22
; Sequence 22, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-10-665-708-22

Query Match 96.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCGCTTTCG 25
Db 1 CAAGTCGAACGGAAGGCGCTTTCG 24

RESULT 5
US-10-697-802A-6
; Sequence 6, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 6
; LENGTH: 1449
; TYPE: DNA
; ORGANISM: Mycobacterium fortuitum
US-10-697-802A-6

Query Match 93.6%; Score 23.4; DB 10; Length 1449;
Best Local Similarity 96.0%; Pred. No. 0.63;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
Db 20 GCAAGTCGAACGGAAGGCGCTTTCG 44

RESULT 6
US-10-697-802A-13
; Sequence 13, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 13
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Mycobacterium mucogenicum
US-10-697-802A-13

Query Match 93.6%; Score 23.4; DB 10; Length 1455;
Best Local Similarity 96.0%; Pred. No. 0.63;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
Db 30 GCAAGTCGAACGGAAGGCGCTTTCG 54

RESULT 7
US-10-697-802A-5
; Sequence 5, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 5
; LENGTH: 1482
; TYPE: DNA
; ORGANISM: Mycobacterium farcinogenes
US-10-697-802A-5

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Query Match      93.6%; Score 23.4; DB 10; Length 1482;
Best Local Similarity 96.0%; Pred. No. 0.63;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTTTCG 25
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DB 28 GCAAGTCGAACGGAAGGCGCTTTTCG 52

RESULT 8
US-10-522-454-1
; Sequence 1, Application US/10522454
; Publication No. US20050244938A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Russell T.
; APPLICANT: Hamann, Mark T.
; APPLICANT: Peraud, Olivier
; APPLICANT: Kasanah, Noer
; TITLE OF INVENTION: MANZAMINE-PRODUCING ACTINOMYCETES
; FILE REFERENCE: 4115-180
; CURRENT APPLICATION NUMBER: US/10/522,454
; PRIOR FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: PCT/US03/24238
; PRIOR FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 1403
; TYPE: DNA
; ORGANISM: Actinomyces sp.
US-10-522-454-1

Query Match      87.2%; Score 21.8; DB 10; Length 1403;
Best Local Similarity 92.0%; Pred. No. 3.7;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 25 GCAAGTCGAACGGAAGGCGCTTTTCG 49

RESULT 9
US-11-035-296-1
; Sequence 1, Application US/11035296
; Publication No. US20050203005A1
; GENERAL INFORMATION:
; APPLICANT: VICURON PHARMACEUTICALS INC.
; APPLICANT: LAZZARINI, Ameriga
; APPLICANT: GASTALDO, Luciano
; APPLICANT: CANDIANI, Gianpaolo
; APPLICANT: CICILIATO, Ismaela
; APPLICANT: LOSI, Daniele
; APPLICANT: MARINELLI, Flavia
; APPLICANT: SELVA, Enrico
; APPLICANT: PARENTI, Franco
; TITLE OF INVENTION: ANTIBIOTIC 107891, ITS FACTORS A1 AND A2, PHARMACEUTICALLY
; FILE REFERENCE: 892,280-195
; CURRENT APPLICATION NUMBER: US/11/035,296
; PRIOR FILING DATE: 2005-01-12
; PRIOR APPLICATION NUMBER: US 10/521,336
; PRIOR FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: PCT/EP2004/007658
; PRIOR FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: EP 03016306.7
; PRIOR FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Microbispora sp. ATCC PTA-5024
US-11-035-296-1

Query Match      87.2%; Score 21.8; DB 13; Length 1443;
Best Local Similarity 92.0%; Pred. No. 3.7;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTTTCG 25
    ||||| ||||| ||||| ||||| |||||
DB 30 GCAAGTCGAACGGAAGGCGCTTTTCG 54

RESULT 11
US-10-697-802A-7
; Sequence 7, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; PRIOR FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: EP 03016306.7
; PRIOR FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 1461
; TYPE: DNA
; ORGANISM: Mycobacterium gordonae
US-10-697-802A-7

US-11-035-296-1
Query Match      87.2%; Score 21.8; DB 13; Length 1443;
Best Local Similarity 92.0%; Pred. No. 3.7;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTTTCG 25
    ||||| ||||| ||||| ||||| |||||
DB 30 GCAAGTCGAACGGAAGGCGCTTTTCG 54

RESULT 10
US-11-045-628-1
; Sequence 1, Application US/11045628
; Publication No. US20050233952A1
; GENERAL INFORMATION:
; APPLICANT: VICURON PHARMACEUTICALS INC.
; APPLICANT: LAZZARINI, Ameriga
; APPLICANT: GASTALDO, Luciano
; APPLICANT: CANDIANI, Gianpaolo
; APPLICANT: CICILIATO, Ismaela
; APPLICANT: LOSI, Daniele
; APPLICANT: MARINELLI, Flavia
; APPLICANT: SELVA, Enrico
; APPLICANT: PARENTI, Franco
; TITLE OF INVENTION: ANTIBIOTIC 107891, ITS FACTORS A1 AND A2, PHARMACEUTICALLY
; FILE REFERENCE: 892,280-500
; CURRENT APPLICATION NUMBER: US/11/045,628
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: US 11/035,296
; PRIOR FILING DATE: 2005-01-12
; PRIOR APPLICATION NUMBER: US 10/521,336
; PRIOR FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: PCT/EP2004/007658
; PRIOR FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: EP 03016306.7
; PRIOR FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Microbispora sp. ATCC PTA-5024
US-11-045-628-1

Query Match      87.2%; Score 21.8; DB 13; Length 1443;
Best Local Similarity 92.0%; Pred. No. 3.7;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTTTCG 25
    ||||| ||||| ||||| ||||| |||||
DB 30 GCAAGTCGAACGGAAGGCGCTTTTCG 54
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Query Match      87.2%; Score 21.8; DB 10; Length 1461;
Best Local Similarity 92.0%; Pred. No. 3.7; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTCG 25
    |||||
Db 20 GCAAGTCGAACGGAAGGCGCTTCG 44

RESULT 12
US-11-228-416-5
; Sequence 5, Application US/11228416
; Publication No. US2006000852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1480
; TYPE: DNA
; ORGANISM: Salinospira sp. CNH898 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1423)..(1423)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
; US-11-228-416-5

Query Match      87.2%; Score 21.8; DB 16; Length 1480;
Best Local Similarity 92.0%; Pred. No. 3.7; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTCG 25
    |||||
Db 50 GCAAGTCGAACGGAAGGCGCTTCG 74

RESULT 13
US-11-228-416-6
; Sequence 6, Application US/11228416
; Publication No. US2006000852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO

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; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1480
; TYPE: DNA
; ORGANISM: Salinospira sp. CNH440 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1423)..(1423)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
; US-11-228-416-6

Query Match      87.2%; Score 21.8; DB 16; Length 1480;
Best Local Similarity 92.0%; Pred. No. 3.7; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTCG 25
    |||||
Db 50 GCAAGTCGAACGGAAGGCGCTTCG 74

RESULT 14
US-11-228-416-8
; Sequence 8, Application US/11228416
; Publication No. US2006000852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 1480
; TYPE: DNA
; ORGANISM: Salinospira sp. CNH725 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature

```

; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1423)..(1423)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
US-11-228-416-8

Query Match 87.2%; Score 21.8; DB 16; Length 1480;
Best Local Similarity 92.0%; Pred. No. 3.7; Mismatches 0; Gaps 0;
Matches 23; Conservative 0; Indels 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGAAAGGCCTTTCG 25
|||||
Db 50 GCAAGTCGAGCGGAAAGGCCCTTCG 74

RESULT 15
US-11-228-416-9
; Sequence 9, Application US/11228416
; Publication No. US20060008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1480
; TYPE: DNA
; ORGANISM: Salinospora sp. CNH964 16S ribosomal RNA gene, partial sequence
; NAME/KEY: misc feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: n is signature nucleotide t position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1423)..(1423)
; OTHER INFORMATION: n is signature nucleotide g position 1456 of 16S rDNA
US-11-228-416-9

Query Match 87.2%; Score 21.8; DB 16; Length 1480;
Best Local Similarity 92.0%; Pred. No. 3.7; Mismatches 0; Gaps 0;
Matches 23; Conservative 0; Indels 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGAAAGGCCTTTCG 25
|||||
Db 50 GCAAGTCGAGCGGAAAGGCCCTTCG 74

RESULT 16
US-11-228-416-3
; Sequence 3, Application US/11228416
; Publication No. US20060008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1481
; TYPE: DNA
; ORGANISM: Salinospora sp. CNH643 16S ribosomal RNA gene, partial sequence
; NAME/KEY: misc feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (352)..(352)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (444)..(444)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1424)..(1424)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
US-11-228-416-3

Query Match 87.2%; Score 21.8; DB 16; Length 1481;
Best Local Similarity 92.0%; Pred. No. 3.7; Mismatches 0; Gaps 0;
Matches 23; Conservative 0; Indels 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGAAAGGCCTTTCG 25
|||||
Db 50 GCAAGTCGAGCGGAAAGGCCCTTCG 74

RESULT 17
US-11-228-416-4
; Sequence 4, Application US/11228416
; Publication No. US20060008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15

; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1482
; TYPE: DNA
; ORGANISM: Salinospora sp. CNH646 16S ribosomal RNA gene, partial sequence
; NAME/KEY: misc feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1425)..(1425)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
US-11-228-416-4

Query Match 87.2%; Score 21.8; DB 16; Length 1482;
Best Local Similarity 92.0%; Pred. No. 3.7; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 2;

Qy 1 GCAAGTCGAACGGAAGGCCTTCG 25
Db 50 GCAAGTCGAGCGGAAGGCCTTCG 74

RESULT 18
US-11-228-416-7
; Sequence 7, Application US/11228416
; Publication No. US2006008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1483
; TYPE: DNA
; ORGANISM: Salinospora sp. CNH536 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:

; NAME/KEY: misc feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (444)..(444)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1426)..(1426)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
US-11-228-416-7

Query Match 87.2%; Score 21.8; DB 16; Length 1483;
Best Local Similarity 92.0%; Pred. No. 3.7; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 2;

Qy 1 GCAAGTCGAACGGAAGGCCTTCG 25
Db 50 GCAAGTCGAGCGGAAGGCCTTCG 74

RESULT 19
US-09-738-972-7
; Sequence 7, Application US/09738972
; Patent No. US20020012918A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: primer
US-09-738-972-7

Query Match 85.6%; Score 21.4; DB 3; Length 32;
Best Local Similarity 95.7%; Pred. No. 4.9;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
Db 1 GCAAGTCGAACGGAAGGCCTCT 23

RESULT 20
US-09-738-972-14/c
; Sequence 14, Application US/09738972
; Patent No. US20020012918A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14

```
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-738-972-14

Query Match      85.6%; Score 21.4; DB 3; Length 32;
Best Local Similarity 95.7%; Pred. No. 4.9;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
Db 32 GCAAGTCGAACGGAAGGCCTCT 10

RESULT 21
US-10-862-026-7
; Sequence 7, Application US/10862026
; Publication No. US20040224348A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GPI19-02.UT
; CURRENT APPLICATION NUMBER: US/10/862,026
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-862-026-7

Query Match      85.6%; Score 21.4; DB 9; Length 32;
Best Local Similarity 95.7%; Pred. No. 4.9;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
Db 1 GCAAGTCGAACGGAAGGCCTCT 23

RESULT 22
US-10-862-026-14/c
; Sequence 14, Application US/10862026
; Publication No. US20040224348A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GPI19-02.UT
; CURRENT APPLICATION NUMBER: US/10/862,026
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
```

```
; OTHER INFORMATION: probe
US-10-862-026-14

Query Match      85.6%; Score 21.4; DB 9; Length 32;
Best Local Similarity 95.7%; Pred. No. 4.9;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
Db 32 GCAAGTCGAACGGAAGGCCTCT 10

RESULT 23
US-10-478-633A-23
; Sequence 23, Application US/10478633A
; Publication No. US20050059000A1
; GENERAL INFORMATION:
; APPLICANT: TAKARA BIO INC.
; TITLE OF INVENTION: A stabilization method and a preservation method for a reagent fo
; FILE REFERENCE: 663232
; CURRENT APPLICATION NUMBER: US/10/478,633A
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: JP 2001-177737
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2001-249689
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 23
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-10-478-633A-23

Query Match      85.6%; Score 21.4; DB 10; Length 560;
Best Local Similarity 95.7%; Pred. No. 5.5;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
Db 30 GCAAGTCGAACGGAAGGCCTCT 52

RESULT 24
US-10-697-802A-12
; Sequence 12, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 12
; LENGTH: 1421
; TYPE: DNA
; ORGANISM: Mycobacterium lentiflavum
US-10-697-802A-12

Query Match      85.6%; Score 21.4; DB 10; Length 1421;
Best Local Similarity 95.7%; Pred. No. 5.7;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
Db 20 GCAAGTCGAACGGAAGGCCTCT 42

RESULT 25
US-10-697-802A-2
; Sequence 2, Application US/10697802A
```

; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 2
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-10-697-802A-2

Query Match 85.6%; Score 21.4; DB 10; Length 1454;
Best Local Similarity 95.7%; Pred. No. 5.7;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
| | | | | | | | | | | | | | | | | | | | | |
Db 30 GCAAGTCGAACGGAAGGCCTCT 52

RESULT 26

US-10-029-397A-32
; Sequence 32, Application US/10029397A
; Publication No. US20030175709A1

; GENERAL INFORMATION:
; APPLICANT: MURPHY, GEORGE L.
; APPLICANT: WHITLEY, J. PENN
; TITLE OF INVENTION: METHOD AND SYSTEM FOR DEPLETING rRNA POPULATIONS
; FILE REFERENCE: AMBI-076US
; CURRENT APPLICATION NUMBER: US/10/029,397A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 1465
; TYPE: DNA
; ORGANISM: Mycobacterium avium
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (298)..(881)
; OTHER INFORMATION: N = A, C, G or T/U
US-10-029-397A-32

Query Match 85.6%; Score 21.4; DB 7; Length 1465;
Best Local Similarity 95.7%; Pred. No. 5.7;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
| | | | | | | | | | | | | | | | | | | | | |
Db 20 GCAAGTCGAACGGAAGGCCTCT 42

RESULT 27

US-09-738-274-23
; Sequence 23, Application US/09738274
; Publication No. US20030165824A1

; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 2000-12-15
; PRIOR FILING DATE: 1999-12-17

; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-23

Query Match 84.0%; Score 21; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GTCGAACGGAAGGCCTTTTCG 25
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GTCGAACGGAAGGCCTTTTCG 21

RESULT 28

US-10-665-708-23
; Sequence 23, Application US/10665708
; Publication No. US20050100915A1

; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-10-665-708-23

Query Match 84.0%; Score 21; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GTCGAACGGAAGGCCTTTTCG 25
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GTCGAACGGAAGGCCTTTTCG 21

RESULT 29

US-10-085-871C-1
; Sequence 1, Application US/10085871C
; Publication No. US20030199047A1

; GENERAL INFORMATION:
; APPLICANT: Lee, Fang-Yu
; APPLICANT: Lee, Ming-Liang
; APPLICANT: Anderson, Hong C.
; APPLICANT: Chiu, Chung-Ching
; TITLE OF INVENTION: New Strains of Saccharothrix, Process for Producing Pravastatin U
; FILE REFERENCE: 004135.0005
; CURRENT APPLICATION NUMBER: US/10/085,871C
; CURRENT FILING DATE: 2002-02-27

Qy 1 GCAAGTCGAACGGAAGGCCCTTCG 25
 |||||
 Db 30 GCAAGTCGAGCGGTAAGGCCCTTCG 54

RESULT 34

US-10-727-643-2
 ; Sequence 2, Application US/10727643
 ; Publication No. US20050064566A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lee, Fang-Yu
 ; APPLICANT: Lee, Ming-Liang
 ; APPLICANT: Anderson, Hong C.
 ; APPLICANT: Chiu, Chung-Ching
 ; TITLE OF INVENTION: New Strains of Saccharothrix, Process for Producing Pravastatin
 ; FILE REFERENCE: 004135.P005
 ; CURRENT APPLICATION NUMBER: US/10/727,643
 ; PRIOR FILING DATE: 2003-12-03
 ; PRIOR APPLICATION NUMBER: US/10/085,871
 ; PRIOR FILING DATE: 2002-02-27
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 1471
 ; TYPE: DNA
 ; ORGANISM: Saccharothrix 45494
 US-10-727-643-2

Query Match 80.8%; Score 20.2; DB 10; Length 1471;
 Best Local Similarity 88.0%; Pred. No. 21;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCCTTCG 25
 |||||
 Db 30 GCAAGTCGAGCGGTAAGGCCCTTCG 54

RESULT 35

US-10-756-683-1
 ; Sequence 1, Application US/10756683
 ; Publication No. US20040180960A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Korea Chungang Educational Foundation
 ; APPLICANT: Hwang, Byong Kook
 ; APPLICANT: Lee, Jung Yeop
 ; TITLE OF INVENTION: Thiobactin and Antifungal Composition for Controlling Plant
 ; TITLE OF INVENTION: Diseases Using the Same
 ; FILE REFERENCE: 4228-102
 ; CURRENT APPLICATION NUMBER: US/10/756,683
 ; CURRENT FILING DATE: 2004-01-13
 ; PRIOR APPLICATION NUMBER: KP 10-2003-0015628
 ; PRIOR FILING DATE: 2003-03-13
 ; PRIOR APPLICATION NUMBER: KP 10-2003-0015629
 ; PRIOR FILING DATE: 2003-03-13
 ; NUMBER OF SEQ ID NOS: 1
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 1
 ; LENGTH: 1488
 ; TYPE: DNA
 ; ORGANISM: Lechevalieria aerocolonigenes
 US-10-756-683-1

Query Match 80.8%; Score 20.2; DB 9; Length 1488;
 Best Local Similarity 88.0%; Pred. No. 21;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCCTTCG 25
 |||||
 Db 42 GCAAGTCGAGCGGTAAGGCCCTTCG 66

RESULT 36

US-10-875-161-2
 ; Sequence 2, Application US/10875161
 ; Publication No. US20050009151A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chase, Matthew
 ; APPLICANT: Clayton, Robert
 ; APPLICANT: Landis, Bryan
 ; APPLICANT: Banerjee, Amit
 ; TITLE OF INVENTION: Methods for the Stereoselective Synthesis and Enantiomeric
 ; FILE REFERENCE: S0-3262-2-PR-US
 ; CURRENT APPLICATION NUMBER: US/10/875,161
 ; CURRENT FILING DATE: 2004-06-22
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 2
 ; LENGTH: 1514
 ; TYPE: DNA
 ; ORGANISM: Rhodococcus opacus
 ; FEATURE:
 ; NAME/KEY: rRNA
 ; LOCATION: (1)..(1514)
 ; OTHER INFORMATION: 16s rRNA gene (rDNA) from Rhodococcus opacus
 ; FEATURE:
 ; NAME/KEY: misc difference
 ; LOCATION: (1)..(1514)
 ; OTHER INFORMATION: Alignment 0.17% different from 16s rRNA gene (rDNA) of
 ; OTHER INFORMATION: Rhodococcus opacus
 US-10-875-161-2

Query Match 80.8%; Score 20.2; DB 9; Length 1514;
 Best Local Similarity 88.0%; Pred. No. 21;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCCTTCG 25
 |||||
 Db 53 GCAAGTCGAGCGGTAAGGCCCTTCG 77

RESULT 37

US-10-831-286A-1517
 ; Sequence 1517, Application US/10831286A
 ; Publication No. US20060046246A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ZENG, QIANDONG
 ; APPLICANT: CHATELLIER, SONIA
 ; APPLICANT: MOIR, DONALD T.
 ; APPLICANT: LACROIX, BRUNA
 ; APPLICANT: CHILDRESS, DARRELL
 ; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
 ; FILE REFERENCE: 032796-174.001
 ; CURRENT APPLICATION NUMBER: US/10/831,286A
 ; CURRENT FILING DATE: 2004-04-26
 ; PRIOR APPLICATION NUMBER: 60/464,955
 ; PRIOR FILING DATE: 2003-04-24
 ; NUMBER OF SEQ ID NOS: 48788
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 1517
 ; LENGTH: 30
 ; TYPE: DNA
 ; ORGANISM: Corynebacterium diphtheriae
 US-10-831-286A-1517

Query Match 80.0%; Score 20; DB 11; Length 30;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CAAAGTCGAACGGAAGGCCCT 21
 |||||
 Db 1 CAAAGTCGAACGGAAGGCCCT 20

```

; CURRENT APPLICATION NUMBER: US/10/697,802A
; NUMBER FILING DATE: 2003-10-31
; CURRENT OF SEQ ID NOS: 145
; SEQ ID NO 11
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Mycobacterium kansasii
; US-10-697-802A-11

Query Match      80.0%; Score 20; DB 10; Length 1321;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCC 20
    |||||
DB 14 GCAAGTCGAACGGAAGGCC 33
    |||||

RESULT 41
US-10-697-802A-14
; Sequence 14, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 14
; LENGTH: 1415
; TYPE: DNA
; ORGANISM: Mycobacterium paraffinicum
; US-10-697-802A-14

Query Match      80.0%; Score 20; DB 10; Length 1415;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCC 20
    |||||
DB 15 GCAAGTCGAACGGAAGGCC 34
    |||||

RESULT 42
US-10-062-777-1
; Sequence 1, Application US/10062777
; Publication No. US20020119514A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: A PROCESS FOR PRODUCING A BRAN PICKLES FLAVORING SOLUTION
; FILE REFERENCE: 11142WO
; CURRENT APPLICATION NUMBER: US/10/062,777
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/463,618
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Corynebacterium sp.NK-1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (166)
; OTHER INFORMATION: n is "a" or "g" or "c" or "t".
; US-10-062-777-1

Query Match      80.0%; Score 20; DB 6; Length 1460;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; CURRENT APPLICATION NUMBER: US/10/830,943
; NUMBER FILING DATE: 2004-04-22
; CURRENT OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: amplicon sequence
; US-10-830-943-11

Query Match      80.0%; Score 20; DB 9; Length 80;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCC 20
    |||||
DB 50 GCAAGTCGAACGGAAGGCC 69
    |||||

RESULT 39
US-10-478-633A-24
; Sequence 24, Application US/10478633A
; Publication No. US20050059000A1
; GENERAL INFORMATION:
; APPLICANT: TAKARA BIO INC.
; TITLE OF INVENTION: A stabilization method and a preservation method for a reagent for
; FILE REFERENCE: 663232
; CURRENT APPLICATION NUMBER: US/10/478,633A
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: JP 2001-177737
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2001-249689
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 24
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Mycobacterium intracellulare
; US-10-478-633A-24

Query Match      80.0%; Score 20; DB 10; Length 560;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCC 20
    |||||
DB 42 GCAAGTCGAACGGAAGGCC 61
    |||||

RESULT 40
US-10-697-802A-11
; Sequence 11, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001

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; CURRENT APPLICATION NUMBER: US/10/697,802A
; NUMBER FILING DATE: 2003-10-31
; CURRENT OF SEQ ID NOS: 145
; SEQ ID NO 11
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Mycobacterium kansasii
; US-10-697-802A-11

Query Match      80.0%; Score 20; DB 10; Length 1321;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCC 20
    |||||
DB 14 GCAAGTCGAACGGAAGGCC 33
    |||||

RESULT 41
US-10-697-802A-14
; Sequence 14, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 14
; LENGTH: 1415
; TYPE: DNA
; ORGANISM: Mycobacterium paraffinicum
; US-10-697-802A-14

Query Match      80.0%; Score 20; DB 10; Length 1415;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCC 20
    |||||
DB 15 GCAAGTCGAACGGAAGGCC 34
    |||||

RESULT 42
US-10-062-777-1
; Sequence 1, Application US/10062777
; Publication No. US20020119514A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: A PROCESS FOR PRODUCING A BRAN PICKLES FLAVORING SOLUTION
; FILE REFERENCE: 11142WO
; CURRENT APPLICATION NUMBER: US/10/062,777
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/463,618
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Corynebacterium sp.NK-1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (166)
; OTHER INFORMATION: n is "a" or "g" or "c" or "t".
; US-10-062-777-1

Query Match      80.0%; Score 20; DB 6; Length 1460;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; CURRENT APPLICATION NUMBER: US/10/830,943
; NUMBER FILING DATE: 2004-04-22
; CURRENT OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: amplicon sequence
; US-10-830-943-11

Query Match      80.0%; Score 20; DB 9; Length 80;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCC 20
    |||||
DB 50 GCAAGTCGAACGGAAGGCC 69
    |||||

RESULT 39
US-10-478-633A-24
; Sequence 24, Application US/10478633A
; Publication No. US20050059000A1
; GENERAL INFORMATION:
; APPLICANT: TAKARA BIO INC.
; TITLE OF INVENTION: A stabilization method and a preservation method for a reagent for
; FILE REFERENCE: 663232
; CURRENT APPLICATION NUMBER: US/10/478,633A
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: JP 2001-177737
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2001-249689
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 24
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Mycobacterium intracellulare
; US-10-478-633A-24

Query Match      80.0%; Score 20; DB 10; Length 560;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCC 20
    |||||
DB 42 GCAAGTCGAACGGAAGGCC 61
    |||||

RESULT 40
US-10-697-802A-11
; Sequence 11, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001

```

Qy 1 GCAAGTCGAACGGAAGGCC 20
|||||
Db 38 GCAAGTCGAACGGAAGGCC 57

RESULT 43

US-10-419-095-1
; Sequence 1, Application US/10419095
; Publication No. US20030162244A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: A PROCESS FOR PRODUCING A BRAN PICKLES FLAVORING SOLUTION
; FILE REFERENCE: 11142WO
; CURRENT APPLICATION NUMBER: US/10/419,095
; CURRENT FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: 2003-04-21
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: H10-166226
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Corynebacterium sp.NK-1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (166)
; OTHER INFORMATION: n is "a" or "g" or "c" or "t".
US-10-419-095-1

Query Match 80.0%; Score 20; DB 7; Length 1460;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCC 20
|||||
Db 38 GCAAGTCGAACGGAAGGCC 57

RESULT 44

US-10-697-802A-16
; Sequence 16, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 16
; LENGTH: 1462
; TYPE: DNA
; ORGANISM: Mycobacterium szulgai
US-10-697-802A-16

Query Match 80.0%; Score 20; DB 10; Length 1462;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCC 20
|||||
Db 20 GCAAGTCGAACGGAAGGCC 39

RESULT 45

US-10-697-802A-15
; Sequence 15, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG

; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 15
; LENGTH: 1484
; TYPE: DNA
; ORGANISM: Mycobacterium simiae
US-10-697-802A-15

Query Match 80.0%; Score 20; DB 10; Length 1484;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCC 20
|||||
Db 20 GCAAGTCGAACGGAAGGCC 39

RESULT 46

US-10-697-802A-8
; Sequence 8, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 8
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Mycobacterium heckeshornense
US-10-697-802A-8

Query Match 80.0%; Score 20; DB 10; Length 1527;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCC 20
|||||
Db 44 GCAAGTCGAACGGAAGGCC 63

RESULT 47

US-09-738-274-14
; Sequence 14, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer

```
; OTHER INFORMATION: oligonucleotide
US-09-738-274-14

Query Match          79.2%; Score 19.8; DB 3; Length 32;
Best Local Similarity 91.3%; Pred. No. 28;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTT 23
Db 1 GCAAGTCGAACGGAAGGCTCT 23

RESULT 48
US-10-665-708-14
; Sequence 14, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GPI07-02.U7
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-665-708-14

Query Match          79.2%; Score 19.8; DB 10; Length 32;
Best Local Similarity 91.3%; Pred. No. 28;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTT 23
Db 1 GCAAGTCGAACGGAAGGCTCT 23

RESULT 49
US-10-697-802A-17
; Sequence 17, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: PHAM, Xiang-Yang
; APPLICANT: PHAM, Audrey S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 17
; LENGTH: 1416
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-697-802A-17

Query Match          79.2%; Score 19.8; DB 10; Length 1416;
Best Local Similarity 91.3%; Pred. No. 33;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 GCAAGTCGAACGGAAGGCGCTTT 23
Db 20 GCAAGTCGAACGGAAGGCTCT 42

RESULT 50
US-10-697-802A-3
; Sequence 3, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, Xiang-Yang
; APPLICANT: PHAM, Audrey S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 3
; LENGTH: 1421
; TYPE: DNA
; ORGANISM: Mycobacterium bovis
US-10-697-802A-3

Query Match          79.2%; Score 19.8; DB 10; Length 1421;
Best Local Similarity 91.3%; Pred. No. 33;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTT 23
Db 20 GCAAGTCGAACGGAAGGCTCT 42

RESULT 51
US-10-697-802A-10
; Sequence 10, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, Xiang-Yang
; APPLICANT: PHAM, Audrey S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 10
; LENGTH: 1463
; TYPE: DNA
; ORGANISM: Mycobacterium kansasii
US-10-697-802A-10

Query Match          79.2%; Score 19.8; DB 10; Length 1463;
Best Local Similarity 91.3%; Pred. No. 33;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTT 23
Db 19 GCAAGTCGAACGGAAGGCTCT 41

RESULT 52
US-09-726-774-7
; Sequence 7, Application US/09726774
; Patent No. US2002008226A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; TITLE OF INVENTION: Composition
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/09/726,774
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
```



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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-726-774-7

Query Match          79.2%; Score 19.8; DB 3; Length 1464;
Best Local Similarity 91.3%; Pred. No. 33;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
    |||||
Db 20 GCAAGTCGAACGGAAGGTCCT 42

RESULT 53
US-10-719-633-7
; Sequence 7, Application US/10719633
; Publication No. US20040137485A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; FILE REFERENCE: Composition
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/10/719,633
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/09/726,774
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-719-633-7

Query Match          79.2%; Score 19.8; DB 8; Length 1464;
Best Local Similarity 91.3%; Pred. No. 33;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
    |||||
Db 20 GCAAGTCGAACGGAAGGTCCT 42

RESULT 54
US-10-220-212A-34
; Sequence 34, Application US/10220212A
; Publication No. US20040110129A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America as represented by the
; APPLICANT: Secretary, Department of Health & Human Services, the National Institutes
; APPLICANT: Health
; APPLICANT: Beckman Coulter, Inc.
; TITLE OF INVENTION: Multiplex Hybridization System for the Identification of Pathogen
; FILE REFERENCE: 4239-58135
; CURRENT APPLICATION NUMBER: US/10/220,212A
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/186,840
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-220-212A-34

Query Match          79.2%; Score 19.8; DB 8; Length 1524;
Best Local Similarity 91.3%; Pred. No. 33;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
    |||||
Db 20 GCAAGTCGAACGGAAGGTCCT 42

RESULT 55
US-10-029-397A-33
; Sequence 33, Application US/10029397A
; Publication No. US20030175709A1
; GENERAL INFORMATION:
; APPLICANT: MURPHY, GEORGE L.
; APPLICANT: WHITLEY, J. PENN
; TITLE OF INVENTION: METHOD AND SYSTEM FOR DEPLETING rRNA POPULATIONS
; FILE REFERENCE: AMBI:076US
; CURRENT APPLICATION NUMBER: US/10/029,397A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-029-397A-33

Query Match          79.2%; Score 19.8; DB 7; Length 1536;
Best Local Similarity 91.3%; Pred. No. 33;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
    |||||
Db 59 GCAAGTCGAACGGAAGGTCCT 81

RESULT 56
US-10-029-397A-34
; Sequence 34, Application US/10029397A
; Publication No. US20030175709A1
; GENERAL INFORMATION:
; APPLICANT: MURPHY, GEORGE L.
; APPLICANT: WHITLEY, J. PENN
; TITLE OF INVENTION: METHOD AND SYSTEM FOR DEPLETING rRNA POPULATIONS
; FILE REFERENCE: AMBI:076US
; CURRENT APPLICATION NUMBER: US/10/029,397A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-029-397A-34

Query Match          79.2%; Score 19.8; DB 7; Length 1536;
Best Local Similarity 91.3%; Pred. No. 33;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
    |||||
Db 59 GCAAGTCGAACGGAAGGTCCT 81

RESULT 57
US-10-831-286A-8212
; Sequence 8212, Application US/10831286A
; Publication No. US20060046246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, QIANDONG
; APPLICANT: CHATELIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
```

```
; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001
; CURRENT APPLICATION NUMBER: US/10/831,286A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/464,955
; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8212
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Corynebacterium kutscheri
US-10-831-286A-8212

Query Match          77.6%; Score 19.4; DB 11; Length 30;
Best Local Similarity 95.2%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  2  CAAGTCGAACGGAAGGCGCTT 22
      ||||| ||||| ||||| ||||| ||
Db  1  CAAGTCGAACGGAAGGCGCTT 21

RESULT 58
US-10-438-774-15
; Sequence 15, Application US/10438774
; Publication No. US20040010504A1
; GENERAL INFORMATION:
; APPLICANT: Hinrichs, Steven
; APPLICANT: Mohammed, Amr
; APPLICANT: Ali, Hesham
; APPLICANT: Kuyper, Dan
; TITLE OF INVENTION: Custom Sequence Databases and Methods of
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: UNMC.63174-US
; CURRENT APPLICATION NUMBER: US/10/438,774
; CURRENT FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: 60/381,015
; PRIOR FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-438-774-15

Query Match          77.6%; Score 19.4; DB 7; Length 454;
Best Local Similarity 95.2%; Pred. No. 49;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  5  GTCGAACGGAAGGCGCTTTTCG 25
      ||||| ||||| ||||| ||||| ||
Db  1  GTCGAACGGAAGGCGCTTTTCG 21

RESULT 59
US-09-925-065A-906221/c
; Sequence 906221, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 906221
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-906221

Query Match          76.8%; Score 19.2; DB 5; Length 600;
Best Local Similarity 87.5%; Pred. No. 62;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  1  GCAAGTCGAACGGAAGGCGCTTTC 24
      ||||| ||||| ||||| ||||| |||||
Db  299 GCAAGTCGACCTGGAAGGCGCTTTC 276

RESULT 60
US-09-925-065A-906221/c
; Sequence 906221, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 906221
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-906221

Query Match          76.8%; Score 19.2; DB 5; Length 600;
Best Local Similarity 87.5%; Pred. No. 62;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  1  GCAAGTCGAACGGAAGGCGCTTTC 24
      ||||| ||||| ||||| ||||| |||||
Db  299 GCAAGTCGACCTGGAAGGCGCTTTC 276

RESULT 61
US-09-925-065A-906221
; Sequence 27, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
```

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; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001
; CURRENT APPLICATION NUMBER: US/10/831,286A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/464,955
; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8212
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Corynebacterium kutscheri
US-10-831-286A-8212

Query Match          77.6%; Score 19.4; DB 11; Length 30;
Best Local Similarity 95.2%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  2  CAAGTCGAACGGAAGGCGCTT 22
      ||||| ||||| ||||| ||||| ||
Db  1  CAAGTCGAACGGAAGGCGCTT 21

RESULT 58
US-10-438-774-15
; Sequence 15, Application US/10438774
; Publication No. US20040010504A1
; GENERAL INFORMATION:
; APPLICANT: Hinrichs, Steven
; APPLICANT: Mohammed, Amr
; APPLICANT: Ali, Hesham
; APPLICANT: Kuyper, Dan
; TITLE OF INVENTION: Custom Sequence Databases and Methods of
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: UNMC.63174-US
; CURRENT APPLICATION NUMBER: US/10/438,774
; CURRENT FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: 60/381,015
; PRIOR FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-438-774-15

Query Match          77.6%; Score 19.4; DB 7; Length 454;
Best Local Similarity 95.2%; Pred. No. 49;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  5  GTCGAACGGAAGGCGCTTTTCG 25
      ||||| ||||| ||||| ||||| ||
Db  1  GTCGAACGGAAGGCGCTTTTCG 21

RESULT 59
US-09-925-065A-906221/c
; Sequence 906221, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 906221
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-906221

Query Match          76.8%; Score 19.2; DB 5; Length 600;
Best Local Similarity 87.5%; Pred. No. 62;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  1  GCAAGTCGAACGGAAGGCGCTTTC 24
      ||||| ||||| ||||| ||||| |||||
Db  299 GCAAGTCGACCTGGAAGGCGCTTTC 276

RESULT 60
US-09-925-065A-906221/c
; Sequence 906221, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 906221
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-906221

Query Match          76.8%; Score 19.2; DB 5; Length 600;
Best Local Similarity 87.5%; Pred. No. 62;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  1  GCAAGTCGAACGGAAGGCGCTTTC 24
      ||||| ||||| ||||| ||||| |||||
Db  299 GCAAGTCGACCTGGAAGGCGCTTTC 276

RESULT 61
US-09-925-065A-906221
; Sequence 27, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
```

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; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-27

Query Match          76.0%; Score 19; DB 3; Length 23;
Best Local Similarity 100.0%; Pred.No. 68;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 CAAGTCGAACGGAAGGCC 20
Db  1 CAAGTCGAACGGAAGGCC 19

RESULT 62
US-10-665-708-27
; Sequence 27, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-10-665-708-27

Query Match          76.0%; Score 19; DB 10; Length 23;
Best Local Similarity 100.0%; Pred.No. 68;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 CAAGTCGAACGGAAGGCC 20
Db  1 CAAGTCGAACGGAAGGCC 19

RESULT 63
US-10-697-802A-9
; Sequence 9, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 9
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Mycobacterium intracellulare
US-10-697-802A-9

Query Match          73.6%; Score 18.4; DB 10; Length 1452;
Best Local Similarity 95.0%; Pred.No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1 GCAAGTCGAACGGAAGGCC 20
Db  10 GCAAGTCGAACGGAAGGCC 29

RESULT 64
US-09-738-274-24
; Sequence 24, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-24

Query Match          72.0%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred.No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  8 GAACGGAAGCCTTTCG 25
Db  1 GAACGGAAGCCTTTCG 18

RESULT 65
US-10-665-708-24
; Sequence 24, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
```

; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-10-665-708-24

Query Match 72.0%; Score 18; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GAACGGAAGGCGTTTCG 25
Db 1 GAACGGAAGGCGTTTCG 18
|||||

RESULT 66
US-10-425-114-30427
; Sequence 30427, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 30427
; LENGTH: 1366
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73019F09_FLI
US-10-425-114-30427

Query Match 71.2%; Score 17.8; DB 8; Length 1366;
Best Local Similarity 90.5%; Pred. No. 3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCGTTT 22
Db 896 CAAGTCGAACGGAAGGCGTTT 916
|||||

RESULT 67
US-09-917-800A-1684
; Sequence 1684, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31

; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1684
; LENGTH: 4540
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_021266
US-09-917-800A-1684

Query Match 71.2%; Score 17.8; DB 3; Length 4540;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCGTTT 22
Db 105 CAAGTCGAACGGAAGGCGTTT 125
|||||

RESULT 68
US-11-136-527-299
; Sequence 299, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays for Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 299
; LENGTH: 4770
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-299

Query Match 71.2%; Score 17.8; DB 16; Length 4770;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCGTTT 22
Db 105 CAAGTCGAACGGAAGGCGTTT 125
|||||

RESULT 69
US-10-972-079-55955/c
; Sequence 55955, Application US/10972079
; Publication No. US20050153317A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: Denise, Sue K.
; APPLICANT: ROSENFELD, David

```
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEER
; TITLE OF INVENTION: LIVESTOCK
; FILE REFERENCE: MM1110-2
; CURRENT APPLICATION NUMBER: US/10/972,079
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,333
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 96631
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55955
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Chicken 19866894310123_1
US-10-972-079-55955

Query Match          70.4%; Score 17.6; DB 10; Length 600;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTC 24
    ||||| ||||| ||||| |||||
Db 481 GCAAGGGGGACGGAAGGACTTTC 458

RESULT 70
US-10-972-079-55956/c
; Sequence 55956, Application US/10972079
; Publication No. US20050153317A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEER
; TITLE OF INVENTION: LIVESTOCK
; FILE REFERENCE: MM1110-2
; CURRENT APPLICATION NUMBER: US/10/972,079
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,333
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 96631
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55956
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Chicken 19866894310123_2
US-10-972-079-55956

Query Match          70.4%; Score 17.6; DB 10; Length 600;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTC 24
    ||||| ||||| ||||| |||||
Db 114 GCAAGGGGGACGGAAGGACTTTC 91

RESULT 71
US-09-925-065A-481777
; Sequence 481777, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 481777
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-481777

Query Match          70.4%; Score 17.6; DB 5; Length 654;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTC 24
    ||||| ||||| ||||| |||||
Db 401 GGAAGTGAACGGAACGCGCTTTC 424

RESULT 72
US-09-925-065A-481777
; Sequence 481777, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 481777
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-481777

Query Match          70.4%; Score 17.6; DB 5; Length 654;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTC 24
    ||||| ||||| ||||| |||||
Db 401 GGAAGTGAACGGAACGCGCTTTC 424

RESULT 73
US-10-087-192-1004
; Sequence 1004, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
```

```
; TITLE OF INVENTION:  CANCER
; FILE REFERENCE:  529452000122
; CURRENT APPLICATION NUMBER:  US/10/087,192
; CURRENT FILING DATE:  2002-03-01
; PRIOR APPLICATION NUMBER:  US 09/747,377
; PRIOR FILING DATE:  2000-12-22
; PRIOR APPLICATION NUMBER:  US 09/798,586
; PRIOR FILING DATE:  2001-03-02
; NUMBER OF SEQ ID NOS:  2059
; SOFTWARE:  FastSeq for Windows Version 4.0
; SEQ ID NO 1004
; LENGTH:  960
; TYPE:  DNA
; ORGANISM:  Mus musculus
US-10-087-192-1004
```

```
Query Match          70.4%; Score 17.6; DB 6; Length 960;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy  2  CAAGTCGAACGGAAGGCGCTTTCG 25
      ||||| ||||| ||||| ||||| |||||
Db  811 CAAGTCGAGCAGAAAGCTCTTACG 834
```

```
RESULT 74
US-10-301-480-553054/c
; Sequence 553054, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
```

```
; APPLICANT:  Wang, David G.
; TITLE OF INVENTION:  Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE:  108827.137
; CURRENT APPLICATION NUMBER:  US/10/301,480
; CURRENT FILING DATE:  2002-11-21
; PRIOR APPLICATION NUMBER:  US 10/215,598
; PRIOR FILING DATE:  2002-08-09
; PRIOR APPLICATION NUMBER:  US 60/311,695
; PRIOR FILING DATE:  2001-08-10
; NUMBER OF SEQ ID NOS:  1226818
; SOFTWARE:  FastSeq for Windows Version 4.0
; SEQ ID NO 553054
; LENGTH:  999
; TYPE:  DNA
; ORGANISM:  Homo sapien
US-10-301-480-553054
```

```
Query Match          70.4%; Score 17.6; DB 12; Length 999;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy  1  GCAAGTCGAACGGAAGGCGCTTTC 24
      ||||| ||||| ||||| ||||| |||||
Db  921 GCAACTGGAACAGAAAGGCGCTTCC 898
```

```
RESULT 75
US-10-301-480-1166463/c
; Sequence 1166463, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
```

```
; APPLICANT:  Wang, David G.
; TITLE OF INVENTION:  Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE:  108827.137
; CURRENT APPLICATION NUMBER:  US/10/301,480
; CURRENT FILING DATE:  2002-11-21
; PRIOR APPLICATION NUMBER:  US 10/215,598
; PRIOR FILING DATE:  2002-08-09
; PRIOR APPLICATION NUMBER:  US 60/311,695
; PRIOR FILING DATE:  2001-08-10
; NUMBER OF SEQ ID NOS:  1226818
```

```
; SOFTWARE:  FastSeq for Windows Version 4.0
; SEQ ID NO 1166463
; LENGTH:  999
; TYPE:  DNA
; ORGANISM:  Homo sapien
US-10-301-480-1166463
```

```
Query Match          70.4%; Score 17.6; DB 12; Length 999;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy  1  GCAAGTCGAACGGAAGGCGCTTTC 24
      ||||| ||||| ||||| ||||| |||||
Db  921 GCAACTGGAACAGAAAGGCGCTTCC 898
```

```
RESULT 76
US-10-956-157-9594
; Sequence 9594, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
```

```
; APPLICANT:  Wyeth
; APPLICANT:  Mounts, William
; TITLE OF INVENTION:  NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE:  031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER:  US/10/956,157
; CURRENT FILING DATE:  2004-10-04
; NUMBER OF SEQ ID NOS:  319805
; SOFTWARE:  PatentIn version 3.2
; SEQ ID NO 9594
; LENGTH:  1400
; TYPE:  DNA
; ORGANISM:  Homo sapiens
US-10-956-157-9594
```

```
Query Match          70.4%; Score 17.6; DB 10; Length 1400;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy  2  CAAGTCGAACGGAAGGCGCTTTCG 25
      ||||| ||||| ||||| ||||| |||||
Db  554 CAAGTCGAATTGAAAGGACTGTCG 577
```

```
RESULT 77
US-10-956-157-4359
; Sequence 4359, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
```

```
; APPLICANT:  Wyeth
; APPLICANT:  Mounts, William
; TITLE OF INVENTION:  NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE:  031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER:  US/10/956,157
; CURRENT FILING DATE:  2004-10-04
; NUMBER OF SEQ ID NOS:  319805
; SOFTWARE:  PatentIn version 3.2
; SEQ ID NO 4359
; LENGTH:  1786
; TYPE:  DNA
; ORGANISM:  Homo sapiens
US-10-956-157-4359
```

```
Query Match          70.4%; Score 17.6; DB 10; Length 1786;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy  2  CAAGTCGAACGGAAGGCGCTTTCG 25
      ||||| ||||| ||||| ||||| |||||
Db  940 CAAGTCGAATTGAAAGGACTGTCG 963
```

```

RESULT 78
US-10-301-480-29919/c
; Sequence 29919, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29919
; LENGTH: 2360
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269,
; LOCATION: 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279,
; LOCATION: 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289,
; LOCATION: 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308,
; LOCATION: 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318,
; LOCATION: 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328,
; LOCATION: 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347,
; LOCATION: 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357,
; LOCATION: 2358, 2359
; OTHER INFORMATION: n = A,T,C or G
US-10-301-480-29919
Query Match 70.4%; Score 17.6; DB 12; Length 2360;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTC 24
||||| ||||| ||||| ||||| |||||
Db 981 GCAACTGGAACAGAAAGGCGCTTCC 958

RESULT 79
US-10-301-480-643328/c
; Sequence 643328, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 643328
; LENGTH: 2360
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-087-192-1003
Query Match 70.4%; Score 17.6; DB 6; Length 43800;
Best Local Similarity 83.3%; Pred. No. 4.3e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCGCTTTC 25
||||| ||||| ||||| ||||| |||||
Db 33651 CAAGTCGAGCAGAAAGTCCTTACG 33674

RESULT 81
US-10-767-701-31297
; Sequence 31297, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

```

```

; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269,
; LOCATION: 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279,
; LOCATION: 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289,
; LOCATION: 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308,
; LOCATION: 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318,
; LOCATION: 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328,
; LOCATION: 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347,
; LOCATION: 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357,
; LOCATION: 2358, 2359
; OTHER INFORMATION: n = A,T,C or G
US-10-301-480-643328
Query Match 70.4%; Score 17.6; DB 12; Length 2360;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTC 24
||||| ||||| ||||| ||||| |||||
Db 981 GCAACTGGAACAGAAAGGCGCTTCC 958

RESULT 80
US-10-087-192-1003
; Sequence 1003, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1003
; LENGTH: 43800
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-087-192-1003
Query Match 70.4%; Score 17.6; DB 6; Length 43800;
Best Local Similarity 83.3%; Pred. No. 4.3e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCGCTTTC 25
||||| ||||| ||||| ||||| |||||
Db 33651 CAAGTCGAGCAGAAAGTCCTTACG 33674

RESULT 81
US-10-767-701-31297
; Sequence 31297, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

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```
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 31297
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 18066455
US-10-767-701-31297

Query Match          68.8%; Score 17.2; DB 8; Length 622;
Best Local Similarity 86.4%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 AGTCGAACGGAAGGCCTTTCG 25
    ||||| ||||| ||||| |||||
Db 31 AGTCGAAGGAATGCGCTTTCG 52

RESULT 82
US-10-027-632-27617/c
; Sequence 27617, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27617
; LENGTH: 708
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-27617

Query Match          68.8%; Score 17.2; DB 6; Length 708;
Best Local Similarity 86.4%; Pred. No. 5.7e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCCTT 22
    ||||| ||||| ||||| |||||
Db 415 GCAAGTCGAACGGGAGCGCCTT 394

RESULT 83
US-10-027-632-27618/c
; Sequence 27618, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27617
; LENGTH: 708
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-27617

Query Match          68.8%; Score 17.2; DB 6; Length 708;
Best Local Similarity 86.4%; Pred. No. 5.7e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCCTT 22
    ||||| ||||| ||||| |||||
Db 415 GCAAGTCGAACGGGAGCGCCTT 394

RESULT 84
US-10-027-632-27617/c
; Sequence 27617, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27617
; LENGTH: 708
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-27617

Query Match          68.8%; Score 17.2; DB 7; Length 708;
Best Local Similarity 86.4%; Pred. No. 5.7e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCCTT 22
    ||||| ||||| ||||| |||||
```



```
Db      415 GCAAGTCGAACGGGAGCGCCTT 394

RESULT 85
US-10-027-632-27618/c
; Sequence 27618, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27618
; LENGTH: 708
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-27618

Query Match      68.8%; Score 17.2; DB 7; Length 708;
Best Local Similarity 86.4%; Pred. No. 5.7e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GCAAGTCGAACGGGAAAGCCTT 22
Db      415 GCAAGTCGAACGGGAGCGCCTT 394

RESULT 86
US-10-027-632-151386/c
; Sequence 151386, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151386
; LENGTH: 708
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-151386

Query Match      68.8%; Score 17.2; DB 7; Length 708;
Best Local Similarity 86.4%; Pred. No. 5.7e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GCAAGTCGAACGGGAAAGCCTT 22
Db      415 GCAAGTCGAACGGGAGCGCCTT 394

RESULT 87
US-10-027-632-151386/c
; Sequence 151386, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151386
; LENGTH: 787
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-151386

Query Match      68.8%; Score 17.2; DB 7; Length 787;
Best Local Similarity 86.4%; Pred. No. 5.7e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GCAAGTCGAACGGGAAAGCCTT 22
Db      494 GCAAGTCGAACGGGAGCGCCTT 473

RESULT 88
US-10-425-114-28596
; Sequence 28596, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425.114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
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; SEQ ID NO 28596
; LENGTH: 1735
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4759-017-C5_FLI
US-10-423-114-28596

Query Match          68.8%; Score 17.2; DB 8; Length 1735;
Best Local Similarity 86.4%; Pred. No. 5.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCCTT 22
    ||||| ||||| ||||| |||||
Db 1163 GCAAGTCGACAGGAAAGGCCTT 1184

RESULT 89
US-10-767-701-13467
; Sequence 59, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihuei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 13467
; LENGTH: 1754
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS3315_1
US-10-767-701-13467

Query Match          68.8%; Score 17.2; DB 8; Length 1754;
Best Local Similarity 86.4%; Pred. No. 5.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCCTT 22
    ||||| ||||| ||||| |||||
Db 150 GCAAGTCGACAGGAAAGGCCTT 171

RESULT 90
US-09-809-391-59
; Sequence 59, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 1776
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (713)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (862)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
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; LOCATION: (1752)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1773)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-809-391-59

Query Match          68.8%; Score 17.2; DB 3; Length 1776;
Best Local Similarity 79.2%; Pred. No. 5.9e+02;
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCCTTTCG 25
    ||||| ||||| ||||| |||||
Db 878 CAAGTCGAATTGAAAGRACTGTCG 901

RESULT 91
US-09-882-171-59
; Sequence 59, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,633
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,583
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,617
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,618
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,503
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,592
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,581
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,584
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,500
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,587
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PRIOR APPLICATION NUMBER:	60/056,911
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,912
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,913
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,914
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,910
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,864
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,892
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,631
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,845
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,864
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,874
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,910
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,864
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,892
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/057,761
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/047,595
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,599
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,588
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,585
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,586
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,590
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,594
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,589
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,593
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,614
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/043,578
PRIOR FILING DATE:	1997-04-11
PRIOR APPLICATION NUMBER:	60/043,576
PRIOR FILING DATE:	1997-04-11
PRIOR APPLICATION NUMBER:	60/047,501
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/043,670
PRIOR FILING DATE:	1997-04-11
PRIOR APPLICATION NUMBER:	60/056,632
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,664
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,876
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,881
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,909
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,875
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,862
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,887
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/056,908
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/048,964
PRIOR FILING DATE:	1997-06-06
PRIOR APPLICATION NUMBER:	60/057,650
PRIOR FILING DATE:	1997-09-05
PRIOR APPLICATION NUMBER:	60/056,884
PRIOR FILING DATE:	1997-08-22
PRIOR APPLICATION NUMBER:	60/057,669
PRIOR FILING DATE:	1997-09-05

Query Match 68.8%; Score 17.2; DB 3; Length 1776;
Best Local Similarity 79.2%; Pred. No. 5.9e+02;
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCTTTTCG 25
|||||
DB 878 CAAGTCGAATTGAAAGRACTGTCTG 901

RESULT 92
US-10-164-861-59
; Sequence 59, Application US/10164861
; Publication No. US20030225248A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; CURRENT APPLICATION NUMBER: US/10/164,861
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 59
; LENGTH: 1776
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (713)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (862)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1752)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1773)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-164-861-59

Query Match 68.8%; Score 17.2; DB 7; Length 1776;
Best Local Similarity 79.2%; Pred. No. 5.9e+02;
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCTTTTCG 25
|||||
DB 878 CAAGTCGAATTGAAAGRACTGTCTG 901

RESULT 93
US-11-144-947-59
; Sequence 59, Application US/11144947
; Publication No. US20060084082A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; CURRENT APPLICATION NUMBER: US/11/144,947
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: 09/882,171
; PRIOR FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/190,068
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 10/164,861

; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 59
; LENGTH: 1776
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (713)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (862)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1752)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1773)
; OTHER INFORMATION: n equals a,t,g, or c
US-11-144-947-59

Query Match 68.8%; Score 17.2; DB 16; Length 1776;
Best Local Similarity 79.2%; Pred. No. 5.9e+02;
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCTTTTCG 25
|||||
DB 878 CAAGTCGAATTGAAAGRACTGTCTG 901

RESULT 94
US-09-809-391-226
; Sequence 226, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 226
; LENGTH: 1791
; TYPE: DNA
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US-09-809-391-226

Query Match 68.8%; Score 17.2; DB 3; Length 1791;
Best Local Similarity 79.2%; Pred. No. 5.9e+02;
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCTTTTCG 25
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DB 973 CAAGTCGAATTGAAAGRACTGTCTG 996

RESULT 95
US-09-882-171-226
; Sequence 226, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002F2
; CURRENT APPLICATION NUMBER: US/09/882.171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
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; PRIOR APPLICATION NUMBER: 60/040,162
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DB      973 CAAGTCGAATTGAAAGRACTGTGC 996
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; Sequence 226, Application US/10164861
; Publication No. US20030225248A1
; GENERAL INFORMATION:
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; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/10/164,861
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 226
; LENGTH: 1791
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-164-861-226
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Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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; Sequence 226, Application US/11144947
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; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2C2
; CURRENT APPLICATION NUMBER: US/11/144,947
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: 09/882,171
; PRIOR FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/190,068
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 10/164,861
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 09/149,476
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; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 761
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; TYPE: DNA
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US-11-144-947-226
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Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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RESULT 98
US-09-925-065A-553599
; Sequence 553599, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-553599

Query Match 68.8%; Score 17.2; DB 4; Length 2258;
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; Sequence 553599, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
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; ORGANISM: Homo sapiens
US-09-925-065A-553599

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Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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; Sequence 35634, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
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; PRIOR FILING DATE: 2002-02-21
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GenCore version 5.1.8
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Listing first 300 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	15	60.0	1157	6	US-10-196-749-391, A
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9	15	60.0	2787	7	US-11-217-529-76324, A
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ALIGNMENTS

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RESULT 1
US-11-217-529-80747
; Sequence 80747, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: S-38-285
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80747
; LENGTH: 1326
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-80747

Query Match 64.0%; Score 16; DB 7; Length 1326;
Best Local Similarity 79.2%; Pred. No. 11;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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DB 265 CAATTCCAACCTGAATGGGCTTTCG 288

RESULT 2
US-11-217-529-79690/c
; Sequence 79690, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79690
; LENGTH: 1824
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79690

Query Match 64.0%; Score 16; DB 7; Length 1824;
Best Local Similarity 79.2%; Pred. No. 11;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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RESULT 3
US-11-217-529-254
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; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
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; NUMBER OF SEQ ID NOS: 197023
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; SEQ ID NO 254
; LENGTH: 2397
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-254

Query Match      64.0%; Score 16; DB 7; Length 2397;
Best Local Similarity 79.2%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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RESULT 4
US-11-217-529-1369/c
; Sequence 1369, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1369
; LENGTH: 3663
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1369

Query Match      61.6%; Score 15.4; DB 7; Length 3663;
Best Local Similarity 76.0%; Pred. No. 25;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      1 GCAAGTCGAACGGAAGGCTTTTCG 25
Db      349 GCAAATCTAACGTAAGGCTTTCTTG 325

RESULT 5
US-11-217-529-5375/c
; Sequence 5375, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5375
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5375

Query Match      60.8%; Score 15.2; DB 6; Length 11611;
Best Local Similarity 85.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 AAGTCGAACGGAAGGCTTT 22
Db      8479 AAGAAGACGGAACGCTT 8498

RESULT 7
US-10-196-749-391
```

RESULT 10
US-11-217-529-4946/c
; Sequence 4946, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALY
; FILE REFERENCE: S-38-285

```
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4946
; LENGTH: 2952
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4946

Query Match          60.0%; Score 15; DB 7; Length 2952;
Best Local Similarity 78.3%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  3 AAGTCGAACGGAAGGCCTTTTCG 25
Db  2664 AATTCGATCTGGAAGGCCCTTCG 2642

RESULT 11
US-11-217-529-3215/c
; Sequence 3215, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3215
; LENGTH: 3093
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3215

Query Match          60.0%; Score 15; DB 7; Length 3093;
Best Local Similarity 78.3%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  1 GCAAGTCGAACGGAAGGCCTTT 23
Db  1580 GCAAGTTGATAAGAAAGCGGTTT 1558

RESULT 12
US-11-217-529-56270/c
; Sequence 56270, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
```

```
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 56270
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-56270

Query Match          59.2%; Score 14.8; DB 7; Length 25;
Best Local Similarity 88.9%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1 GCAAGTCGAACGGAAGG 18
Db  20 GTAAGTCGATGGAAGG 3

RESULT 13
US-10-488-619-2075
; Sequence 2075, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2075
; LENGTH: 497
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2075

Query Match          59.2%; Score 14.8; DB 6; Length 497;
Best Local Similarity 88.9%; Pred. No. 37;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 CAAGTCGAACGGAAGGC 19
Db  69 CCAGTCGCACGGAAGGC 86

RESULT 14
US-10-488-619-2156
; Sequence 2156, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2156
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2156

Query Match          59.2%; Score 14.8; DB 6; Length 599;
Best Local Similarity 88.9%; Pred. No. 38;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 CAAGTCGAACGGAAGGC 19
Db  537 CCAGTCGCACGGAAGGC 554

RESULT 15
```

```
US-10-488-619-2155/c
; Sequence 2155, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2155
; LENGTH: 784
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2155

Query Match      59.2%; Score 14.8; DB 6; Length 784;
Best Local Similarity 88.9%; Pred. No. 40;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CAAGTCGAACGGAAGGC 19
DB      397 CCAGTCGCACGGAAGGC 380

RESULT 16
US-11-217-529-4529/c
; Sequence 4529, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4529
; LENGTH: 4365
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4529

Query Match      59.2%; Score 14.8; DB 7; Length 4365;
Best Local Similarity 88.9%; Pred. No. 51;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GCAAGTCGAACGGAAGG 18
DB      4149 GTAAGTCGAATGGAAGG 4132

RESULT 17
US-11-217-529-110320
; Sequence 110320, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 110320
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-110320

Query Match      58.4%; Score 14.6; DB 7; Length 25;
Best Local Similarity 81.0%; Pred. No. 30;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      5 GTCGAACGGAAGGCCTTTCG 25
DB      5 GTCCAACGGAAGGCCTTTCG 25

RESULT 18
US-11-217-529-77805
; Sequence 77805, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77805
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77805

Query Match      58.4%; Score 14.6; DB 7; Length 471;
Best Local Similarity 81.0%; Pred. No. 47;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      5 GTCGAACGGAAGGCCTTTCG 25
DB      152 GTCCAACGGAAGGCCTTTCG 172

RESULT 19
US-11-217-529-730
; Sequence 730, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 730
; LENGTH: 172
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-730
```

```
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 110320
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-110320

Query Match      58.4%; Score 14.6; DB 7; Length 25;
Best Local Similarity 81.0%; Pred. No. 30;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      5 GTCGAACGGAAGGCCTTTCG 25
DB      5 GTCCAACGGAAGGCCTTTCG 25

RESULT 18
US-11-217-529-77805
; Sequence 77805, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77805
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77805

Query Match      58.4%; Score 14.6; DB 7; Length 471;
Best Local Similarity 81.0%; Pred. No. 47;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      5 GTCGAACGGAAGGCCTTTCG 25
DB      152 GTCCAACGGAAGGCCTTTCG 172

RESULT 19
US-11-217-529-730
; Sequence 730, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 730
; LENGTH: 172
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-730
```

```
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 730
; LENGTH: 1350
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-730

Query Match      58.4%; Score 14.6; DB 7; Length 1350;
Best Local Similarity 81.0%; Pred. No. 54;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2 CAAGTCGAACGGAAGGCCTT 22
      ||||| ||||| ||||| |||||
Db      1128 CAAGCTTAACGACAAAGTCCTT 1148

RESULT 20
US-11-217-529-514/c
; Sequence 514, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 514
; LENGTH: 2541
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-514

Query Match      58.4%; Score 14.6; DB 7; Length 2541;
Best Local Similarity 81.0%; Pred. No. 60;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      3 AAGTCGAACGGAAGGCCTTT 23
      ||||| ||||| ||||| |||||
Db      2480 AAGTCCAATGTAATGGCCTTT 2460

RESULT 21
US-11-217-529-82268/c
; Sequence 82268, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82268
; LENGTH: 2883
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82268

Query Match      58.4%; Score 14.6; DB 7; Length 2883;
Best Local Similarity 81.0%; Pred. No. 61;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      3 AAGTCGAACGGAAGGCCTTT 23
      ||||| ||||| ||||| |||||
Db      2230 AAGTAGAAGGAACGCGCTTT 2210

RESULT 22
US-11-217-529-94649
; Sequence 94649, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 94649
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-94649

Query Match      57.6%; Score 14.4; DB 7; Length 25;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      1 GCAAGTCGAACGGAAGGCCTTTC 24
      ||||| ||||| ||||| |||||
Db      1 GCAACGGCAGCGGAACACTACTTTC 24

RESULT 23
US-11-217-529-4661
; Sequence 4661, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4661
; LENGTH: 750
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4661

Query Match      57.6%; Score 14.4; DB 7; Length 750;
Best Local Similarity 75.0%; Pred. No. 63;
```

```
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 2 CAAGTCGAACGGAAGGCGCTTTCG 25
    ||||| | | | | | | | |
Db 297 CAAGTCGCATGAAGAGCGCGTTAG 320

RESULT 24
US-09-949-925-62/c
; Sequence 62, Application US/09949925
; Publication No. US20060099575A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2023P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-949-925-62

Query Match 57.6%; Score 14.4; DB 1; Length 1452;
Best Local Similarity 75.0%; Pred. No. 69;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 GCAAGTCGAACGGAAGGCGCTTTC 24
    ||||| | | | | | | | |
Db 949 GGAAGTATAAGGTAAGGCGCTTTC 926

RESULT 25
US-11-256-221-1
; Sequence 1, Application US/11256221
; Publication No. US20060094094A1
; GENERAL INFORMATION:
; APPLICANT: Sugio, Tsuyoshi
; APPLICANT: Miura, Akira
; APPLICANT: Parada Valdecantos, Pilar A.
; APPLICANT: Badilla Ohlbaum, Ricardo
; TITLE OF INVENTION: BACTERIA STRAIN WENELN DSM 16786, USE OF SAID BACTERIA FOR
; TITLE OF INVENTION: LEACHING OF ORES OR CONCENTRATES CONTAINING METALLIC SULFIDE
; TITLE OF INVENTION: MINERAL SPECIES AND LEACHING PROCESSES BASED ON THE USE OF SAID
; TITLE OF INVENTION: BACTERIA OR MIXTURES THAT CONTAIN SAID BACTERIA
; FILE REFERENCE: 15053.15U801
; CURRENT APPLICATION NUMBER: US/11/256,221
; CURRENT FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: CL 2731-2004
; PRIOR FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 1
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```
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 1531
; TYPE: DNA
; ORGANISM: Bacteria
US-11-256-221-1

Query Match 57.6%; Score 14.4; DB 7; Length 1531;
Best Local Similarity 93.8%; Pred. No. 70;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GCAAGTCGAACGGAAG 16
    ||||| | | | | | | |
Db 53 GCAAGTCGAACGGTAA 68

RESULT 26
US-11-324-517-36
; Sequence 36, Application US/11324517
; Publication No. US20060099221A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, MARY
; APPLICANT: GICQUEL, BRIGITTE
; TITLE OF INVENTION: METHOD OF SCREENING ANTI-MYCObACTERIAL MOLECULES
; FILE REFERENCE: 03495.0182-01
; CURRENT APPLICATION NUMBER: US/11/324,517
; CURRENT FILING DATE: 2006-01-04
; PRIOR APPLICATION NUMBER: US/10/914,165
; PRIOR FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: US/10/383,675
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 09/429,370
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/113,375
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/111,813
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 09/181,934
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 1600
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (549)..(1562)
US-11-324-517-36

Query Match 57.6%; Score 14.4; DB 7; Length 1600;
Best Local Similarity 75.0%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 2 CAAGTCGAACGGAAGGCGCTTTCG 25
    ||||| | | | | | | | |
Db 1476 CAAGTCGACGGGAAGCGCGTACG 1499

RESULT 27
US-11-217-529-3010/c
; Sequence 3010, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
```



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; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3010
; LENGTH: 1872
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3010

Query Match          57.6%; Score 14.4; DB 7; Length 1872;
Best Local Similarity 75.0%; Pred. No. 72;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  2 CAAGTCGAACGGAAGGCGCTTTCG 25
Db  163 CGATTTCGTATGGAATGCGCTTTG 140

RESULT 28
US-11-217-529-1992
; Sequence 1992, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1992
; LENGTH: 1893
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1992

Query Match          57.6%; Score 14.4; DB 7; Length 1893;
Best Local Similarity 75.0%; Pred. No. 72;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  1 GCAAGTCGAACGGAAGGCGCTTTC 24
Db  768 GCAAGATGGATGGAAGGCGCTTTC 791

RESULT 29
US-11-217-529-75610/c
; Sequence 75610, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75610
; LENGTH: 2013
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75610

Query Match          57.6%; Score 14.4; DB 7; Length 2013;
Best Local Similarity 75.0%; Pred. No. 73;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  2 CAAGTCGAACGGAAGGCGCTTTCG 25
Db  527 CAATTCAATCTGAAAGTCCTTTG 504

RESULT 30
US-11-217-529-3183
; Sequence 3183, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3183
; LENGTH: 2376
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3183

Query Match          57.6%; Score 14.4; DB 7; Length 2376;
Best Local Similarity 75.0%; Pred. No. 74;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  2 CAAGTCGAACGGAAGGCGCTTTCG 25
Db  1306 CAAGTCGAAGCTAACGGGATTTTCG 1329

RESULT 31
US-10-946-650-35
; Sequence 35, Application US/10946650
; Publication No. US20060101535A1
; GENERAL INFORMATION:
; APPLICANT: FORSTER, RICHARD L.
; APPLICANT: ROTTMANN, WILLIAM H.
; APPLICANT: CONNETT, MARIE B.
; APPLICANT: SANDERS, PAUL
; APPLICANT: ZHANG, GARY
; APPLICANT: FITZGERALD, SANDRA JOANNE
; APPLICANT: EAGLETON, CLARE
; TITLE OF INVENTION: MODIFICATION OF PLANT LIGNIN CONTENT
; FILE REFERENCE: 044463-0348
; CURRENT APPLICATION NUMBER: US/10/946,650
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 35
; LENGTH: 2435
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-946-650-35
```

QY 1 GCAAGTCGAACGGAAGGCCTTC 24

```
Db      838 GAAATTCAAACGGAATAGGCTTC 815
; Sequence 77141, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77141
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77141

Query Match      56.8%; Score 14.2; DB 7; Length 858;
Best Local Similarity 84.2%; Pred. No. 81;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      6 TCGAACGGAAGGCTTTC 24
      ||||| ||||| ||||| |||||
Db      187 TCGAAGAGAAAGGCTTTC 169

RESULT 39
US-11-217-529-60921/c
; Sequence 60921, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 60921
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-60921

Query Match      56.0%; Score 14; DB 7; Length 25;
Best Local Similarity 77.3%; Pred. No. 61;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      3 AAGTCGAACGGAAGGCTTTC 24
      ||||| ||||| ||||| |||||
Db      22 AATTCGATCTTGAAGGCTTC 1

RESULT 40
US-11-217-529-117575/c
; Sequence 117575, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
```

```
Db      838 GAAATTCAAACGGAATAGGCTTC 815
; Sequence 75552, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75552
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75552

Query Match      56.8%; Score 14.2; DB 7; Length 480;
Best Local Similarity 84.2%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 AAGTCGACGGAAGGCTTTC 21
      ||||| ||||| ||||| |||||
Db      212 AAGACGAATGGAGGCTTTC 230

RESULT 37
US-11-217-529-1257/c
; Sequence 1257, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1257
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1257

Query Match      56.8%; Score 14.2; DB 7; Length 858;
Best Local Similarity 84.2%; Pred. No. 81;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      6 TCGAACGGAAGGCTTTC 24
      ||||| ||||| ||||| |||||
Db      187 TCGAAGAGAAAGGCTTTC 169

RESULT 38
US-11-217-529-77141/c
```

```
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 117575
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-117575

Query Match          56.0%; Score 14; DB 7; Length 25;
Best Local Similarity 77.3%; Pred. No. 61;
Matches 17; Conservative 0; Mismatches 5; Indels 5; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTTT 23
   |||||
Db 22 CAGGTCGAAGGTAATGACTTT 1

RESULT 41
US-11-217-529-152173
; Sequence 152173, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 152173
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-152173

Query Match          56.0%; Score 14; DB 7; Length 25;
Best Local Similarity 77.3%; Pred. No. 61;
Matches 17; Conservative 0; Mismatches 5; Indels 5; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTTT 23
   |||||
Db 4 CAAGTTCTTCGGAAGGCCTCT 25

RESULT 42
US-11-217-529-188129
; Sequence 188129, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
```

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; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 188129
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-188129

Query Match          56.0%; Score 14; DB 7; Length 25;
Best Local Similarity 77.3%; Pred. No. 61;
Matches 17; Conservative 0; Mismatches 5; Indels 5; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTT 22
   |||||
Db 1 GAAACTCTACCTGAAGGCCTT 22

RESULT 43
US-11-139-257-9
; Sequence 9, Application US/11139257
; Publication No. US20060088849A1
; GENERAL INFORMATION:
; APPLICANT: HAPPE, SCOTT
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis of Group B
; TITLE OF INVENTION: Streptococcus Infection
; FILE REFERENCE: 25436/2512
; CURRENT APPLICATION NUMBER: US/11/139,257
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: US 60/575,124
; PRIOR FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 150
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-139-257-9

Query Match          56.0%; Score 14; DB 7; Length 150;
Best Local Similarity 77.3%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 5; Indels 5; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTTT 23
   |||||
Db 10 CATGACAAACGGCAAGGCCTTT 31

RESULT 44
US-11-139-257-14
; Sequence 14, Application US/11139257
; Publication No. US20060088849A1
; GENERAL INFORMATION:
; APPLICANT: HAPPE, SCOTT
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis of Group B
; TITLE OF INVENTION: Streptococcus Infection
; FILE REFERENCE: 25436/2512
; CURRENT APPLICATION NUMBER: US/11/139,257
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: US 60/575,124
; PRIOR FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 210
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Positive internal control
```

```
US-11-139-257-14
Query Match          56.0%; Score 14; DB 7; Length 210;
Best Local Similarity 77.3%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTTT 23
Db 40 CATGACAAACGGCAAGGCTTTT 61

RESULT 45
US-11-139-257-12
; Sequence 12, Application US/11139257
; Publication No. US2006008849A1
; GENERAL INFORMATION:
; APPLICANT: Happe, Scott
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis of Group B
; FILE REFERENCE: 25436/2512
; CURRENT APPLICATION NUMBER: US/11/139,257
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: US 60/575,124
; PRIOR FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 213
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Control Sequence
US-11-139-257-12

Query Match          56.0%; Score 14; DB 7; Length 213;
Best Local Similarity 77.3%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTTT 23
Db 41 CATGACAAACGGCAAGGCTTTT 62

RESULT 46
US-11-217-529-81114
; Sequence 81114, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81114
; LENGTH: 363
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-81114

Query Match          56.0%; Score 14; DB 7; Length 363;
Best Local Similarity 77.3%; Pred. No. 89;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTT 22
```

```
Db 16 GCCAGTCGAAAGAAAGGGCTT 37

RESULT 47
US-11-217-529-81538
; Sequence 81538, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81538
; LENGTH: 363
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-81538

Query Match          56.0%; Score 14; DB 7; Length 363;
Best Local Similarity 77.3%; Pred. No. 89;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTTT 23
Db 90 CAAGTTCTTCGAAAGGCCTCT 111

RESULT 48
US-11-217-529-79564/c
; Sequence 79564, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79564
; LENGTH: 381
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79564

Query Match          56.0%; Score 14; DB 7; Length 381;
Best Local Similarity 77.3%; Pred. No. 90;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTTT 23
Db 108 CAAGTCGATCGGAAGTCACTCT 87

RESULT 49
```

```
US-11-217-529-78815
; Sequence 78815, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78815
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78815
Query Match 56.0%; Score 14; DB 7; Length 438;
Best Local Similarity 77.3%; Pred. No. 92;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 AAGTCGAACGGAAGGCCTTTC 24
||| ||| ||| ||| ||| ||| |||
Db 1 ATGTCGAAGGGAAGGTTTGC 22

RESULT 50
US-11-217-529-2487
; Sequence 2487, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2487
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-2487
Query Match 56.0%; Score 14; DB 7; Length 579;
Best Local Similarity 77.3%; Pred. No. 96;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTTT 23
||| ||| ||| ||| ||| ||| |||
Db 86 CAATTCGAACGGAAGGACTTT 107

RESULT 51
US-11-217-529-81387
; Sequence 81387, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81387
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-81387
Query Match 56.0%; Score 14; DB 7; Length 666;
Best Local Similarity 77.3%; Pred. No. 98;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 AAGTCGAACGGAAGGCCTTTC 24
||| ||| ||| ||| ||| ||| |||
Db 374 AAGTGAATGGAAGGCTCTCC 395

RESULT 52
US-11-217-529-4416
; Sequence 4416, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4416
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4416
Query Match 56.0%; Score 14; DB 7; Length 837;
Best Local Similarity 77.3%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 AAGTCGAACGGAAGGCCTTTC 24
||| ||| ||| ||| ||| ||| |||
Db 176 AAGTCGAAGGATGTCATTTC 197

RESULT 53
US-11-217-529-174359
; Sequence 174359, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174359
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-174359
Query Match 56.0%; Score 14; DB 7; Length 837;
Best Local Similarity 77.3%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174359
; LENGTH: 984
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-11-217-529-174359

Query Match          56.0%; Score 14; DB 7; Length 984;
Best Local Similarity 77.3%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCCTT 22
    ||||| ||||| ||||| |||||
Db 835 GAAACTCTACCTGGAAGGCCTT 856

RESULT 54
US-10-975-697-7
; Sequence 7, Application US/10975697
; Publication No. US20060094099A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: Inactivated Enzyme Variants And Associated Process and Reagent
; FILE REFERENCE: 5727-76273
; CURRENT APPLICATION NUMBER: US/10/975,697
; CURRENT FILING DATE: 2004-10-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GlucDH variant RC-21
US-10-975-697-7

Query Match          56.0%; Score 14; DB 6; Length 1080;
Best Local Similarity 77.3%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 AGTCGAACGGAAGGCCTTTTCG 25
    ||||| ||||| ||||| |||||
Db 1014 AGTCGAAAGACTGGCCTTTTCG 1035

RESULT 55
US-10-975-697-9
; Sequence 9, Application US/10975697
; Publication No. US20060094099A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: Inactivated Enzyme Variants And Associated Process and Reagent
; FILE REFERENCE: 5727-76273
; CURRENT APPLICATION NUMBER: US/10/975,697
; CURRENT FILING DATE: 2004-10-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GlucDH variant RC-28
US-10-975-697-9
```

```
Query Match          56.0%; Score 14; DB 6; Length 1080;
Best Local Similarity 77.3%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 AGTCGAACGGAAGGCCTTTTCG 25
    ||||| ||||| ||||| |||||
Db 1014 AGTCGAAAGACTGGCCTTTTCG 1035

RESULT 56
US-10-975-697-11
; Sequence 11, Application US/10975697
; Publication No. US20060094099A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: Inactivated Enzyme Variants And Associated Process and Reagent
; FILE REFERENCE: 5727-76273
; CURRENT APPLICATION NUMBER: US/10/975,697
; CURRENT FILING DATE: 2004-10-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GlucDH Variant RC-35
US-10-975-697-11

Query Match          56.0%; Score 14; DB 6; Length 1080;
Best Local Similarity 77.3%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 AGTCGAACGGAAGGCCTTTTCG 25
    ||||| ||||| ||||| |||||
Db 1014 AGTCGAAAGACTGGCCTTTTCG 1035

RESULT 57
US-11-217-529-78457/c
; Sequence 78457, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78457
; LENGTH: 1194
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-11-217-529-78457

Query Match          56.0%; Score 14; DB 7; Length 1194;
Best Local Similarity 77.3%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 CAAAGTCGAACGGAAGGCCTTT 23
    ||||| ||||| ||||| |||||
Db 980 CAGGTCGAAGGTTATGACTTT 959
```

```
RESULT 58
US-10-196-749-223/c
; Sequence 223, Application US/10196749
; Publication No. US200600948641
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 223
; LENGTH: 1245
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-749-223

Query Match          56.0%; Score 14; DB 6; Length 1245;
Best Local Similarity 77.3%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      3  AAGTCGAACGGAAGGCCTTTC 24
      ||| ||| ||| ||| ||| ||| |||
Db      807 AAGGCGCCGGAAGGCGGTGC 786

RESULT 59
US-11-217-529-1925/c
; Sequence 1925, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
```

```
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1925
; LENGTH: 1887
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1925

Query Match          56.0%; Score 14; DB 7; Length 1887;
Best Local Similarity 77.3%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      3  AAGTCGAACGGAAGGCCTTTC 24
      ||| ||| ||| ||| ||| ||| |||
Db      971 AAGTCTAACGGTAATACCTTGC 950

RESULT 60
US-09-949-925-78/c
; Sequence 78, Application US/09949925
; Publication No. US20060099575A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2023P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1212)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-949-925-78

Query Match          56.0%; Score 14; DB 1; Length 1931;
Best Local Similarity 77.3%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1  GCAAGTCGAACGGAAGGCCTT 22
      ||| ||| ||| ||| ||| ||| |||
Db      253 GCTCATCGAAGGGAAGGCATT 232

RESULT 61
US-09-949-925-112/c
```



```

; Sequence 12, Application US/09949925
; Publication No. US20060099575A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2023P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1932
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-949-925-12

```

```
Query Match      56.0%; Score 14; DB 1; Length 1932;
Best Local Similarity 77.3%; Pred. NO. 1.1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

Qy 1 GCAAGTCGAACGGAAGGCCTT 22
|||
Db 253 GCTCATCGAAGGGAAGGCATT 232

```

RESULT 62
US-11-217-529-77876
; Sequence 77876, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77876
; LENGTH: 1950
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77876

```

```
Query Match          56.0%; Score 14; DB 7; Length 1950;
Best Local Similarity 77.3%; Pred. NO. 1.1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

QY 4 AGTCGAACGGAAGGCCTTTCG 25
 | | | | | | | | | |
Db 1230 ACTGGAACTGAAAAGGCTTTCG 1251

RESULT 63
US-11-217-529-82283/c
; Sequence 82283, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIRO
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 8-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82283
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82283

Query Match	56.0%	Score 14;	DB 7;	Length 2436;
Best Local Similarity	77.3%	Pred. No.	1.2e+02;	
Matches	17:	Conservative	0:	Mismatches 5; Indels 0; Gaps 0;

Qy

1 GCAAGTCGAACGGAAAGGCCTT 22
| | | | | | | | | |
Dβ

1922 GAAACTTGAAGGGGAAAGCCCTT 1901

```

RESULT 64
US-11-217-529-522
; Sequence 522, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 522
; LENGTH: 2511
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-522

```

Query Match	56.0%	Score 14;	DB 7;	Length 2511;
Best Local Similarity	77.3%	Pred.	No. 1.2e+02;	
Matches	17:	Conservative	0:	Mismatches 5; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAAGGCCTT 23
 ||| ||| ||| ||| ||| |||
Db 357 CAACTCCAATGGAAGGACGT 378

RESULT 65
US-11-217-529-75493
; Sequence 75493, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75493
; LENGTH: 2700
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75493

Query Match 56.0%; Score 14; DB 7; Length 2700;
Best Local Similarity 77.3%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 AAGTCGAACGGAAGGCCTTTC 24
||||| ||||| ||||| ||||| |||||
DB 691 AAGTCATACAGAAAGCCGATC 712

RESULT 66
US-11-217-529-3368/c
; Sequence 3368, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3368
; LENGTH: 2706
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3368

Query Match 56.0%; Score 14; DB 7; Length 2706;
Best Local Similarity 77.3%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCCTTT 23
||||| ||||| ||||| ||||| |||||
DB 1768 CAAGACCAGAGTAAGGCCTTT 1747

RESULT 67
US-10-520-210-29/c
; Sequence 29, Application US/10520210
; Publication No. US20060099692A1

; GENERAL INFORMATION:
; APPLICANT: Yocum , R. Rogers
; APPLICANT: Patterson, Thomas A.
; APPLICANT: Pero, Janice G.
; APPLICANT: Hermann, Theron
; TITLE OF INVENTION: MICROORGANISMS AND PROCESSES FOR ENHANCED PRODUCTION OF
; FILE REFERENCE: BGI-154US
; CURRENT APPLICATION NUMBER: US/10/520,210
; CURRENT FILING DATE: 2005-01-03
; PRIOR APPLICATION NUMBER: PCT/US2003/021336
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 6805
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:plasmid
US-10-520-210-29

Query Match 56.0%; Score 14; DB 6; Length 6805;
Best Local Similarity 77.3%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 AGTCGAACGGAAGGCCTTTTCG 25
||||| ||||| ||||| ||||| |||||
DB 1258 AGTCGAAGACTGGCCCTTTCG 1237

RESULT 68
US-10-520-210-31/c
; Sequence 31, Application US/10520210
; Publication No. US20060099692A1
; GENERAL INFORMATION:
; APPLICANT: Yocum , R. Rogers
; APPLICANT: Patterson, Thomas A.
; APPLICANT: Pero, Janice G.
; APPLICANT: Hermann, Theron
; TITLE OF INVENTION: MICROORGANISMS AND PROCESSES FOR ENHANCED PRODUCTION OF
; FILE REFERENCE: BGI-154US
; CURRENT APPLICATION NUMBER: US/10/520,210
; CURRENT FILING DATE: 2005-01-03
; PRIOR APPLICATION NUMBER: PCT/US2003/021336
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 7330
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:plasmid
US-10-520-210-31

Query Match 56.0%; Score 14; DB 6; Length 7330;
Best Local Similarity 77.3%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 AGTCGAACGGAAGGCCTTTTCG 25
||||| ||||| ||||| ||||| |||||
DB 1258 AGTCGAAGACTGGCCCTTTCG 1237

RESULT 69
US-10-520-210-25/c
; Sequence 25, Application US/10520210
; Publication No. US20060099692A1
; GENERAL INFORMATION:
; APPLICANT: Yocum , R. Rogers
; APPLICANT: Patterson, Thomas A.

; APPLICANT: Pero, Janice G.
; APPLICANT: Hermann, Theron
; TITLE OF INVENTION: MICROORGANISMS AND PROCESSES FOR ENHANCED PRODUCTION OF
; TITLE OF INVENTION: PANTOTHENATE
; FILE REFERENCE: BGI-154US
; CURRENT APPLICATION NUMBER: US/10/520,210
; CURRENT FILING DATE: 2005-01-03
; PRIOR APPLICATION NUMBER: PCT/US2003/021336
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 7701
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:glyA overexpression
; FEATURE:
; OTHER INFORMATION: plasmid
US-10-520-210-25

Query Match 56.0%; Score 14; DB 6; Length 7701;
Best Local Similarity 77.3%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 4 AGTCGAACGGAAGCCCTTCG 25
Db 1263 AGTCGAAGACTGGCCCTTCG 1242

RESULT 70
US-10-520-210-24/c
; Sequence 24, Application US/10520210
; Publication No. US20060099692A1
; GENERAL INFORMATION:
; APPLICANT: Yocum, R. Rogers
; APPLICANT: Patterson, Thomas A.
; APPLICANT: Pero, Janice G.
; APPLICANT: Hermann, Theron
; TITLE OF INVENTION: MICROORGANISMS AND PROCESSES FOR ENHANCED PRODUCTION OF
; TITLE OF INVENTION: PANTOTHENATE
; FILE REFERENCE: BGI-154US
; CURRENT APPLICATION NUMBER: US/10/520,210
; CURRENT FILING DATE: 2005-01-03
; PRIOR APPLICATION NUMBER: PCT/US2003/021336
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 7926
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:serA overexpression
; FEATURE:
; OTHER INFORMATION: plasmid
US-10-520-210-24

Query Match 56.0%; Score 14; DB 6; Length 7926;
Best Local Similarity 77.3%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 4 AGTCGAACGGAAGCCCTTCG 25
Db 1263 AGTCGAAGACTGGCCCTTCG 1242

RESULT 71
US-11-297-317-15
; Sequence 15, Application US/11297317
; Publication No. US20060088525A1
; GENERAL INFORMATION:
; APPLICANT: Gregorio Aversa

; APPLICANT: Frank Kolbinger
; APPLICANT: Jose M. Carballido Herrera
; APPLICANT: Andras Aszodi
; APPLICANT: Jose W. Saldanha
; APPLICANT: Bruce M. Hall
; TITLE OF INVENTION: Therapeutic binding molecules
; FILE REFERENCE: Not Yet Known
; CURRENT APPLICATION NUMBER: US/11/297,317
; CURRENT FILING DATE: 2005-12-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 8687
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Nucleotide sequence of the expression vector HCMV-G1 HuAb-VHQ
; OTHER INFORMATION: (Complete DNA Sequence of a humanised heavy chain expression vect
; OTHER INFORMATION: or comprising SEQ ID NO:12 (VHQ) from 3921-4274)
US-11-297-317-15

Query Match 56.0%; Score 14; DB 7; Length 8687;
Best Local Similarity 77.3%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 GCAAGTCGAACGGAAGGCCTT 22
Db 6871 GCAATTCGAAGGAAGTCCTT 6892

RESULT 72
US-11-297-317-16
; Sequence 16, Application US/11297317
; Publication No. US20060088525A1
; GENERAL INFORMATION:
; APPLICANT: Gregorio Aversa
; APPLICANT: Frank Kolbinger
; APPLICANT: Jose M. Carballido Herrera
; APPLICANT: Andras Aszodi
; APPLICANT: Jose W. Saldanha
; APPLICANT: Bruce M. Hall
; TITLE OF INVENTION: Therapeutic binding molecules
; FILE REFERENCE: Not Yet Known
; CURRENT APPLICATION NUMBER: US/11/297,317
; CURRENT FILING DATE: 2005-12-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 8687
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Nucleotide sequence of the expression vector HCMV-G1 HuAb-VHE
; OTHER INFORMATION: (Complete DNA Sequence of a humanised heavy chain expression vect
; OTHER INFORMATION: or comprising SEQ ID NO: 11 (VHE) from 3921-4274)
US-11-297-317-16

Query Match 56.0%; Score 14; DB 7; Length 8687;
Best Local Similarity 77.3%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 GCAAGTCGAACGGAAGGCCTT 22
Db 6871 GCAATTCGAAGGAAGTCCTT 6892

RESULT 73
US-11-297-317-18
; Sequence 18, Application US/11297317
; Publication No. US20060088525A1
; GENERAL INFORMATION:

; APPLICANT: Gregorio Aversa
; APPLICANT: Frank Kolbinger
; APPLICANT: Jose M. Carballido Herrera
; APPLICANT: Andras Aszodi
; APPLICANT: Jose W. Saldanha
; APPLICANT: Bruce M. Hall
; TITLE OF INVENTION: Therapeutic binding molecules
; FILE REFERENCE: Not Yet Known
; CURRENT APPLICATION NUMBER: US/11/297,317
; CURRENT FILING DATE: 2005-12-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 9362
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Nucleotide sequence of the expression vector HCMV-K HuAb-VL1 hum
; OTHER INFORMATION: V2
; OTHER INFORMATION: (Complete DNA Sequence of a humanised light chain expression vect
; OTHER INFORMATION: or comprising SEQ ID NO: 13 (humV2=VLm) from 3926-4246)
US-11-297-317-18

Query Match 56.0%; Score 14; DB 7; Length 9362;
Best Local Similarity 77.3%; Pred. No. 1.4e+02;
Matches 17; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCTT 22
Db 7548 GCAATTCCTGAAGGAAGTCCTT 7569

RESULT 74
US-11-297-317-17
; Sequence 17, Application US/11297317
; Publication No. US20060088525A1
; GENERAL INFORMATION:
; APPLICANT: Gregorio Aversa
; APPLICANT: Frank Kolbinger
; APPLICANT: Jose M. Carballido Herrera
; APPLICANT: Andras Aszodi
; APPLICANT: Jose W. Saldanha
; APPLICANT: Bruce M. Hall
; TITLE OF INVENTION: Therapeutic binding molecules
; FILE REFERENCE: Not Yet Known
; CURRENT APPLICATION NUMBER: US/11/297,317
; CURRENT FILING DATE: 2005-12-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 9400
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Nucleotide sequence of the expression vector HCMV-K HuAb-VL1 hum
; OTHER INFORMATION: V1
; OTHER INFORMATION: (Complete DNA Sequence of a humanised light chain expression vect
; OTHER INFORMATION: or comprising SEQ ID NO: 14 (humV1=VLh) from 3964-4284
US-11-297-317-17

Query Match 56.0%; Score 14; DB 7; Length 9400;
Best Local Similarity 77.3%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCTT 22
Db 7586 GCAATTCCTGAAGGAAGTCCTT 7607

RESULT 75
US-10-541-993-4/c

; Sequence 4, Application US/10541993
; Publication No. US20060099670A1
; GENERAL INFORMATION:
; APPLICANT: Matuschek, Markus
; APPLICANT: Heinekamp, Thorsten
; APPLICANT: Schmidt, Andre
; APPLICANT: Brakhage, Axel
; TITLE OF INVENTION: Method for the genetic modification of organisms of the genus
; FILE REFERENCE: 13311-00010-US
; CURRENT APPLICATION NUMBER: US/10/541,993
; CURRENT FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: PCT/EP2004/000100
; PRIOR FILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: DE 103 00 649.4
; PRIOR FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: DE 103 41 272.7
; PRIOR FILING DATE: 2003-09-08
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 11611
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Vector
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (227)..(227)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (318)..(318)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (526)..(526)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8946)..(8946)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10028)..(10028)
; OTHER INFORMATION: n is a, c, g, or t
US-10-541-993-4

Query Match 56.0%; Score 14; DB 6; Length 11611;
Best Local Similarity 77.3%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCTT 22
Db 5488 GCAATTCCTGAAGGAAGTCCTT 5467

RESULT 76
US-10-519-335-37/c
; Sequence 37, Application US/10519335
; Publication No. US20060099210A1
; GENERAL INFORMATION:
; APPLICANT: Cavarec, Laurent
; APPLICANT: Chumakov, Ilya
; APPLICANT: Destenaves, Benoit
; APPLICANT: Gonther, Catherine
; APPLICANT: Elias, Isabelle
; TITLE OF INVENTION: NOVEL KCNQ POLYPEPTIDES, MODULATORS THEREOF, AND THEIR USES IN T
; FILE REFERENCE: G-194US03PCT
; CURRENT APPLICATION NUMBER: US/10/519,335
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 60/391,359

```
; PRIOR FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 151830
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (60402)..(60402)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (61110)..(61110)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (98207)..(98207)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (98208)..(98208)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (98209)..(98209)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (98210)..(98210)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (98211)..(98211)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (99743)..(99743)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (108055)..(108055)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (109094)..(109094)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (109125)..(109125)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (118900)..(118900)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (119024)..(119024)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (119053)..(119112)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (119115)..(119121)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (119123)..(119123)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (141674)..(141674)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (142063)..(142063)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (142137)..(142137)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (142967)..(142967)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (143077)..(143077)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (143506)..(143506)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (143587)..(143587)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (143629)..(143629)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (149079)..(149079)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5363)..(5363)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8080)..(8080)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10296)..(10296)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14528)..(14528)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15336)..(15336)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15457)..(15457)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16288)..(16288)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16306)..(16307)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16316)..(16316)
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OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (16357)..(16397)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (56012)..(56012)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (57662)..(57662)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: 5'UTR
LOCATION: (1)..(54)
OTHER INFORMATION: exon 1
FEATURE:
NAME/KEY: exon
LOCATION: (55)..(124)
OTHER INFORMATION: exon 1
FEATURE:
NAME/KEY: exon
LOCATION: (91147)..(91244)
OTHER INFORMATION: exon 2
FEATURE:
NAME/KEY: exon
LOCATION: (93669)..(93834)
OTHER INFORMATION: exon 3
FEATURE:
NAME/KEY: exon
LOCATION: (96310)..(96422)
OTHER INFORMATION: exon 4
FEATURE:
NAME/KEY: exon
LOCATION: (99546)..(99723)
OTHER INFORMATION: exon 5
FEATURE:
NAME/KEY: exon
LOCATION: (125441)..(125605)

Query Match 56.0%; Score 14; DB 6; Length 151830;
Best Local Similarity 77.3%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCCTTT 23
DB 127951 CAAGGCGATCACAGGGCCTTT 127930

RESULT 77
US-10-506-549-3/c
; Sequence 3, Application US/10506549
; Publication No. US20060100417A1
; GENERAL INFORMATION:
; APPLICANT: APPLERA CORPORATION
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001361-US
; CURRENT APPLICATION NUMBER: US/10/506,549
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/361,343
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 394191
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(394191)

OTHER INFORMATION: n = A,T,C or G
US-10-506-549-3
Query Match 56.0%; Score 14; DB 6; Length 394191;
Best Local Similarity 77.3%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 4 AGTCGAACGGAAGGCCTTTTCG 25
DB 388331 AGGCAATGGAAAGGCCTTTAG 388310
RESULT 78
US-11-217-529-4473/c
; Sequence 4473, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4473
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4473

Query Match 55.2%; Score 13.8; DB 7; Length 987;
Best Local Similarity 72.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 GCAAGTCGAACGGAAGGCCTTTTCG 25
DB 745 GCAAGGCGACTGCGAAGGCGCTAG 721

RESULT 79
US-11-217-529-82631
; Sequence 82631, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82631
; LENGTH: 1200
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82631
Query Match 55.2%; Score 13.8; DB 7; Length 1200;
Best Local Similarity 72.0%; Pred. No. 1.3e+02;

```
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 GCAAGTCGAACGGAAGCCCTTCG 25
Db 558 GCACGGCGACCTGAAACTCTTCG 582

RESULT 80
US-10-473-173-97
; Sequence 97, Application US/10473173
; Publication No. US2006008823A1
; GENERAL INFORMATION:
; APPLICANT: VAN ANDEL INSTITUTE
; TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
; FILE REFERENCE: 38345-170094
; CURRENT APPLICATION NUMBER: US/10/473.173
; CURRENT FILING DATE: 2003-09-29
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 498
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 97
; LENGTH: 1212
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-473-173-97

Query Match 55.2%; Score 13.8; DB 6; Length 1212;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GCAAGTCGAACGGAAG 17
Db 1002 GCAAGTCGAACGGAAG 1018

RESULT 81
US-11-529-75992
; Sequence 75992, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75992
; LENGTH: 1236
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-529-75992

Query Match 55.2%; Score 13.8; DB 7; Length 1236;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 CAAGTCGAACGGAAGG 18
Db 1176 CAAGTCGAACGGAAGATG 1192

RESULT 82
US-11-217-529-79704
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; Sequence 79704, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79704
; LENGTH: 1380
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79704

Query Match 55.2%; Score 13.8; DB 7; Length 1380;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 AAGTCGAACGGAAGGC 19
Db 1061 AATTGGAACGGAAGGC 1077

RESULT 83
US-11-217-529-2853
; Sequence 2853, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2853
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-2853

Query Match 55.2%; Score 13.8; DB 7; Length 1647;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GCAAGTCGAACGGAAG 17
Db 189 GCACATCGAACGGAAG 205

RESULT 84
US-11-217-529-80937
; Sequence 80937, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
```

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; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80937
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-80937

Query Match      55.2%; Score 13.8; DB 7; Length 1647;
Best Local Similarity 72.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      1  GCAAGTCGACGGAAGGCCTTTG 25
Db      1230 GCATTTCGATGAAAAGGCATTGG 1254

RESULT 85
US-10-196-749-275
; Sequence 275, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 275
; LENGTH: 1915
; TYPE: DNA
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; ORGANISM: Homo Sapien
US-10-196-749-275

Query Match      55.2%; Score 13.8; DB 6; Length 1915;
Best Local Similarity 72.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      1  GCAAGTCGACGGAAGGCCTTTG 25
Db      560  GCAAGTCGAGTGATGAGGCCTGTG 584

RESULT 86
US-11-217-529-173838
; Sequence 173838, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 173838
; LENGTH: 2157
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-173838

Query Match      55.2%; Score 13.8; DB 7; Length 2157;
Best Local Similarity 72.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      1  GCAAGTCGACGGAAGGCCTTTG 25
Db      1981 GCAAGTCAATTTCAATGCCTGTCG 2005

RESULT 87
US-11-217-529-76817
; Sequence 76817, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76817
; LENGTH: 2454
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76817

Query Match      55.2%; Score 13.8; DB 7; Length 2454;
Best Local Similarity 72.0%; Pred. No. 1.5e+02;
```


Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTTCG 25
Db 1598 GGAAGCCGACAGTCAGGCGCTTACG 1622

RESULT 88

US-10-505-928-84

; Sequence 84, Application US/10505928
; Publication No. US20060089532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 84
; LENGTH: 3588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-84

Query Match 55.2%; Score 13.8; DB 6; Length 3588;
Best Local Similarity 72.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTTCG 25
Db 377 GCACGCTCTCGGAAGACCTGCGC 401

RESULT 89

US-11-217-529-98883
; Sequence 98883, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 98883
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-98883

Query Match 54.4%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 AAGTCGAACGGAAGGCCTT 22
Db 6 AAGTCACACGCAAGGCCTT 25

RESULT 90

US-11-217-529-130040/c
; Sequence 130040, Application US/11217529

; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 130040
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-130040

Query Match 54.4%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCT 21
Db 21 CAAGTCGATCGGAAGTGACT 2

RESULT 91

US-10-488-619-2026
; Sequence 2026, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2026
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2026

Query Match 54.4%; Score 13.6; DB 6; Length 523;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 AGTCGAACGGAAGGCCTTT 23
Db 257 AATCAAAAAGGAAGGACTTT 276

RESULT 92

US-11-217-529-4440
; Sequence 4440, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529

; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4440
; LENGTH: 903
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4440

Query Match 54.4%; Score 13.6; DB 7; Length 903;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 TCGAACGGAAGGCTTTTCG 25
|||||
DB 268 TCGAACGGAAGAGACTTTGG 287
|||||

RESULT 93
US-10-473-173-107/c
; Sequence 107, Application US/10473173
; Publication No. US2006008823A1
; GENERAL INFORMATION:
; APPLICANT: VAN ANDEL INSTITUTE
; TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
; TITLE OF INVENTION: Carcinoma: Prognosis and Drug Target Identification
; FILE REFERENCE: 38345-170094
; CURRENT APPLICATION NUMBER: US/10/473,173
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/279,411
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 498
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 107
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-473-173-107

Query Match 54.4%; Score 13.6; DB 6; Length 927;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCT 21
|||
DB 564 CAGGAAGCAGGAAGGCT 545
|||||

RESULT 94
US-11-217-529-3863
; Sequence 3863, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3863
; LENGTH: 1224
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus

US-11-217-529-3863

Query Match 54.4%; Score 13.6; DB 7; Length 1224;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 GTCGAACGGAAGGCTTTTC 24
|||||
DB 309 GTCGAAGGAAGGCTTGC 328
|||||

RESULT 95
US-11-217-529-78935
; Sequence 78935, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78935
; LENGTH: 1242
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78935

Query Match 54.4%; Score 13.6; DB 7; Length 1242;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 TCGAACGGAAGGCTTTTCG 25
|||||
DB 63 TCGAACAGTAAGGCTTTTG 82
|||||

RESULT 96
US-11-217-529-2620
; Sequence 2620, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2620
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-2620

Query Match 54.4%; Score 13.6; DB 7; Length 1443;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82107
; LENGTH: 1797
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82107

Query Match          54.4%; Score 13.6; DB 7; Length 1797;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2 CAAGTCGAACGGAAGGCCT 21
Db      485 CAAGCTCAACGATAGGCCT 504

RESULT 100
US-11-217-529-5081
; Sequence 5081, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5081
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5081

Query Match          54.4%; Score 13.6; DB 7; Length 2040;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      4 AGTCGAACGGAAGGCCTTT 23
Db      62 AGACGAACCTTAAAGGCATTT 81

Search completed: May 19, 2006, 05:38:11
Job time : 18.512 secs
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```
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76764
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76764

Query Match          54.4%; Score 13.6; DB 7; Length 1479;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      4 AGTCGAACGGAAGGCCTTT 23
Db      7 AGTCGAACACTACAGGCCTTT 26

RESULT 98
US-10-505-928-419
; Sequence 419, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 419
; LENGTH: 1667
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-419

Query Match          54.4%; Score 13.6; DB 6; Length 1667;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2 CAAGTCGAACGGAAGGCCT 21
Db      370 CAAGTCGAGCGGCAAGCACT 389

RESULT 99
US-11-217-529-82107
; Sequence 82107, Application US/11217529
; Publication No. US20060099612A1
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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 02:22:49 ; Search time 282.94 Seconds
(without alignments)
591.412 Million cell updates/sec

Title: US-10-665-708-22

Perfect score: 24

Sequence: 1 caagtcgaacggaagcccttcg 24

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489940

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

N_Geneseq_8:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

14: Geneseqn2005s:*

15: Geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	24	100.0	24	4	AAD11272 Mycobacte
2	24	100.0	24	10	ADG88353 Mycobacte
3	24	100.0	24	14	AEA08228 Mycobacte
4	24	100.0	25	4	AAD11271 Mycobacte
5	24	100.0	25	10	ADG88352 Mycobacte
6	24	100.0	25	14	AEA08227 Mycobacte
7	22.4	93.3	500	13	ADZ20587 Formaldeh
8	22.4	93.3	1449	14	AEA22405 Mycobacte
9	22.4	93.3	1455	14	AEA22412 Mycobacte
10	22.4	93.3	1482	14	AEA22404 Mycobacte
11	21	87.5	22	4	AAD11273 Mycobacte
12	21	87.5	22	10	ADG88354 Mycobacte
13	21	87.5	22	14	AEA08229 Mycobacte
14	20.8	86.7	50	12	ADP94057 Microorga
15	20.8	86.7	166	2	AAX32481 Preferred
16	20.8	86.7	460	8	ABZ76674 Microtr
17	20.8	86.7	497	14	ABE72673 Streptosp
18	20.8	86.7	500	14	AED64356 Rhodococc

c	19	20.8	86.7	1343	12	ADO80217	Ado80217 Rhodococc
	20	20.8	86.7	1390	14	ADW16264	Adw16264 DNA copy
	21	20.8	86.7	1403	12	ADJ38609	Adj38609 Micromono
	22	20.8	86.7	1427	14	ADW16290	Adw16290 DNA copy
	23	20.8	86.7	1440	14	ADZ35975	Adz35975 verrucosi
	24	20.8	86.7	1443	14	ADX38843	Adx38843 Microbiisp
	25	20.8	86.7	1461	14	AEA22406	Aea22406 Mycobacte
	26	20.8	86.7	1483	14	AED35651	Aed35651 Pseudonoc
	27	20.8	86.7	1511	13	ADR90327	Adr90327 Rhodococc
	28	20.8	86.7	1511	13	ADR90325	Adr90325 Rhodococc
	29	20.8	86.7	1511	14	AED11327	Aed11327 Aliphatic
	30	20.8	86.7	1584	10	ADE41084	Ade41084 . coralli
c	31	20.8	86.7	84222	14	AED48445	Aed48445 M. echino
c	32	20.4	85.0	32	4	AAD11024	Aad11024 Probe #4
	33	20.4	85.0	32	4	AAD11017	Aad11017 PCR prime
	34	20.4	85.0	50	2	AAX99195	Aax99195 M. avium
	35	20.4	85.0	50	2	AAX99196	Aax99196 M. fortui
	36	20.4	85.0	50	12	ADF94050	Adf94050 Microorga
	37	20.4	85.0	209	14	AEb98762	Aeb98762 Mycobacte
	38	20.4	85.0	560	10	ABT23571	Abt23571 Stabillisi
	39	20.4	85.0	1421	14	AEA22411	Aea22411 Mycobacte
	40	20.4	85.0	1431	12	ADK66476	Adk66476 Coryneb
	41	20.4	85.0	1431	12	ADK66445	Adk66445 Coryneb
	42	20.4	85.0	1449	2	AAQ37639	Aaq37639 Mycobacte
	43	20.4	85.0	1454	14	AEA22401	Aea22401 Mycobacte
	44	20.4	85.0	1465	10	ADB61680	Adb61680 16S rRNA
	45	20.4	85.0	1472	13	ADR90572	Adr90572 M avium 1
	46	20	83.3	39	14	AEb98771	Aeb98771 Mycobacte
	47	20	83.3	1391	2	AA745276	Aat45276 Coryneb
	48	19.8	82.5	1457	6	ABN86276	Abn86276 G. polyis
	49	19.8	82.5	1457	6	ABN86275	Abn86275 G. polyis
c	50	19.8	82.5	2743	4	AA559540	Aas59540 Propionib
c	51	19.8	82.5	2743	8	ACF64469	Acf64469 Propionib
	52	19.4	80.8	50	2	AAX99198	Aax99198 M. smegma
	53	19.4	80.8	50	2	AAX99201	Aax99201 M. simium
	54	19.2	80.0	535	13	AD575567	Ad575567 Rhodococc
	55	19.2	80.0	1437	12	ADF56670	Adf56670 YS-44442
	56	19.2	80.0	1437	12	ADG64519	Adg64519 Saccharot
	57	19.2	80.0	1437	14	ADY86147	Ady86147 Saccharot
	58	19.2	80.0	1439	10	ADC61232	Adc61232 Baeyer-Vi
	59	19.2	80.0	1471	12	ADF56671	Adf56671 YS-45494
	60	19.2	80.0	1471	12	ADG64520	Adg64520 Saccharot
	61	19.2	80.0	1471	14	ADY86148	Ady86148 Saccharot
	62	19.2	80.0	1477	14	AED47485	Aed47485 Nocardia
	63	19.2	80.0	1488	13	AD517269	Ad517269 Lechevali
	64	19.2	80.0	1514	14	ADW12667	Adw12667 Rhodococc
	65	19	79.2	23	4	AAD11277	Aad11277 Mycobacte
	66	19	79.2	23	10	ADG88358	Adg88358 Mycobacte
	67	19	79.2	23	14	AEA08233	Aea08233 Mycobacte
	68	19	79.2	39	14	AEb98776	Aeb98776 Mycobacte
	69	19	79.2	50	12	ADF94053	Adf94053 Microorga
	70	19	79.2	80	14	ADU66542	Adu66542 Cut base
	71	19	79.2	209	14	AEb98763	Aeb98763 Mycobacte
	72	19	79.2	560	10	ABT23572	Abt23572 Stabillisi
	73	19	79.2	1321	14	AEA22410	Aea22410 Mycobacte
c	74	19	79.2	1344	12	ADO85868	Ado85868 Gordonia
	75	19	79.2	1415	14	AEA22413	Aea22413 Mycobacte
	76	19	79.2	1460	3	AAX22765	Aax22765 Coryneb
	77	19	79.2	1462	14	AEA22415	Aea22415 Mycobacte
	78	19	79.2	1484	14	AEA22414	Aea22414 Mycobacte
	79	19	79.2	1517	12	ADM92517	Adm92517 Gordonia
	80	19	79.2	1517	12	ADO71823	Ado71823 DNA of RN
	81	19	79.2	1527	14	AEA22407	Aea22407 Mycobacte
	82	18.8	78.3	32	4	AAD11264	Aad11264 Mycobacte
	83	18.8	78.3	32	10	ADG88345	Adg88345 Mycobacte
	84	18.8	78.3	32	14	AEA08220	Aea08220 Mycobacte
	85	18.8	78.3	50	2	AAX99199	Aax99199 M. Kansas
	86	18.8	78.3	50	2	AAX99194	Aax99194 M. bovis
	87	18.8	78.3	50	2	AAX99193	Aax99193 M. tuberc
	88	18.8	78.3	50	12	ADF94055	Adf94055 Microorga
	89	18.8	78.3	50	12	ADF94047	Adf94047 Microorga
	90	18.8	78.3	203	2	AAQ94742	Aaq94742 DNA fragm
	91	18.8	78.3	209	14	AEb98764	Aeb98764 Mycobacte

92	18.8	78.3	211	14	AEb98761 Mycobacte	165	16.6	69.2	4456	4	ABL04788	AbL04788 Drosophil
93	18.8	78.3	349	13	Adv99481 Meningiti	c 166	16.6	69.2	18900	13	ADM00484	Adw00484 Escherich
94	18.8	78.3	1271	2	Aav24293 Mycobacte	167	16.4	68.3	25	2	AAV24418	Aav24418 Target se
95	18.8	78.3	1416	14	Aea22416 Mycobacte	168	16.4	68.3	25	2	AAV13026	Aav13026 Mycobacte
96	18.8	78.3	1421	14	Aea22402 Mycobacte	169	16.4	68.3	25	4	AAS30718	Aas30718 Mycobacte
97	18.8	78.3	1463	14	Aea22409 Mycobacte	170	16.4	68.3	25	4	AAS30716	Aas30716 Mycobacte
98	18.8	78.3	1464	3	Aaz35571 Mycobacte	171	16.4	68.3	549	4	ABL15533	AbL15533 Drosophil
99	18.8	78.3	1464	5	Aas11027 Mycobacte	172	16.4	68.3	1456	15	AEg07725	Aeg07725 Nocardi
100	18.8	78.3	1469	13	Adr90574 M kansasi	173	16.4	68.3	5503	4	ABL15532	AbL15532 Drosophil
101	18.8	78.3	1524	4	Aas30719 Mycobacte	174	16.2	67.5	587	8	ABZ53802	AbZ53802 Aspergill
102	18.8	78.3	1536	10	Adb61681 16S rRNA	c 175	16.2	67.5	590	8	ABQ83792	AbQ83792 Normal co
103	18.8	78.3	1536	10	Adb61682 16S rRNA	176	16.2	67.5	637	3	AAF14590	Aaf14590 Aspergill
104	18.8	78.3	1537	10	Adf41649 Mycobacte	177	16.2	67.5	637	13	ADU58631	AdU58631 Aspergill
c 105	18.8	78.3	36241	10	Adb74385 Mycobacte	178	16.2	67.5	637	14	AD296634	Ad296634 Aspergill
c 106	18.8	78.3	36470	10	Adb74374 Mycobacte	c 179	16.2	67.5	655	14	AEb88183	Aeb88183 Human CDN
107	18.8	78.3	110000	4	Continuation (15 o	c 180	16.2	67.5	755	14	AEb88269	Aeb88269 Human DNA
108	18.8	78.3	110000	4	Continuation (15 o	181	16.2	67.5	788	3	AAC33114	Aac33114 Arabidops
109	18.4	76.7	36	14	Adu69991 LAMP reac	c 182	16.2	67.5	790	14	AEb88271	Aeb88271 Human DNA
110	18.4	76.7	37	14	Adu69988 LAMP reac	c 183	16.2	67.5	813	14	AEb88267	Aeb88267 Human DNA
111	18.4	76.7	39	14	Adu69984 LAMP reac	c 184	16.2	67.5	972	6	ABK77386	Abk77386 Bacillus
112	18.4	76.7	39	14	Adu69983 LAMP reac	c 185	16.2	67.5	1049	13	ADS95257	AdS95257 Murine th
113	18.4	76.7	39	14	Adu69985 LAMP reac	c 186	16.2	67.5	1049	13	ADV68114	Adv68114 Biologica
114	18.4	76.7	39	14	AEb98765 Mycobacte	c 187	16.2	67.5	1498	4	AAF63387	Aaf63387 cDNA enco
115	18.4	76.7	39	14	AEb98779 Mycobacte	c 188	16.2	67.5	1588	4	AAF63423	Aaf63423 Human CD3
116	18.4	76.7	39	15	Aef95350 Nucleic a	c 189	16.2	67.5	1735	13	ADX53856	AdX53856 Plant ful
117	18.4	76.7	41	14	Adu69960 LAMP reac	c 190	16.2	67.5	1902	13	ADT48449	Adt48449 Bacterial
118	18.4	76.7	41	14	Adu69958 LAMP reac	c 191	16.2	67.5	2226	13	ACN43714	Acn43714 Human dia
119	18.4	76.7	42	14	Adu69959 LAMP reac	c 192	16.2	67.5	2239	4	ABL02095	AbL02095 Drosophil
120	18.4	76.7	42	14	Adu69957 LAMP reac	c 193	16.2	67.5	2294	4	AAF63419	Aaf63419 Human CD3
121	18.2	75.8	1158	14	Adw16249 DNA copy	c 194	16.2	67.5	2371	4	AAF63416	Aaf63416 Human CD3
122	18	75.0	19	4	AdL11274 Mycobacte	c 195	16.2	67.5	2497	4	AAF63421	Aaf63421 Human CD3
123	18	75.0	19	10	Adg88355 Mycobacte	c 196	16.2	67.5	2597	13	ACN43713	Acn43713 Human dia
124	18	75.0	19	14	AEa08230 Mycobacte	c 197	16.2	67.5	2648	6	ABT05471	Abt05471 DNA of NO
125	18	75.0	50	2	Aax99197 M. sorofu	c 198	16.2	67.5	2693	4	AAF63418	Aaf63418 Human CD3
c 126	18	75.0	1137	9	AdS57239 Human CGD	c 199	16.2	67.5	2693	4	ABT05470	Abt05470 DNA of NO
127	17.8	74.2	1366	13	AdX59584 Plant ful	c 200	16.2	67.5	2729	12	AQ87074	Adq87074 Human tum
128	17.8	74.2	1418	8	ABZ25595 Rhodococc	c 201	16.2	67.5	2736	6	ABL39778	AbL39778 Human NS
129	17.8	74.2	4540	6	ABK63777 Rat sequ	c 202	16.2	67.5	2762	3	AAA96066	Aaa96066 Human ect
130	17.8	74.2	4540	10	ADB58396 Toxicity-	c 203	16.2	67.5	2762	4	AAF63422	Aaf63422 Human CD3
c 131	17.6	73.3	465	10	ADB57680 Toxicity-	c 204	16.2	67.5	2762	4	AAF63386	Aaf63386 Human CD3
132	17.6	73.3	960	11	ACN44517 Mouse mRN	c 205	16.2	67.5	2762	6	AAD31693	Aad31693 Human CD3
133	17.6	73.3	1561	13	ADR07240 Full leng	c 206	16.2	67.5	2762	12	ADQ99441	Adq99441 Human CD3
134	17.6	73.3	1763	15	AEe88040 Human cDN	c 207	16.2	67.5	2762	13	ADR69170	Adr69170 Human CD3
135	17.6	73.3	1787	4	AAH14162 Human cDN	c 208	16.2	67.5	2762	13	ADR69004	Adr69004 Human CD3
136	17.6	73.3	1792	12	ADQ84493 Human tum	c 209	16.2	67.5	2762	13	ACN40734	Acn40734 Tumour-as
137	17.6	73.3	1792	12	ADQ85308 Human tum	c 210	16.2	67.5	2762	13	ACN417884	Acn417884 Human CD3
138	17.6	73.3	43800	11	ACN44516 Mouse gen	c 211	16.2	67.5	2762	13	ADR87780	Adr87780 Human CD3
139	17.4	72.5	36	14	Adu69990 LAMP reac	c 212	16.2	67.5	2762	13	ADR65838	Adr65838 Human pro
140	17.4	72.5	1452	14	AEA22408 Mycobacte	c 213	16.2	67.5	2762	13	ADR66522	Adr66522 Human pro
141	17.2	71.7	1417	12	ADJ87468 Tomato Le	c 214	16.2	67.5	2762	13	ADQ909773	Adq909773 Human the
142	17.2	71.7	1776	2	AAV59559 Human sec	c 215	16.2	67.5	2762	14	ADV16894	Adv16894 Human CD3
143	17.2	71.7	1776	6	ABs73546 Human cDN	c 216	16.2	67.5	2762	14	ADZ66963	Adz66963 Human CD3
144	17.2	71.7	1776	9	ACd82689 cDNA sequ	c 217	16.2	67.5	2762	14	ADZ74432	Adz74432 Human CD3
145	17.2	71.7	1776	10	ADI22774 cDNA enco	c 218	16.2	67.5	2805	4	AAF63420	Aaf63420 Human CD3
146	17.2	71.7	1776	12	ADH73776 Human sec	219	16.2	67.5	2837	5	AA887012	Aas87012 DNA enco
147	17.2	71.7	1776	12	ADH73776 Human sec	c 220	16.2	67.5	2882	4	AAF63424	Aaf63424 Human CD3
148	17.2	71.7	1791	6	ABs73713 Human cDN	c 221	16.2	67.5	2888	10	ADCl14273	Adc14273 Human enz
149	17.2	71.7	1791	9	ACd82856 cDNA sequ	c 222	16.2	67.5	3200	4	ABL25250	AbL25250 Drosophil
150	17.2	71.7	1791	10	ADI22941 cDNA enco	223	16.2	67.5	3757	4	ABL14492	AbL14492 Drosophil
151	17.2	71.7	1791	12	ADH73943 Human sec	c 224	16.2	67.5	5417	4	ABL02094	AbL02094 Drosophil
c 152	17.2	71.7	2919	13	ADs59960 Bacterial	225	16.2	67.5	5498	4	ABL08702	AbL08702 Drosophil
153	17	70.8	23	2	AAV59060 Primer KY	226	16.2	67.5	5656	4	ABL14490	AbL14490 Drosophil
154	17	70.8	23	10	ADF41650 Mycobacte	227	16.2	67.5	13206	4	ABL14494	AbL14494 Drosophil
155	17	70.8	23	13	ADR90575 Mycobacte	228	16.2	67.5	110000	14	AEb35724_2	Continuation (3 of
156	17	70.8	50	2	Aax99200 M. intrac	229	16.2	67.5	110000	14	AEb35724_3	Continuation (4 of
157	17	70.8	1452	13	ADR90573 M intrac	230	16.2	67.5	110000	14	AEb39175_23	Continuation (24 o
158	16.8	70.0	36538	10	ABV75558 Saccharop	231	16.2	67.5	110000	14	AEb39175_24	Continuation (25 o
c 159	16.6	69.2	508	5	AA354274 Human cDN	232	16.2	67.5	110000	14	AEb42401_23	Continuation (24 o
c 160	16.6	69.2	671	13	ADQ79174 Novel can	233	16	66.7	17	14	ADU70004	AdU70004 LAMP reac
161	16.6	69.2	780	6	AQ90469 M. capsul	234	16	66.7	26	4	AAD11278	AdA11278 Mycobacte
162	16.6	69.2	1392	8	ACA23504 Prokaryot	235	16	66.7	26	10	ADG88359	AdG88359 Mycobacte
163	16.6	69.2	1436	14	ADw16288 DNA copy	236	16	66.7	26	14	AEa08234	Aea08234 Mycobacte
164	16.6	69.2	2077	4	ABL04789 Drosophil	237	16	66.7	60	6	AAL42509	Aal42509 Self-asse

238	16	66.7	60	6	AA142505	Aa142505 Self-asse	XX
239	16	66.7	161	6	ABK79321	Abk79321 Bacillus	DT
c 240	16	66.7	330	4	AA527929	Aa527929 Novel cDN	XX
241	16	66.7	330	10	ADG40833	Adg40833 Human res	DE
242	16	66.7	330	11	ADI96607	Adi96607 Human res	XX
c 243	16	66.7	339	6	ABN18591	Abn18591 Human ORF	KW
c 244	16	66.7	360	6	ABQ92667	Abq92667 Human imm	KW
c 245	16	66.7	417	11	ABD04111	Abd04111 Pseudomon	XX
246	16	66.7	463	8	ABZ76675	Abz76675 Streptomy	OS
247	16	66.7	463	8	ABZ76673	Abz76673 Streptomy	XX
248	16	66.7	496	5	AA587009	Aa587009 DNA encod	PN
249	16	66.7	500	14	ABE72672	Abe72672 Streptosp	XX
c 250	16	66.7	506	12	ACH77915	Ach77915 Human gen	PD
251	16	66.7	552	11	ABD07597	Abd07597 Pseudomon	XX
252	16	66.7	553	13	ADQ55635	Adq55635 Novel can	PF
253	16	66.7	633	8	ABZ53337	Abz53337 Aspergill	XX
254	16	66.7	913	15	AEF74691	Aef74691 Human pol	PR
255	16	66.7	981	8	ACA27357	Act27357 Prokaryot	XX
256	16	66.7	1221	13	ADT43292	Adt43292 Bacterial	PA
257	16	66.7	1269	3	AA99893	Aa99893 C. minita	PA
258	16	66.7	1420	14	ADW16254	Adw16254 DNA copy	XX
259	16	66.7	1449	4	AAF32669	Aaf32669 Human cDN	PI
260	16	66.7	1468	14	AED50856	Aed50856 M. haemof	XX
c 261	16	66.7	1476	14	ABE94382	Abe94382 Streptomy	DR
262	16	66.7	1487	14	ABE94381	Abe94381 Streptomy	XX
263	16	66.7	1698	11	ABD02283	Abd02283 Pseudomon	PT
264	16	66.7	1705	2	AA975793	Aa975793 Extended	PT
265	16	66.7	1705	12	ADP18860	Adp18860 Human sec	XX
266	16	66.7	1712	10	ADC28975	Adc28975 Human nov	XX
267	16	66.7	1766	10	ADC29974	Adc29974 Human nov	PS
268	16	66.7	1770	4	AAH15708	Aah15708 Human cDN	XX
269	16	66.7	1797	4	AAH76747	Aah76747 Human COP	CC
c 270	16	66.7	1822	4	AAH17113	Aah17113 Human cDN	CC
c 271	16	66.7	1857	4	AA544870	Aa544870 Human con	CC
c 272	16	66.7	1857	10	ADC31910	Adc31910 Human nov	CC
c 273	16	66.7	1857	10	ADC31911	Adc31911 Human nov	CC
c 274	16	66.7	1934	4	AA544698	Aa544698 Human ful	CC
c 275	16	66.7	2000	11	ACL36279	Abt36279 Rice stre	CC
c 276	16	66.7	2103	6	ABZ11376	Abz11376 Human pol	CC
277	16	66.7	2103	12	ADMA43894	Adm43894 Novel hum	CC
c 278	16	66.7	2106	11	ABD08113	Abd08113 Pseudomon	CC
c 279	16	66.7	2199	8	ACA43833	Act43833 Prokaryot	CC
c 280	16	66.7	2325	4	AA551444	Aa551444 Pseudomon	CC
c 281	16	66.7	2325	8	ACA19423	Act19423 Prokaryot	CC
c 282	16	66.7	2427	11	ABD04295	Abd04295 Pseudomon	CC
283	16	66.7	2556	11	ABD04470	Abd04470 Human tum	CC
c 284	16	66.7	2633	10	ADD29575	Add29575 Human tum	CC
c 285	16	66.7	3689	13	ADRI14442	Adri14442 Human NF-	CC
286	16	66.7	4839	4	ABL14642	Ab114642 Drosophil	CC
c 287	16	66.7	31248	9	ACC58250	Acc58250 Coumermyc	CC
c 288	16	66.7	35058	4	ABL05556	Ab105556 Drosophil	CC
c 289	16	66.7	35359	9	ACC58251	Acc58251 Coumermyc	CC
c 290	16	66.7	36063	10	ADB74391	Abd74391 Mycobacte	CC
c 291	16	66.7	89328	6	ABL61995	Ab161995 Colon ade	CC
c 292	16	66.7	110000	6	ABA03041_07	Continuation (8 of	CC
c 293	16	66.7	152141	8	ACA64961	Act64961 Human BCR	CC
294	15.8	65.8	330	4	AA182750	Aai82750 Human pol	XX
295	15.8	65.8	375	11	ACH95596	Ach95596 Klebsiell	XX
c 296	15.8	65.8	381	5	AA577874	Aas77874 DNA encod	AC
c 297	15.8	65.8	510	14	ABE04097	Abe04097 Cryptococ	XX
c 298	15.8	65.8	510	14	ABE04098	Abe04098 Cryptococ	XX
c 299	15.8	65.8	510	14	ABE04147	Abe04147 Cryptococ	XX
c 300	15.8	65.8	510	14	ABE04146	Abe04146 Cryptococ	XX

ALIGNMENTS

RESULT 1
 AAD11272
 ID AAD11272 standard; DNA; 24 BP.
 XX
 AC AAD11272;

XX	24-SEP-2001	(first entry)	XX
DT	Mycobacterium 16S rRNA amplifying primer #16.		XX
DE	Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;		XX
KW	Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.		XX
OS	Mycobacterium sp.		XX
PN	WO200144510-A2.		XX
PD	21-JUN-2001.		XX
PF	17-DEC-1999; 99WO-US030346.		XX
XX	17-DEC-1999; 99WO-US030346.		XX
PA	(GENP-) GEN-PROBE INC.		XX
PA	(INMR) BIOMERIEUX SA.		XX
PI	Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;		XX
XX	WPI; 2001-398170/42.		XX
DR	Detecting Mycobacterium species, involves in vitro amplification of 16S		XX
PT	rRNA or DNA encoding RNA in nucleic acid amplification mixture using		XX
PT	specific primers, and detecting the amplified nucleic acid.		XX
XX	Claim 1; Page 36; 4app; English.		XX
PS	The invention relates to a method of detecting Mycobacterium species,		XX
CC	that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA		XX
CC	encoding 16S rRNA in an in vitro nucleic acid amplification mixture		XX
CC	comprising a polymerase, and at least two primers, and then detecting the		XX
CC	amplified nucleic acid. The method is relatively simple and useful for		XX
CC	detecting the presence of various Mycobacterium species in a biological		XX
CC	sample, and thus important for diagnosis of infections resulting from		XX
CC	them. The method is especially important for screening opportunistic		XX
CC	infections caused by M. tuberculosis or a Mycobacterium other than		XX
CC	tuberculosis (MOTT). The present sequence is a PCR primer used for		XX
CC	amplifying Mycobacterium 16S rRNA		XX
SQ	Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;		XX
Query Match	100.0%; Score 24; DB 4; Length 24;		
Best Local Similarity	100.0%; Pred. No. 0.1;		
Matches	24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1 CAAGTCGAACGGAAGGCGCTTCG 24		
Db	1 CAAGTCGAACGGAAGGCGCTTCG 24		
RESULT 2			
ADG88353			
ID	ADG88353 standard; DNA; 24 BP.		
XX			
AC	ADG88353;		
XX			
DT	11-MAR-2004 (first entry)		
XX			
DE	Mycobacterium amplifying PCR primer #22.		
XX			
KW	In vitro amplification; PCR; primer; ss.		
XX			
OS	Mycobacterium celatum.		
PN	US2003165824-A1.		
XX			
PD	04-SEP-2003.		
XX			
PF	15-DEC-2000; 2000US-00738274.		

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XX PR 17-DEC-1999; 99US-0172190P.
XX PA (BREN/) BRENTANO S T.
XX PA (JUCK/) JUCKER M T.
XX PA (DELG/) DELGADO F D.
XX PA (CLEU/) CLEUZAT P.
XX PA (RODR/) RODRIGUE M.
XX PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX DR WPI; 2003-898044/82.
XX PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX PT in a biological sample comprises performing in vitro nucleic acid
XX PT amplification and detection of amplified products.
XX PS Claim 1; SEQ ID NO 22; 20pp; English.
XX CC The present invention relates to a method of detecting Mycobacterium
XX CC species present in a biological sample comprises performing an in vitro
XX CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
XX CC detecting the amplified Mycobacterium nucleic acid. The present sequence
XX CC is Mycobacterium amplifying PCR primer.
XX SQ Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
Db 1 CAAGTCGAACGGAAGGCGCTTTCG 24

RESULT 3
ID AEA08228 standard; DNA; 24 BP.
XX AC AEA08228;
XX DT 14-JUL-2005 (first entry)
XX DE Mycobacterium celatum 16S rRNA amplifying non-T7 primer, SEQ ID NO: 22.
XX KW Microorganism detection; DNA amplification; 16s ribosomal RNA; 16s rRNA;
XX KW PCR; primer; ss.
XX OS Mycobacterium celatum.
XX PN US2005100915-A1.
XX PD 12-MAY-2005.
XX PF 18-SEP-2003; 2003US-00665708.
XX PR 17-DEC-1999; 99US-0172190P.
XX PR 15-DEC-2000; 2000US-00738274.
XX PA (BREN/) BRENTANO S T.
XX PA (JUCK/) JUCKER M T.
XX PA (DELG/) DELGADO F D.
XX PA (CLEU/) CLEUZAT P.
XX PA (RODR/) RODRIGUE M.
XX PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX DR WPI; 2005-345392/35.
XX PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX PT in a biological sample, comprises using in vitro nucleic acid
XX PT amplification and detection of amplified products.

XX PS Claim 8; SEQ ID NO 22; 21pp; English.
XX CC The present invention relates to a method of detecting Mycobacterium
XX CC species present in a biological sample. The method involves using in
XX CC vitro nucleic acid amplification and detection of amplified products. The
XX CC invention is useful for diagnostic detection of pathogenic bacteria such
XX CC as Mycobacterium species. The present sequence is the Mycobacterium
XX CC celatum (ATCC 51130 and ATCC 51131) 16S ribosomal RNA (16S rRNA)
XX CC amplifying non-T7 PCR primer.
XX SQ Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 14; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
Db 1 CAAGTCGAACGGAAGGCGCTTTCG 24

RESULT 4
ID AAD11271 standard; DNA; 25 BP.
XX AC AAD11271;
XX DT 24-SEP-2001 (first entry)
XX DE Mycobacterium 16S rRNA amplifying primer #15.
XX KW Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
XX KW Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
XX OS Mycobacterium sp.
XX PN WO200144510-A2.
XX PD 21-JUN-2001.
XX PF 17-DEC-1999; 99WO-US030346.
XX PR 17-DEC-1999; 99WO-US030346.
XX PA (GENP-) GEN-PROBE INC.
XX PA (INMR ) BIOMERIEUX SA.
XX PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX DR WPI; 2001-398170/42.
XX PT Detecting Mycobacterium species, involves in vitro amplification of 16S
XX PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using
XX PT specific primers, and detecting the amplified nucleic acid.
XX PS Claim 1; Page 36; 44pp; English.
XX CC The invention relates to a method of detecting Mycobacterium species,
XX CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
XX CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture
XX CC comprising a polymerase, and at least two primers, and then detecting the
XX CC amplified nucleic acid. The method is relatively simple and useful for
XX CC detecting the presence of various Mycobacterium species in a biological
XX CC sample, and thus important for diagnosis of infections resulting from
XX CC them. The method is especially important for screening opportunistic
XX CC infections caused by M. tuberculosis or a Mycobacterium other than
XX CC tuberculosis (MOTT). The present sequence is a PCR primer used for
XX CC amplifying Mycobacterium 16S rRNA
XX SQ Sequence 25 BP; 7 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 4; Length 25;

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Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTCG 24
Db 2 CAACTCGAACGGAAGGCGCTTTCG 25

RESULT 5
ADG88352
ID ADG88352 standard; DNA; 25 BP.
XX AC ADG88352;
XX DT 11-MAR-2004 (first entry)
XX DE Mycobacterium amplifying PCR primer #21.
XX KW In vitro amplification; PCR; primer; ss.
XX OS Mycobacterium celatum.
XX PN US2003165824-A1.
XX PD 04-SEP-2003.
XX PF 15-DEC-2000; 2000US-00738274.
XX PR 17-DEC-1999; 99US-0172190P.
XX PS Claim 1; SEQ ID NO 21; 20pp; English.
XX PA (BREN/) BRENTANO S T.
XX PA (JUCK/) JUCKER M T.
XX PA (DELG/) DELGADO F D.
XX PA (CLEU/) CLEUZIAT P.
XX PA (RODR/) RODRIGUE M.
XX PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX DR WPI; 2003-898044/82.
XX PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX PT in a biological sample comprises performing in vitro nucleic acid
XX PT amplification and detection of amplified products.
XX PS Claim 1; SEQ ID NO 21; 20pp; English.
XX CC The present invention relates to a method of detecting Mycobacterium
XX CC species present in a biological sample. The method involves using in
XX CC vitro nucleic acid amplification and detection of amplified products.
XX CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
XX CC detecting the amplified Mycobacterium nucleic acid. The present sequence
XX CC is Mycobacterium amplifying PCR primer.
XX SQ Sequence 25 BP; 7 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTCG 24
Db 2 CAACTCGAACGGAAGGCGCTTTCG 25

RESULT 6
AEA08227
ID AEA08227 standard; DNA; 25 BP.
XX AC AEA08227;
XX DT 14-JUL-2005 (first entry)
XX DE Mycobacterium celatum 16SrRNA amplifying non-T7 primer, SEQ ID NO: 21.
XX
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Microorganism detection; DNA amplification; 16s ribosomal RNA; 16s rRNA;
PCR; primer; ss.
Mycobacterium celatum.
US2005100915-A1.
12-MAY-2005.
18-SEP-2003; 2003US-00665708.
17-DEC-1999; 99US-0172190P.
15-DEC-2000; 2000US-00738274.
(BREN/) BRENTANO S T.
(JUCK/) JUCKER M T.
(DELG/) DELGADO F D.
(CLEU/) CLEUZIAT P.
(RODR/) RODRIGUE M.
Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
WPI; 2005-345392/35.
Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
in a biological sample, comprises using in vitro nucleic acid
amplification and detection of amplified products.
Claim 8; SEQ ID NO 21; 21pp; English.
The present invention relates to a method of detecting Mycobacterium
species present in a biological sample. The method involves using in
vitro nucleic acid amplification and detection of amplified products. The
invention is useful for diagnostic detection of pathogenic bacteria such
as Mycobacterium species. The present sequence is the Mycobacterium
celatum (ATCC 51130 and ATCC 51131) 16S ribosomal RNA (16SrRNA)
amplifying non-T7 PCR primer.
Sequence 25 BP; 7 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTCG 24
Db 2 CAACTCGAACGGAAGGCGCTTTCG 25

RESULT 7
ADZ20587
ID ADZ20587 standard; DNA; 500 BP.
XX AC ADZ20587;
XX DT 16-JUN-2005 (first entry)
XX DE Formaldehyde decomposition related Mycobacterium sp. DNA.
XX KW decomposition; formaldehyde; ds.
XX OS Mycobacterium sp.
XX PN JP2003284548-A.
XX PD 07-OCT-2003.
XX PF 27-MAR-2002; 2002JP-00089307.
XX PR 27-MAR-2002; 2002JP-00089307.
XX PA (KUMO-) KUMONOTO KEN PREFECTURE.
XX PA (MITS-) MITSUWA CORP YG.
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PA (MTS-) MITSUWA BIPRO KK.
 DR WPI; 2004-172963/17.
 XX Decomposing formaldehyde by Mycobacterium and/or growth medium of the
 PT cells.
 PT
 XX Example 1; SEQ ID NO 1; 20pp; Japanese.
 XX
 CC The invention relates to a novel method for decomposing formaldehyde by
 CC using microbial cells that belong to Mycobacterium sp. or Fusarium
 CC oxysporum, and/or the growth medium of the microbial cells. The invention
 CC further comprises: microbial cells which belong to Mycobacterium sp.
 CC having the ability to decompose formaldehyde; a formaldehyde
 CC decomposition agent comprising Mycobacterium sp. and/or the growth medium
 CC of the microbial cells; and a formaldehyde decomposition agent comprising
 CC F. oxysporum and/or its growth medium. The method is useful for
 CC decomposing formaldehyde in sea water by Mycobacterium sp. or F.
 CC oxysporum that is deposited under FERM P-818690 or FERM P-18403,
 CC respectively. This polynucleotide sequence represents the Mycobacterium
 CC sp. DNA of the invention.
 XX
 SQ Sequence 500 BP; 108 A; 119 C; 178 G; 95 T; 0 U; 0 Other;
 Query Match 93.3%; Score 22.4; DB 13; Length 500;
 Best Local Similarity 95.8%; Pred. No. 0.85;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CAAGTCGAACGGAAGGCGCTTTCG 24
 DB 54 CAAGTCGAACGGAAGGCGCTTTCG 77
 RESULT 8
 AEA22405
 ID AEA22405 standard; DNA; 1449 BP.
 XX
 AC AEA22405;
 XX
 DT 25-AUG-2005 (first entry)
 DE
 DE Mycobacterium fortuitum 16S rRNA sequence SEQ ID NO:6.
 XX
 XX microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
 XX
 OS Mycobacterium fortuitum.
 XX
 XX US2005130168-A1.
 PN
 PD 16-JUN-2005.
 XX
 XX 31-OCT-2003; 2003US-00697802.
 PF
 XX 31-OCT-2003; 2003US-00697802.
 XX
 XX (HANX/) HAN X.
 PA (PHAM/) PHAM A S.
 XX
 XX Han X, Pham AS;
 PI
 XX WPI; 2005-424597/43.
 DR
 XX Determining a bacterium species comprises providing oligonucleotide
 PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
 XX
 XX Disclosure; SEQ ID NO 6; 74pp; English.
 XX
 CC The invention relates to a method (M1) for determining a bacterium
 CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
 CC extracting a genomic nucleotide from the bacterium to provide a
 CC nucleotide template; (c) annealing a region of a nucleotide template to a
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
 CC complimentary fashion, the primer set designed to provide a product

CC having a predetermined size dictated by a complementary primer set; (d)
 CC amplifying the region of the nucleotide template to produce the product;
 CC and (e) determining a species of a bacterium in a nucleotide sequence of
 CC the product. Also described is an alternative method (M2) for determining
 CC a bacterium species comprising: (a) providing a specimen or a sample
 CC having a template; (b) providing a pair of primers selected from: (i) a
 CC first forward primer having consecutive bases of an AFB-f comprising any
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
 CC or variations; and a first reverse primer having consecutive bases of an
 CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
 CC or their fragments or variations, (ii) a second forward primer having
 CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
 CC bp (AEA22489-AEA22516) or their fragments or variations and a second
 CC reverse primer having consecutive bases of an UB-r comprising any of the
 CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
 CC variations, or (iii) a first forward primer having consecutive bases of
 CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
 CC second reverse primer having consecutive bases of an UB-r of AEA22517-
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)
 CC comparing the product from the specimen with a nucleotide sequence from a
 CC database to determine the bacterium species present in the specimen. The
 CC methods are useful for determining a bacterium species. The present
 CC sequence represents a Mycobacterium fortuitum 16S rRNA nucleotide
 CC sequence, which is used in the exemplification of the present invention.
 XX
 SQ Sequence 1449 BP; 322 A; 342 C; 495 G; 290 T; 0 U; 0 Other;
 Query Match 93.3%; Score 22.4; DB 14; Length 1449;
 Best Local Similarity 95.8%; Pred. No. 0.95;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRAAGTCGAACGGAAGGCGCTTTCG 24
 DB 21 CAAGTCGAACGGAAGGCGCTTTCG 44
 RESULT 9
 AEA22412
 ID AEA22412 standard; DNA; 1455 BP.
 XX
 AC AEA22412;
 XX
 DT 25-AUG-2005 (first entry)
 DE
 DE Mycobacterium mucogenicum 16S rRNA sequence SEQ ID NO:13.
 XX
 XX microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
 XX
 OS Mycobacterium mucogenicum.
 XX
 XX US2005130168-A1.
 PN
 PD 16-JUN-2005.
 XX
 XX 31-OCT-2003; 2003US-00697802.
 PF
 XX 31-OCT-2003; 2003US-00697802.
 XX
 XX (HANX/) HAN X.
 PA (PHAM/) PHAM A S.
 XX
 XX Han X, Pham AS;
 PI
 XX WPI; 2005-424597/43.
 DR
 XX Determining a bacterium species comprises providing oligonucleotide
 PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
 XX
 XX Disclosure; SEQ ID NO 13; 74pp; English.
 XX
 CC The invention relates to a method (M1) for determining a bacterium
 CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
 CC extracting a genomic nucleotide from the bacterium to provide a
 CC nucleotide template; (c) annealing a region of a nucleotide template to a
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
 CC complimentary fashion, the primer set designed to provide a product

CC nucleotide template; (c) annealing a region of a nucleotide template to a
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
 CC complementary fashion, the primer set designed to provide a product
 CC having a predetermined size dictated by a complementary primer set; (d)
 CC amplifying the region of the nucleotide template to produce the product;
 CC and (e) determining a species of a bacterium in a nucleotide sequence of
 CC the product. Also described is an alternative method (M2) for determining
 CC a bacterium species comprising: (a) providing a specimen or a sample
 CC having a template; (b) providing a pair of primers selected from: (i) a
 CC first forward primer having consecutive bases of an AFB-f comprising any
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
 CC or variations, and a first reverse primer having consecutive bases of an
 CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
 CC or their fragments or variations, (ii) a second forward primer having
 CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
 CC bp (AEA22489-AEA22516) or their fragments or variations, and a second
 CC reverse primer having consecutive bases of an UB-r comprising any of the
 CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
 CC variations, or (iii) a first forward primer having consecutive bases of
 CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
 CC second reverse primer having consecutive bases of an UB-r of AEA22517-
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)
 CC comparing the product from the specimen with a nucleotide sequence from a
 CC database to determine the bacterium species present in the specimen. The
 CC methods are useful for determining a bacterium species. The present
 CC sequence represents a Mycobacterium mucogenicum 16S rRNA nucleotide
 CC sequence, which is used in the exemplification of the present invention.

XX
 SQ Sequence 1455 BP; 321 A; 347 C; 500 G; 287 T; 0 U; 0 Other;

Query Match 93.3%; Score 22.4; DB 14; Length 1455;
 Best Local Similarity 95.8%; Pred. No. 0.95;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
 |||||
 Db 31 CAAGTCGAACGGAAGGCGCTTTCG 54

RESULT 10
 AEA22404
 ID AEA22404 standard; DNA; 1482 BP.
 XX
 AC AEA22404;
 XX
 XX
 DT 25-AUG-2005 (first entry)
 XX
 XX
 DE Mycobacterium farcinogenes 16S rRNA sequence SEQ ID NO:5.
 XX
 KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
 XX
 OS Mycobacterium farcinogenes.
 XX
 OS US2005130168-A1.
 PN
 XX
 PD 16-JUN-2005.
 XX
 XX
 PF 31-OCT-2003; 2003US-00697802.
 XX
 XX
 PR 31-OCT-2003; 2003US-00697802.

XX
 PA (HANX//) HAN X.
 PA (PHAM//) PHAM A S.
 XX
 XX Han X, Pham AS;
 PI
 XX WPI; 2005-424597/43.
 DR
 XX
 PT Determining a bacterium species comprises providing oligonucleotide
 PT primer set comprising SEQ-FOR and SEQ-REV in a complementary fashion.
 XX
 XX Disclosure; SEQ ID NO 5; 74pp; English.

CC The invention relates to a method (M1) for determining a bacterium
 CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
 CC extracting a genomic nucleotide from the bacterium to provide a
 CC nucleotide template; (c) annealing a region of a nucleotide template to a
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
 CC complementary fashion, the primer set designed to provide a product
 CC having a predetermined size dictated by a complementary primer set; (d)
 CC amplifying the region of the nucleotide template to produce the product;
 CC and (e) determining a species of a bacterium in a nucleotide sequence of
 CC the product. Also described is an alternative method (M2) for determining
 CC a bacterium species comprising: (a) providing a specimen or a sample
 CC having a template; (b) providing a pair of primers selected from: (i) a
 CC first forward primer having consecutive bases of an AFB-f comprising any
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
 CC or variations, and a first reverse primer having consecutive bases of an
 CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
 CC or their fragments or variations, (ii) a second forward primer having
 CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
 CC bp (AEA22489-AEA22516) or their fragments or variations, and a second
 CC reverse primer having consecutive bases of an UB-r comprising any of the
 CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
 CC variations, or (iii) a first forward primer having consecutive bases of
 CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
 CC second reverse primer having consecutive bases of an UB-r of AEA22517-
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)
 CC comparing the product from the specimen with a nucleotide sequence from a
 CC database to determine the bacterium species present in the specimen. The
 CC methods are useful for determining a bacterium species. The present
 CC sequence represents a Mycobacterium farcinogenes 16S rRNA nucleotide
 CC sequence, which is used in the exemplification of the present invention.

XX
 SQ Sequence 1482 BP; 327 A; 353 C; 507 G; 295 T; 0 U; 0 Other;

Query Match 93.3%; Score 22.4; DB 14; Length 1482;
 Best Local Similarity 95.8%; Pred. No. 0.95;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
 |||||
 Db 29 CAAGTCGAACGGAAGGCGCTTTCG 52

RESULT 11
 AAD11273
 ID AAD11273 standard; DNA; 22 BP.
 XX
 AC AAD11273;
 XX
 DT 24-SEP-2001 (first entry)
 XX
 DE Mycobacterium 16S rRNA amplifying primer #17.
 XX
 KW Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
 KW Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
 XX
 OS Mycobacterium sp.
 OS
 XX WO200144510-A2.
 PN
 XX
 PD 21-JUN-2001.
 XX
 XX
 PF 17-DEC-1999; 99WO-US030346.
 PF
 PR 17-DEC-1999; 99WO-US030346.
 PR
 PA (GENP-) GEN-PROBE INC.
 PA (INMR) BIOMERIEUX SA.
 XX
 XX Brentano ST, Jucker WT, Delgado FD, Cleuziat P, Rodrigue M;
 PI WPI; 2001-398170/42.

XX
 PT Detecting Mycobacterium species, involves in vitro amplification of 16S

PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using
 PT specific primers, and detecting the amplified nucleic acid.
 XX
 PS Claim 1; Page 36; 44pp; English.

CC The invention relates to a method of detecting Mycobacterium species,
 CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
 CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture
 CC comprising a polymerase, and at least two primers, and then detecting the
 CC amplified nucleic acid. The method is relatively simple and useful for
 CC detecting the presence of various Mycobacterium species in a biological
 CC sample, and thus important for diagnosis of infections resulting from
 CC them. The method is especially important for screening opportunistic
 CC infections caused by *M. tuberculosis* or a Mycobacterium other than
 CC *tuberculosis* (MOTT). The present sequence is a PCR primer used for
 CC amplifying Mycobacterium 16S rRNA

XX
 SQ Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 87.5%; Score 21; DB 4; Length 22;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTCGAACGGAAGGCTTTTCG 24
 Db 1 GTCGAACGGAAGGCTTTTCG 21

RESULT 12
 ADG88354
 ID ADG88354 standard; DNA; 22 BP.
 XX
 AC ADG88354;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Mycobacterium amplifying PCR primer #23.
 XX
 KW In vitro amplification; PCR; primer; ss.

XX Mycobacterium celatum.
 XX US2003165824-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 15-DEC-2000; 2000US-00738274.
 XX
 PR 17-DEC-1999; 99US-0172190P.

XX (BREN/) BRENTANO S T.
 PA (JUCK/) JUCKER M T.
 PA (DELG/) DELGADO F D.
 PA (CLEU/) CLEUZIAT P.
 PA (RODR/) RODRIGUE M.
 XX
 PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
 XX WPI; 2003-898044/82.

XX
 XX
 PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
 PT in a biological sample comprises performing in vitro nucleic acid
 PT amplification and detection of amplified products.

XX Claim 1; SEQ ID NO 23; 20pp; English.
 XX
 XX The present invention relates to a method of detecting Mycobacterium
 CC species present in a biological sample comprises performing an in vitro
 CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
 CC detecting the amplified Mycobacterium nucleic acid. The present sequence
 CC is Mycobacterium amplifying PCR primer.

XX Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 87.5%; Score 21; DB 10; Length 22;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTCGAACGGAAGGCTTTTCG 24
 Db 1 GTCGAACGGAAGGCTTTTCG 21

RESULT 13
 AEA08229
 ID AEA08229 standard; DNA; 22 BP.

XX
 AC AEA08229;

XX
 DT 14-JUL-2005 (first entry)

XX Mycobacterium celatum 16SrRNA amplifying non-T7 primer, SEQ ID NO: 23.
 DE
 KW Microorganism detection; DNA amplification; 16s ribosomal RNA; 16s rRNA;
 KW PCR; primer; ss.

XX Mycobacterium celatum.

XX US2005100915-A1.

XX 12-MAY-2005.

XX 18-SEP-2003; 2003US-00665708.

XX 17-DEC-1999; 99US-0172190P.

XX 15-DEC-2000; 2000US-00738274.

XX (BREN/) BRENTANO S T.
 PA (JUCK/) JUCKER M T.
 PA (DELG/) DELGADO F D.
 PA (CLEU/) CLEUZIAT P.
 PA (RODR/) RODRIGUE M.

XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
 XX WPI; 2005-345392/35.

XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
 PT in a biological sample, comprises using in vitro nucleic acid
 PT amplification and detection of amplified products.

XX Claim 8; SEQ ID NO 23; 21pp; English.

XX The present invention relates to a method of detecting Mycobacterium
 CC species present in a biological sample. The method involves using in
 CC vitro nucleic acid amplification and detection of amplified products. The
 CC invention is useful for diagnostic detection of pathogenic bacteria such
 CC as Mycobacterium species. The present sequence is the Mycobacterium
 CC celatum (ATCC 51130 and ATCC 51131) 16S ribosomal RNA (16SrRNA)
 CC amplifying non-T7 PCR primer.

XX Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 87.5%; Score 21; DB 14; Length 22;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTCGAACGGAAGGCTTTTCG 24
 Db 1 GTCGAACGGAAGGCTTTTCG 21

RESULT 14
 ADF94057
 ID ADF94057 standard; DNA; 50 BP.

XX

AC ADF94057;
 XX 11-MAR-2004 (first entry)
 XX Microorganism detection probe, SEQ ID 150.
 DE Probe; detection; identification; microorganism; food; drug;
 XX 16S rRNA V1 region; 16S rRNA V2 region; 16S rRNA V3 region; ss.
 KW Mycobacterium gordonae.
 XX WO2003106676-A1.
 PN 24-DEC-2003.
 XX 16-JUN-2003; 2003WO-JP007620.
 PD 14-JUN-2002; 2002JP-00174564.
 XX (HISF) HITACHI SOFTWARE ENG CO LTD.
 PA (MITS-) MITSUBISHI KAGAKU BIO-CLINICAL LAB INC.
 XX Hashida J, Ueno S, Muto I, Naruse K, Tamura M, Matsuda K;
 XX Shimadzu M, Kobayashi I, Ishiko H;
 XX WPI; 2004-071565/07.
 DR 20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a
 PT microorganism for specific detection and identification of the
 PT microorganism in foods and drug compositions.
 XX Claim 2; SEQ ID NO 150; 150pp; Japanese.
 XX The present invention relates to probes (ADP93908-ADP94059) for the
 CC specific detection and identification of harmful microorganisms in
 CC samples of foods and drug compositions. The probe sequences are derived
 CC from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism,
 CC or its complementary sequence. Detection and identification of the
 CC microorganism is by amplification of the complete 16S rRNA gene using
 CC primers ADF94060 and ADF94061, labelling the amplification product (a
 CC fluorescence label is preferred), and hybridising to the probe or probes
 CC of the invention. The probes may be immobilised on a DNA chip. The
 CC microorganism is selected from Actinobacillus actinomycetemcomitans,
 CC Acinetobacter calcoaceticus, Haemophilus influenzae, Stenotrophomonas
 CC maltophilia, Proteus mirabilis, Streptococcus pneumoniae, Pseudomonas
 CC aeruginosa, Citrobacter freundii, Veillonella parvula, Providencia
 CC stuartii, Neisseria gonorrhoeae, Streptococcus agalactiae, Morganella
 CC morganii, Bacteroides fragilis, Staphylococcus hominis, Staphylococcus
 CC warneri, Staphylococcus haemolyticus, Enterobacter cloacae, Enterobacter
 CC aerogenes, Staphylococcus epidermidis, Streptococcus constellatus,
 CC Serratia marcescens, Streptococcus anginosus, Escherichia coli,
 CC Klebsiella pneumoniae, Enterococcus faecalis, Enterococcus faecium,
 CC Streptococcus sanguinis, Streptococcus mitis, Streptococcus intermedius,
 CC Listeria monocytogenes, Clostridium perfringens, Corynebacterium
 CC aquatium, Streptococcus oralis, Staphylococcus aureus, Neisseria
 CC meningitidis, Campylobacter fetus, Enterococcus gallinarum, Enterococcus
 CC casseliflavus, Aeromonas hydrophila, Salmonella paratyphi, Salmonella
 CC typhi, Streptococcus equisimilis, Streptococcus canis, Klebsiella
 CC oxytoca, Staphylococcus saprophyticus, Pasteurella multocida, Eikenella
 CC corrodens, Streptococcus pyogenes, Moraxella catarrhalis, Legionella
 CC pneumophila, Mycobacterium tuberculosis, Mycobacterium avium,
 CC Mycobacterium intracellulare, Mycobacterium kansasii or Mycobacterium
 CC gordonae.
 XX Sequence 50 BP; 12 A; 11 C; 19 G; 8 T; 0 U; 0 Other;
 SQ Query Match 86.7%; Score 20.8; DB 12; Length 50;
 Best Local Similarity 91.7%; Pred. No. 4;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CAAGTCGAACGGAAGGCGCTTCG 24
 |||||||
 DB 4 CAAGTCGAACGGAAGGCGCTTCG 27

RESULT 15
 AAX32481
 ID AAX32481 standard; DNA; 166 BP.
 XX AAX32481;
 AC AAX32481;
 XX 22-JUN-1999 (first entry)
 DT Preferred probe of the invention.
 DE 16S rRNA; maduromycetes; hybridisation; streptomycetes; probe; ss.
 KW Synthetic.
 XX Streptomyces ambofaciens.
 OS WO9914361-A1.
 PN 25-MAR-1999.
 XX 16-SEP-1998; 98WO-EP006038.
 PF 18-SEP-1997; 97US-0059295P.
 PR 16-DEC-1997; 97US-0069748P.
 XX (MERI) MERCK SHARP & DOHME ESPANA SAE.
 PA Genilloud O, Mellado RP, Parro V, Rodriguez V;
 XX WPI; 1999-229548/19.
 DR New probes used for detection of maduromycetes bacteria and to
 PT differentiate between maduromycetes and streptomycetes.
 PT Disclosure; Fig 1; 22pp; English.
 PS The invention relates to a novel nucleic acid probe hybridises to a
 CC nucleic acid encoding a portion of 16S rRNA of maduromycetes bacteria
 CC under hybridisation conditions, and does not hybridise to nucleic acids
 CC encoding a portion of 16S rRNA of streptomycetes under identical
 CC hybridisation conditions. The probes can be used for detecting the
 CC presence of maduromycetes bacteria in a sample and for differentiating
 CC between maduromycetes and streptomycetes bacteria in a sample. The
 CC present sequence represents a preferred probe of the invention
 CC Sequence 166 BP; 39 A; 43 C; 55 G; 29 T; 0 U; 0 Other;
 SQ Query Match 86.7%; Score 20.8; DB 2; Length 166;
 Best Local Similarity 91.7%; Pred. No. 4.5;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CAAGTCGAACGGAAGGCGCTTCG 24
 |||||||
 DB 57 CAAGTCGAACGGAAGGCGCTTCG 80
 RESULT 16
 ABZ76674
 ID ABZ76674 standard; DNA; 460 BP.
 XX ABZ76674;
 AC 30-APR-2003 (first entry)
 DT Microtetraspora recticatenata IFO14525 DNA sequence SEQ ID NO.15.
 DE Streptomyces sp. TM-7; pravastatin; compactin; hyperlipidaemia;
 XX antilipaeamic; microorganism; gene; ds.
 KW Nonomuraea recticatenata.
 OS WO200299109-A1.
 XX

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XX PD 12-DEC-2002.
XX PF
XX PR 30-MAY-2002; 2002WO-JP005252.
XX PR
XX PR 01-JUN-2001; 2001JP-00166412.
XX PR
XX PA (SAOC ) MERCIAN CORP.
XX PI
XX PI Fujii T, Hirose S, Aritoku Y, Morimiya T, Johdo O, Ieshiki K;
XX DR WPI; 2003-148672/14.
XX DR
XX PT Novel Streptomyces sp. produced polypeptide for hydroxylation of
XX PT compactin at 6beta-position and its encoded DNA, applicable in
XX PT constructing transformant microbes to synthesize pravastatin for treating
XX PT hyperlipidemia.
XX PS
XX PS Disclosure; Page 50-51; 67pp; Japanese.
XX CC
XX CC The present invention describes a DNA sequence which contains a base
XX CC sequence from bases 544-1758 in the sequence of (I) with 1992 base pairs,
XX CC or a DNA hybridizable with the DNA under stringent conditions and
XX CC encoding a polypeptide with hydroxylase activity on compactin at 6beta-
XX CC position. Also described: (1) DNA containing base sequences from bases
XX CC 544-1758 and from bases 1782-1970 in the sequence of (I) or a DNA
XX CC hybridizable with the DNA under stringent conditions and encoding a
XX CC polypeptide with hydroxylase activity on compactin at the 6beta-position;
XX CC (2) a polypeptide encoded by any of the DNA or containing an amino acid
XX CC sequence based on the polypeptide but with some amino acids deleted,
XX CC substituted or added and having hydroxylase activity on compactin at the
XX CC 6beta-position; (3) a recombinant DNA obtained by integrating with any of
XX CC the DNA; (4) a microorganism transferred with the recombinant DNA; (5) a
XX CC process for producing pravastatin by culturing the transformant
XX CC microorganism before isolating the culture liquor or cells, and addition
XX CC of compactin for reaction to give pravastatin for recovery; and (6)
XX CC Streptomyces sp. TM-6 (FERM BP-8002) or TM-7 (FERM BP-8003). (I) has
XX CC antilipemic activity. The polypeptide and its encoded DNA are applicable
XX CC in constructing transformant microorganisms to synthesize pravastatin for
XX CC treating hyperlipidemia. With the recombinant microorganisms,
XX CC pravastatin can be produced efficiently, with much less galpha
XX CC hydroxylated epimer formed. The present sequence represents a
XX CC Microtetraspora recticatenata IPO14525 nucleotide sequence, which is given
XX CC in the exemplification of the present invention
XX CC
XX SQ Sequence 460 BP; 97 A; 119 C; 166 G; 78 T; 0 U; 0 Other;
Query Match 86.7%; Score 20.8; DB 8; Length 460;
Best Local Similarity 91.7%; Pred. No. 5;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
Db 31 CAAGTCGAGCGGAAGGCGCTTTCG 54

RESULT 17
AEB72673
ID AEB72673 standard; DNA; 497 BP.
XX AC
XX AC AEB72673;
XX DT
XX DT 06-OCT-2005 (first entry)
XX DE Streptosporangium sp. AF935 16S rDNA, SEQ ID 2.
XX DE cyclosporin; cyclosporin A; ds.
XX OS Streptosporangium sp.
XX OS JP2005198543-A.
XX PN
XX PD 28-JUL-2005.

XX SQ Sequence 497 BP; 105 A; 121 C; 178 G; 93 T; 0 U; 0 Other;
Query Match 86.7%; Score 20.8; DB 14; Length 497;
Best Local Similarity 91.7%; Pred. No. 5.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
Db 54 CAAGTCGAGCGGAAGGCGCTTTCG 77

RESULT 18
AED64356
ID AED64356 standard; DNA; 500 BP.
XX AC
XX AC AED64356;
XX DT
XX DT 12-JAN-2006 (first entry)
XX DE Rhodococcus sp. 16S rDNA, SEQ ID 1.
XX DE 16S ribosomal RNA; 16S rRNA; ds.
XX OS Rhodococcus sp.; Z-35-1 strain.
XX PN JP2005304498-A.
XX PD
XX PD 04-NOV-2005.
XX PF
XX PF 22-MAR-2005; 2005JP-00081977.
XX PR
XX PR 23-MAR-2004; 2004JP-00083956.
XX PA (SANY-) SANYO FINE KK.
XX PI Isobe K, Matsura A, Sakaguchi T;
XX DR WPI; 2005-762911/78.
XX PT Producing alpha-L- or -D-amino adipic acid semialdehyde derivative or its
XX PT salt, involves oxidatively deaminating aminomethyl group of alpha-amino
XX PT protecting group of L- or D-lysine, by utilizing oxidase derived from
XX PT Rhodococcus.
XX PS
XX PS Disclosure; SEQ ID NO 1; 30pp; Japanese.

```

XX The present invention relates to a method (M1) for producing alpha-L- or
CC -D-amino acid semialdehyde derivatives. The method involves
CC oxidatively deaminating the aminomethyl group of the alpha-amino
CC protecting group of L- or D-lysine into an aldehyde group, by utilizing
CC an oxidase derived from Rhodococcus. The present sequence was used to
XX illustrate the invention.

XX Sequence 500 BP; 113 A; 120 C; 173 G; 88 T; 0 U; 6 Other;
SQ

Query Match 86.7%; Score 20.8; DB 14; Length 500;
Best Local Similarity 91.7%; Pred. No. 5.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTTTCG 24
||||||| ||| ||||| |||||
Db 54 CAAGTCGAGCGGTAAAGGCTTTTCG 77

RESULT 19
AD080217/c
ID AD080217 standard; DNA; 1343 BP.
XX
AC AD080217;
XX
DT 29-JUL-2004 (first entry)
XX
DE Rhodococcus sp. GR-002 strain 16S rDNA.
XX
KW cyclic hydrocarbon degrading agent; Rhodococcus; gram positive bacillus;
KW catalase test positive; nitrate-reduction ability positive;
KW pyrazinamidase negative; pyrrolidonyl allyl amidase negative;
KW alkali phosphatase positive; beta-glucuronidase negative;
KW beta-galactosidase negative; alpha-glucosidase positive;
KW N-acetyl-beta-glucosaminidase negative; urease positive; GR-002 strain;
KW FERM P-18804; waste engine oil; aromatic hydrocarbon;
KW cycloaliphatic hydrocarbon; polycyclic aromatic hydrocarbon; ds.
XX
OS Rhodococcus sp.
XX
PN JP2004113197-A.
XX
PD 15-APR-2004.
XX
PF 27-SEP-2002; 2002JP-00284521.
XX
PR 27-SEP-2002; 2002JP-00284521.
XX
PA (GEIT-) GEITO KK.
XX
DR WPI; 2004-322544/30.
XX
XX Novel cyclic hydrocarbon degrading Rhodococcus species GR-002 strain
PT having biochemical properties e.g. gram positive bacillus, catalase test
PT positive, pyrazinamidase negative, useful for degrading waste engine oil.
XX
PS Claim 2; SEQ ID NO 1; 13pp; Japanese.

XX The invention relates to a novel cyclic hydrocarbon degrading agent from
CC the Rhodococcus genus. The cyclic hydrocarbon degrading agent having
CC biochemical properties such as: gram positive bacillus, catalase test
CC positive, nitrate-reduction ability positive, pyrazinamidase negative,
CC pyrrolidonyl allyl amidase negative, alkali phosphatase positive, beta-
CC glucuronidase negative, beta-galactosidase negative, alpha-glucosidase
CC positive, N-acetyl-beta-glucosaminidase negative, urease positive. The
CC novel Rhodococcus microorganism is Rhodococcus sp. GR-002 strain having
CC the accession number FERM P-18804. The cyclic hydrocarbon degrading agent
CC is useful for processing a cyclic hydrocarbon-containing substance, such
CC as a waste engine oil. The novel Rhodococcus microorganism is useful for
CC degrading cyclic hydrocarbons containing aromatic hydrocarbons.
CC cycloaliphatic hydrocarbons, and/or polycyclic aromatic hydrocarbons.
CC This polynucleotide represents the novel Rhodococcus microorganism 16S
CC rDNA sequence of the invention.

XX Sequence 1343 BP; 263 A; 452 C; 320 G; 308 T; 0 U; 0 Other;
SQ

Query Match 86.7%; Score 20.8; DB 12; Length 1343;
Best Local Similarity 91.7%; Pred. No. 5.7;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTTTCG 24
||||||| ||| ||||| |||||
Db 1293 CAAGTCGAGCGGTAAAGGCTTTTCG 1270

RESULT 20
ADW16264
ID ADW16264 standard; DNA; 1390 BP.
XX
AC ADW16264;
XX
DT 07-APR-2005 (first entry)
XX
DE DNA copy of the N_albus 16S ribosomal RNA EN46 isolate Seq 16.
XX
KW 16S ribosomal RNA; ds; 16S rRNA; medicinal plant; plant breeding;
KW disease resistance; insect resistance; crop improvement;
KW plant growth factor; antibacterial; antimicrobial; fungicide;
KW insecticide; nematocide.
XX
OS Nocardioides albus.
XX
PN WO2005003328-A1.
XX
PD 13-JAN-2005.
XX
PF 07-JUL-2004; 2004WO-AU0000914.
XX
PR 07-JUL-2003; 2003US-0485241P.
PR 22-SEP-2003; 2003US-0504703P.
XX
PA (FLIN-) FLINDERS TECHNOLOGIES PTY LTD.
XX
XX Franco CMM, Coombs JT;
PI
XX WPI; 2005-091806/10.
DR
XX Improving plant productivity comprises introducing into the plant or
PT propagation material an endophytic actinomycete that facilitates
PT induction of at least one characteristic related to improved
PT productivity.
XX
XX Claim 1; SEQ ID NO 16; 235pp; English.

XX This invention relates to a novel method for improving plant
CC productivity. Specifically, it refers to introducing into the plant or
CC propagation material an endophytic actinomycetes or variant thereof,
CC where the actinomycetes facilitate induction of a characteristic related
CC to improved productivity. The present invention further describes
CC metabolites of the actinomycetes microorganism such as auxin, gibberellin
CC or cytokinin that are able to induce disease resistance in plants i.e.
CC provide disease bio-control capabilities against pathogen infection.
CC Accordingly, the method facilitates the improvement of cereal crop
CC productivity including increasing germination by up-regulating plant
CC growth promoting activities, as well as improving plant vigor or flower
CC and fruit yield. Furthermore, the new actinomycete or metabolite is
CC useful in the manufacture of a medicament for the therapeutic and/or
CC prophylactic treatment of a mammalian or non-mammalian subject i.e.
CC plant. As such, this method provides plant protectants and plant growth
CC stimulants that exhibit antibacterial, antimicrobial, fungicide,
CC insecticide and nematocide activities. This polynucleotide is the DNA
CC sequence of an actinomycetes 16S ribosomal RNA sequence of the invention.

XX Sequence 1390 BP; 324 A; 348 C; 443 G; 266 T; 0 U; 9 Other;
SQ

Query Match 86.7%; Score 20.8; DB 14; Length 1390;

Best Local Similarity 91.7%; Pred. No. 5.7;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTCG 24
Db 4 CAAGTCGAGCGGAAGGCGCTTCG 27

RESULT 21
ADJ38609
ID ADJ38609 standard; DNA; 1403 BP.
XX AC
XX ADJ38609;
XX 06-MAY-2004 (first entry)
XX Micromonospora sp. M42 16S rRNA, SEQ ID 1.
DE XX
XX Protozoacide; Tuberculostatic; Antitubercular; Antimalarial;
KW Cerebroprotective; Actinomycete; manzamine; 16S rRNA; antibiotic; ds.
XX OS
XX Micromonospora sp. M42.
PN WO2004013297-A2.
XX 12-FEB-2004.
XX 01-AUG-2003; 2003WO-US024238.
XX 01-AUG-2002; 2002US-0400330P.
XX (UYMA-) UNIV MARYLAND BIOTECHNOLOGY.
PA (UMIS) UNIV MISSISSIPPI.
XX Hill RT, Hamann MT, Peraud O, Kasanah N;
XX WPI; 2004-169330/16.
XX New isolated actinomycete useful for producing antibiotics produces
PT manzamine having antituberculosis and antimalarial activity.
XX Claim 19; SEQ ID NO 1; 46pp; English.
XX The present invention relates to an isolated actinomycete (A1) producing
CC manzamine, which comprises a 16S rRNA (ADJ38609). (A1) is useful for
CC producing manzamine by fermentation, which involves culturing (A1) having
CC manzamine producing ability in a culture medium suitable for the growth
CC of manzamine compounds and production of manzamine and separating the
CC manzamine from the culturing medium. (A1) is useful for producing
CC antibiotics.
XX Sequence 1403 BP; 304 A; 361 C; 484 G; 254 T; 0 U; 0 Other;

Query Match 86.7%; Score 20.8; DB 12; Length 1403;
Best Local Similarity 91.7%; Pred. No. 5.7;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTCG 24
Db 26 CAAGTCGAGCGGAAGGCGCTTCG 49

RESULT 22
ADW16290
ID ADW16290 standard; DNA; 1427 BP.
XX AC
XX ADW16290;
XX 07-APR-2005 (first entry)
XX DNA copy of the Actinomycete 16S ribosomal RNA EM47 isolate.
DE 16S ribosomal RNA; ds; 16S rRNA; medicinal plant; plant breeding;

KW disease resistance; insect resistance; crop improvement;
KW plant growth factor; antibacterial; antimicrobial; fungicide;
KW insecticide; nematocide.
XX Actinomycetales.
XX WO2005003328-A1.
XX 13-JAN-2005.
XX 07-JUL-2004; 2004WO-AU000914.
XX 07-JUL-2003; 2003US-0485241P.
XX 22-SEP-2003; 2003US-0504703P.
XX (FLIN-) FLINDERS TECHNOLOGIES PTY LTD.
XX Franco CMW, Coombs JT;
XX WPI; 2005-091806/10.
XX Improving plant productivity comprises introducing into the plant or
PT propagation material an endophytic actinomycete that facilitates
PT induction of at least one characteristic related to improved
PT productivity.
XX Example 18; Fig 19; 235pp; English.
XX This invention relates to a novel method for improving plant
CC productivity. Specifically, it refers to introducing into the plant or
CC propagation material an endophytic actinomycetes or variant thereof,
CC where the actinomycetes facilitate induction of a characteristic related
CC to improved productivity. The present invention further describes
CC metabolites of the actinomycetes microorganism such as auxin, gibberellin
CC or cytokinin that are able to induce disease resistance in plants i.e.
CC provide disease bio-control capabilities against pathogen infection.
CC Accordingly, the method facilitates the improvement of cereal crop
CC productivity including increasing germination by up-regulating plant
CC growth promoting activities, as well as improving plant vigor or flower
CC and fruit yield. Furthermore, the new actinomycete or metabolite is
CC useful in the manufacture of a medicament for the therapeutic and/or
CC prophylactic treatment of a mammalian or non-mammalian subject i.e.
CC plant. As such, this method provides plant protectants and plant growth
CC stimulants that exhibit antibacterial, antimicrobial, fungicide,
CC insecticide and nematocide activities. This polynucleotide is the DNA
CC sequence of an actinomycetes 16S ribosomal RNA sequence of the invention.
XX Sequence 1427 BP; 326 A; 351 C; 471 G; 277 T; 0 U; 2 Other;

Query Match 86.7%; Score 20.8; DB 14; Length 1427;
Best Local Similarity 91.7%; Pred. No. 5.7;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTCG 24
Db 25 CAAGTCGAGCGGAAGGCGCTTCG 48

RESULT 23
ADZ35975
ID ADZ35975 standard; DNA; 1440 BP.
XX AC
XX ADZ35975;
XX 30-JUN-2005 (first entry)
XX Verrucosisspora sp. AB-18-032 16S rRNA gene.
XX ds; antibiotic; antimalarial; protozoacide; 16S rRNA;
KW polycyclic macrolactone; abysomicin; p-Aminobenzoic acid; folic acid;
KW vitamin; abysomicin B; abysomicin C; abysomicin D;
KW Staphylococcus aureus infection; protozoal infection;
KW plasmodium infection; Leishmania infection; chagas disease;

Gram positive bacteria infection; mrsa infection .

Verrucosisporea sp. AB-18-032.

WO2005033114-A1.

14-APR-2005.

23-SEP-2004; 2004WO-EP010661.

01-OCT-2003; 2003DE-01047472.

11-NOV-2003; 2003DE-01053300.

(UVTU-) UNIV TUEBINGEN.

Fiedler H, Suesmuth R, Zaehner H, Bull A;

WPI; 2005-296122/30.

New abyssomicin polycyclic macrolactone compounds, useful as antibiotics and antiprotzoal agents effective against multiresistant strains, prepared using bacteria of genus Verrucosisporea.

Disclosure; SEQ ID NO 1; 47pp; German.

This invention describes novel polycyclic macrolactones and their derivatives, prepared using bacteria of genus Verrucosisporea and designated abyssomicins. The polycyclic macrolactones have at least one oxo-bicyclo system as a partial structure and at least one Michael system as a double bond system. The polycyclic macrolactones are prepared by culturing Verrucosisporea strain AB 18-032, recovering a culture supernatant from the culture, optionally preparing a culture filtrate and optionally isolating one or more polycyclic macrolactones from the supernatant and/or filtrate. Alternatively the microorganism is cultured followed by isolating one or more polycyclic macrolactones from the microorganism. The Verrucosisporea strain AB 18-032 was isolated from marine sediment collected at a depth of 1000m in Sagami Bay in the Japanese Sea and is deposited as DSM No. 15899. The polycyclic macrolactones inhibit the biosynthesis of p-Aminobenzoic acid, (an essential component in the biosynthesis of folic acid) from chorismic acid, thus inhibiting folic acid biosynthesis. The vitamin folic acid is essential to the life of microorganisms, especially prokaryotes and protozoa. The polycyclic macrolactones do not inhibit the biosynthesis of folic acid in mammals (including humans), and thus have no adverse effects on mammalian cells. Three polycyclic macrolactones are specifically claimed, i.e. abyssomicin B, abyssomicin C and abyssomicin D. Abyssomicin C strongly inhibited growth of methicillin-resistant Staphylococcus aureus strain N315 and vancomycin-resistant Staphylococcus aureus strain Mu50. The products of the invention are useful as antibiotics (especially effective against Gram positive bacteria) and antiprotzoal agents, specifically effective against bacteria and protozoa resistant (especially multi-resistant) to conventional antibiotics. Typically polycyclic macrolactones are useful for combating tropical protozoal diseases (e.g. malaria, leishmaniasis, sleeping sickness and Chagas disease) and infections caused by resistant Gram positive bacteria such as methicillin- and vancomycin-resistant Staphylococcus aureus strains. Polycyclic macrolactones are also useful as disinfectants (especially in hospitals and other medical establishments) and as lead structures for the development of further active agents. This sequence represents the Verrucosisporea strain AB 18-032 16S rRNA DNA which is used to phylogenically classify the bacterial strain.

Sequence 1440 BP; 313 A; 363 C; 500 G; 264 T; 0 U; 0 Other;

Query Match 86.7%; Score 20.8; DB 14; Length 1440;
Best Local Similarity 91.7%; Pred. No. 5.7;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAAGTCGAACGGAAGGCGCTTTCG 24

DB 1 CAAAGTCGAACGGAAGGCGCTTTCG 24

RESULT 24

ADX38843

ID ADX38843 standard; DNA; 1443 BP.

XX AC ADX38843;

XX DT 05-MAY-2005 (first entry)

XX DE Microbispora 16S rDNA.

XX antitibiotic; bacterial infection; animal growth; 16S rDNA; ds;
KW antibacterial; anabolic.

XX OS Microbispora sp. ATCC PTA-5024.

XX PN WO2005014628-A1.

XX PD 17-FEB-2005.

XX PF 12-JUL-2004; 2004WO-EP007658.

XX PR 18-JUL-2003; 2003EP-00016306.

XX PA (VICU-) VICURON PHARM INC.

XX PI Lazzarini A, Gastaldo L, Candiani G, Ciciliato I, Losi D;
PI Marinelli F, Selva E, Parenti F;

XX DR WPI; 2005-173079/18.

XX New antibiotic 107891 complex comprising Factor A1 and Factor A2 and
PT having specified physico-chemical characteristics, used to form
PT medicament for the treatment or prevention of bacterial infections, or
PT used as animal growth promoter.

XX PS Disclosure; SEQ ID NO 1; 85pp; English.

XX The invention relates to an antibiotic 107891 complex comprising Factor
CC A1 and Factor A2. The antibiotic is used to form a pharmaceutical
CC composition used as medicament for the treatment or prevention of
CC bacterial infections, or as animal growth promoter. The present sequence
CC represents the Microbispora 16S rDNA.

XX SQ Sequence 1443 BP; 308 A; 352 C; 504 G; 279 T; 0 U; 0 Other;

Query Match 86.7%; Score 20.8; DB 14; Length 1443;

Best Local Similarity 91.7%; Pred. No. 5.7;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAAGTCGAACGGAAGGCGCTTTCG 24

DB 31 CAAAGTCGAACGGAAGGCGCTTTCG 54

RESULT 25

AEA22406

ID AEA22406 standard; DNA; 1461 BP.

XX AC AEA22406;

XX DT 25-AUG-2005 (first entry)

XX DE Mycobacterium gordonae 16S rRNA sequence SEQ ID NO:7.

XX KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.

XX OS Mycobacterium gordonae.

XX PN US2005130168-A1.

XX PD 16-JUN-2005.

PF 31-OCT-2003; 2003US-00697802.
XX
PR 31-OCT-2003; 2003US-00697802.
XX
PA (HANX/) HAN X.
PA (PHAM/) PHAM A S.
XX
PI Han X, Pham AS;
XX
XX WPI; 2005-424597/43.
XX
XX
XX Determining a bacterium species comprises providing oligonucleotide
PT primer set comprising SEQ-FOR and SEQ-REV in a complementary fashion.
XX
XX
XX Disclosure; SEQ ID NO 7; 74pp; English.
XX
XX The invention relates to a method (M1) for determining a bacterium
CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
CC extracting a genomic nucleotide from the bacterium to provide a
CC nucleotide template; (c) annealing a region of a nucleotide template to a
CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
CC complementary fashion, the primer set designed to provide a product
CC having a predetermined size dictated by a complementary primer set; (d)
CC amplifying the region of the nucleotide template to produce the product;
CC and (e) determining a species of a bacterium in a nucleotide sequence of
CC the product. Also described is an alternative method (M2) for determining
CC a bacterium species comprising: (a) providing a specimen or a sample
CC having a template; (b) providing a pair of primers selected from: (i) a
CC first forward primer having consecutive bases of an AFB-f comprising any
CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
CC or variations and a first reverse primer having consecutive bases of an
CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
CC or their fragments or variations, (ii) a second forward primer having
CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
CC bp (AEA22489-AEA22516) or their fragments or variations and a second
CC reverse primer having consecutive bases of an UB-r comprising any of the
CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
CC variations, or (iii) a first forward primer having consecutive bases of
CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
CC second reverse primer having consecutive bases of an UB-r of AEA22517-
CC AEA22544 or their fragments or variations; (c) the specimen; and (d)
CC comparing the product from the specimen with a nucleotide sequence from a
CC database to determine the bacterium species present in the specimen. The
CC methods are useful for determining a bacterium species. The present
CC sequence represents a Mycobacterium goodii 16S rRNA nucleotide
CC sequence, which is used in the exemplification of the present invention.
XX
XX
XX Sequence 1461 BP; 319 A; 350 C; 500 G; 292 T; 0 U; 0 Other;
XX
XX Query Match 86.7%; Score 20.8; DB 14; Length 1461;
XX Best Local Similarity 91.7%; Pred. No. 5.7;
XX Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 1 CAAGTCGAACGGAAGCCCTTCG 24
XX |||||
XX Db 21 CAAGTCGAACGGAAGCCCTTCG 44
XX
XX RESULT 26
XX AED35651
XX ID AED35651 standard; DNA; 1483 BP.
XX
XX AC AED35651;
XX
XX XX 15-DEC-2005 (first entry)
XX
XX Pseudonocardia sp. 727713 melanocortin receptor modulator WS727713.
XX
XX ds; melanocortin receptor; cosmetics; brain injury; cerebroprotective;
XX inflammation; renal disease; nephrotropic; ischemia;
XX cardiovascular disease; vasotrophic; reperfusion injury; inflammation;
XX hepatitis; hepatotropic; virucide; sepsis; septic shock; Antibacterial;
XX immunosuppressive; respiratory distress syndrome; Respiratory-Gen.;

respiratory disease; rheumatoid arthritis; arthritis; Antirheumatic;
Antiathritic; immune disorder; gout; Antigout; osteoarthritis;
osteopathic; nephritis; genitourinary disease; nephrotropic;
hypersensitivity; Antiallergic; inflammatory bowel disease;
Gastrointestinal-Gen.; gastrointestinal disease; Endocrine-Gen.;
genitourinary disease; female sexual dysfunction;
male sexual dysfunction; Gynecological; transplant rejection; Analgesic;
pain; neurological disease; HIV infection; Anti-HIV; hypopigmentation;
Dermatological; dermatological disease; tinea; Fungicide;
diabetes mellitus; Antidiabetic; metabolic disorder; anorexia nervosa;
Eating-Disorders-General.; Cardiovascular-Gen.; Anorectic;
nutritional disorder; psychiatric disorder; fever; Antipyretic;
temperature disorder; functional bowel disorder; obesity; pancreatitis;
fibroid; scar tissue; keloid; scleroderma; graft versus host disease;
liver cirrhosis; pulmonary fibrosis; nephropathy; Ophthalmological;
uveitis; Behcet's disease; hematological disease; sarcoidosis; vasculitis;
infection; antimicrobial; celiac disease; melanoma; neoplasm; Cytostatic;
Anabolic.
Pseudonocardia sp. 727713.
OS WO2005097973-A1.
XX
XX PN 20-OCT-2005.
XX
XX PD 22-MAR-2005; 2005WO-JP005653.
XX
XX PF 08-APR-2004; 2004AU-00901919.
XX
XX PR (FUJI) FUJISAWA PHARM CO LTD.
XX
XX PA
XX
XX PI Otsuka T, Ueda H, Fujie K, Muramatsu H, Hashimoto M, Takase S;
XX
XX DR WPI; 2005-703551/72.
XX
XX New pure WS727713 compound which is a melanocortin receptor modulator
XX useful as antiinflammatory and for treating e.g. hypoxic shock, acute
XX respiratory distress syndrome, rheumatic arthritis and melanoma invasion.
XX
XX Disclosure; SEQ ID NO 1; 41pp; English.
XX
XX This invention describes a novel compound WS727713 isolated from
XX Pseudonocardia sp. 727713 in a leaf litter sample. The compound is
XX capable of modulating the melanocortin receptor and has a potent anti-
XX inflammatory effect. The compound can be used as a medicament or a
XX cosmetic for treating or preventing ischemic or reperfusion injury, brain
XX shock, acute respiratory distress syndrome (ARDS), rheumatic arthritis,
XX gouty arthritis, aortic regurgitation, juvenile chronic arthritis,
XX osteoarthritis, nephritis, induction of tolerance, contact
XX hypersensitivity, inflammatory bowel disease, sexual dysfunction,
XX transplantation, pain, disease progression of HIV, post inflammatory hypo
XX pigmentation, tinea versicolor, idiopathic guttate hypomelanosis, fever,
XX functional bowel disease, obesity, satiety effect, diabetes mellitus,
XX modulation of dermal exocrine function, canities (canities
XX circumscripta), gray hair, pancreatitis, fibrotic disorders (hypertrophic
XX scars, keloids, localized scleroderma, systematic sclerosis, sclerodermic
XX graft versus host disease of the skin, cirrhosis of the liver, idiopathic
XX and bleomycin induced lung fibrosis, cyclosporin induced nephropathy),
XX uveitis (especially in Behcet's syndrome and sarcoidosis), vasculitis,
XX microbial infections, celiac disease, vulvar vestibulitis syndrome,
XX melanoma invasion or anorexia in human or an animal.
XX
XX
XX Sequence 1483 BP; 320 A; 360 C; 509 G; 289 T; 0 U; 5 Other;
XX
XX Query Match 86.7%; Score 20.8; DB 14; Length 1483;
XX Best Local Similarity 91.7%; Pred. No. 5.7;
XX Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 1 CAAGTCGAACGGAAGCCCTTCG 24
XX |||||
XX Db 32 CAAGTCGAACGGAAGCCCTTCG 55

```
RESULT 27
ADR90327
ID ADR90327 standard; DNA; 1511 BP.
XX
XX
AC ADR90327;
XX
XX DT 16-DEC-2004 (first entry)
XX
XX DE Rhodococcus sp. M-15 bioremediation-related 16S rDNA.
XX
XX KW alkane; petroleum; bioremediation; 16S ribosomal RNA; 16S rRNA; ds.
XX
XX OS Rhodococcus sp.
XX
XX PN JP2004261126-A.
XX
XX PD 24-SEP-2004.
XX
XX PF 03-MAR-2003; 2003JP-00056155.
XX
XX PR 03-MAR-2003; 2003JP-00056155.
XX
XX PA (EBAR ) EBARA CORP.
XX
XX DR WPI; 2004-665486/65.
XX
XX PT Evaluating the ability of an environmental sample to degrade alkanes for
XX providing alkane degrading bacteria, comprises measuring alkane degrading
XX bacteria having high resolving power of alkane present in petroleum.
XX
XX PS Claim 1; SEQ ID NO 3; 33pp; Japanese.
XX
XX SQ Sequence 1511 BP; 342 A; 362 C; 510 G; 297 T; 0 U; 0 Other;
XX
XX Query Match 86.7%; Score 20.8; DB 13; Length 1511;
XX Best Local Similarity 91.7%; Pred. No. 5.7;
XX Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 1 CAAGTCGACGGAAGGCGCTTTCG 24
XX Db 51 CAAGTCGACGGAAGGCGCTTTCG 74
XX
XX RESULT 28
ADR90325
ID ADR90325 standard; DNA; 1511 BP.
XX
XX AC ADR90325;
XX
XX DT 16-DEC-2004 (first entry)
XX
XX DE Rhodococcus sp. M-13 bioremediation-related 16S rDNA.
XX
XX KW alkane; petroleum; bioremediation; 16S ribosomal RNA; 16S rRNA; ds.
XX
XX OS Rhodococcus sp.
XX
XX PN JP2004261126-A.
XX
XX PD 24-SEP-2004.
XX
XX Query Match 86.7%; Score 20.8; DB 13; Length 1511;
XX Best Local Similarity 91.7%; Pred. No. 5.7;
XX Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 1 CAAGTCGACGGAAGGCGCTTTCG 24
XX Db 51 CAAGTCGACGGAAGGCGCTTTCG 74
XX
XX RESULT 29
AED11327
ID AED11327 standard; DNA; 1511 BP.
XX
XX AC AED11327;
XX
XX DT 01-DEC-2005 (first entry)
XX
XX DE Aliphatic hydrocarbon degrading R. erythropolis strain 16S rRNA gene.
XX
XX KW degradation; aliphatic hydrocarbon; bioremediation; oil degradation;
XX pollutant; degradation; groundwater decontamination; 16S rRNA;
XX 16S ribosomal RNA; gene; ds.
XX
XX OS Rhodococcus erythropolis.
XX
XX PN JP2005261218-A.
XX
XX PD 29-SEP-2005.
XX
XX PF 16-MAR-2004; 2004JP-00074370.
XX
XX PR 16-MAR-2004; 2004JP-00074370.
XX
XX PA (EBAR ) EBARA CORP.
XX
XX PI Karube M, Tamatsubo K, Miya A;
XX
XX DR WPI; 2005-678804/70.
XX
XX PT Novel Rhodococcus erythropolis M-13 strain capable of degrading aliphatic
XX hydrocarbon, useful for bioremediation of oil-polluted environment such
XX as river water, underground water, ocean, sea coast.
XX
XX PS Claim 1; SEQ ID NO 1; 14pp; Japanese.
```



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OS Mycobacterium avium.
XX WO9935284-A1.
XX PN
XX PD
XX PF 15-JUL-1999.
XX PR
XX PS 30-DEC-1997; 97WO-BR0000087.
XX PT
XX PA 30-DEC-1997; 97WO-BR0000087.
XX PY (UYMI-) UNIV FEDERAL MINAS GERAIS.
XX PI Peregrino Ferreira PC, Geessien Kroon E;
XX PN Bernardes Margutti Pinto ME, Aleixo AW;
XX DR WPI; 1999-444201/37.
XX PS
XX PT Detection of mycobacteria by shift mobility assay.
XX PS Disclosure; Fig 7; 20pp; English.
XX CC The invention describes a new method for diagnosis, identification and
CC characterisation of Mycobacterium tuberculosis or any other mycobacteria
CC by using polymerase chain reaction (PCR) and shift mobility assay (SMA)
CC in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,
CC DNA amplification and shift mobility assay. The method is based on
CC divergence in sequences found in 16S rRNA to identify mycobacteria
CC species, since a remarkable shift of heteroduplex bands are obtained
CC between single stranded and homoduplex bands in UPAGE. The method is
CC fast, simple and can produce information not easily obtained when
CC compared with other detection methods. The sensitivity of other assays
CC suffer due to the tendency of the denatured PCR product strands to
CC reassociate and exclude oligonucleotide probes, and stearic interference
CC between the bound oligonucleotides and the solid support which impede
CC hybridization to nucleic acids in solution. Sequences AAX99193-237
CC represent 16S rRNA gene regions of some mycobacterial species
XX SQ Sequence 50 BP; 15 A; 12 C; 14 G; 9 T; 0 U; 0 Other;
Query Match 85.0%; Score 20.4; DB 2; Length 50;
Best Local Similarity 95.5%; Pred. No. 6.2;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCCTTT 22
Db 10 CAAGTCGAACGGAAGGCCTCT 31
RESULT 35
AAX99196
ID AAX99196 standard; DNA; 50 BP.
XX AC
XX AC AAX99196;
XX DT 28-SEP-1999 (first entry)
XX DE
XX DE M. fortuitum 16S rRNA gene fragment.
XX KW Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA;
XX KW shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.
XX OS Mycobacterium fortuitum.
XX PN WO9935284-A1.
XX PD 15-JUL-1999.
XX PF 30-DEC-1997; 97WO-BR0000087.
XX PR 30-DEC-1997; 97WO-BR0000087.
XX PY (UYMI-) UNIV FEDERAL MINAS GERAIS.
XX PA
XX PS Claim 2; SEQ ID NO 143; 150pp; Japanese.
XX
PI Peregrino Ferreira PC, Geessien Kroon E;
PI Bernardes Margutti Pinto ME, Aleixo AW;
DR WPI; 1999-444201/37.
PT Detection of mycobacteria by shift mobility assay.
PS Disclosure; Fig 7; 20pp; English.
CC The invention describes a new method for diagnosis, identification and
CC characterisation of Mycobacterium tuberculosis or any other mycobacteria
CC by using polymerase chain reaction (PCR) and shift mobility assay (SMA)
CC in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,
CC DNA amplification and shift mobility assay. The method is based on
CC divergence in sequences found in 16S rRNA to identify mycobacteria
CC species, since a remarkable shift of heteroduplex bands are obtained
CC between single stranded and homoduplex bands in UPAGE. The method is
CC fast, simple and can produce information not easily obtained when
CC compared with other detection methods. The sensitivity of other assays
CC suffer due to the tendency of the denatured PCR product strands to
CC reassociate and exclude oligonucleotide probes, and stearic interference
CC between the bound oligonucleotides and the solid support which impede
CC hybridization to nucleic acids in solution. Sequences AAX99193-237
CC represent 16S rRNA gene regions of some mycobacterial species
XX SQ Sequence 50 BP; 14 A; 12 C; 14 G; 9 T; 0 U; 1 Other;
Query Match 85.0%; Score 20.4; DB 2; Length 50;
Best Local Similarity 95.5%; Pred. No. 6.2;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCCTTT 22
Db 10 CAAGTCGAACGGAAGGCCTCT 31
RESULT 36
ADF94050
ID ADF94050 standard; DNA; 50 BP.
XX AC
XX AC ADF94050;
XX DT 11-MAR-2004 (first entry)
XX DE
XX DE Microorganism detection probe, SEQ ID 143.
XX KW Probe; detection; identification; microorganism; food; drug;
XX KW 16S rRNA VI region; 16S rRNA V2 region; 16S rRNA V3 region; ss.
XX OS Mycobacterium avium.
XX PN WO2003106676-A1.
XX PD 24-DEC-2003.
XX PF 16-JUN-2003; 2003WO-JP007620.
XX PR 14-JUN-2002; 2002JP-00174564.
XX PY (HISF) HITACHI SOFTWARE ENG CO LTD.
XX PA (MITS-) MITSUBISHI KAGAKU BIO-CLINICAL LAB INC.
XX PI Hashida J, Ueno S, Muto I, Naruse K, Tamura M, Matsuda K;
XX PI Shimadzu M, Kobayashi I, Ishiko H;
XX DR WPI; 2004-071565/07.
XX PT 20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a
XX PT microorganism for specific detection and identification of the
XX PT microorganism in foods and drug compositions.
XX PS Claim 2; SEQ ID NO 143; 150pp; Japanese.
XX

```

CC The present invention relates to probes (ADP93908-ADP94059) for the
 CC specific detection and identification of harmful microorganisms in
 CC samples of foods and drug compositions. The probe sequences are derived
 CC from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism,
 CC or its complementary sequence. Detection and identification of the
 CC microorganism is by amplification of the complete 16S rRNA gene using
 CC primers ADP94060 and ADP94061, labelling the amplification product (a
 CC fluorescence label is preferred), and hybridising to the probe or probes
 CC of the invention. The probes may be immobilised on a DNA chip. The
 CC microorganism is selected from Actinobacillus actinomycetocombitans,
 CC Acinetobacter calcoaceticus, Haemophilus influenzae, Stenotrophomonas
 CC maltophilia, Proteus mirabilis, Streptococcus pneumoniae, Pseudomonas
 CC aeruginosa, Citrobacter freundii, Veillonella parvula, Providencia
 CC stuartii, Neisseria gonorrhoeae, Streptococcus agalactiae, Morganella
 CC morganii, Bacteroides fragilis, Staphylococcus hominis, Staphylococcus
 CC warneri, Staphylococcus haemolyticus, Enterobacter cloacae, Enterobacter
 CC aerogenes, Staphylococcus epidermidis, Streptococcus constellatus,
 CC Serratia marcescens, Streptococcus anginosus, Escherichia coli,
 CC Klebsiella pneumoniae, Streptococcus faecalis, Enterococcus faecium,
 CC Streptococcus sanguis, Streptococcus mitis, Streptococcus intermedius,
 CC Listeria monocytogenes, Clostridium perfringens, Corynebacterium
 CC aquatium, Streptococcus oralis, Staphylococcus aureus, Neisseria
 CC meningitidis, Campylobacter fetus, Enterococcus gallinarum, Enterococcus
 CC casseliflavus, Aeromonas hydrophila, Salmonella paratyphi, Salmonella
 CC typhi, Streptococcus equisimilis, Streptococcus canis, Klebsiella
 CC oxytoca, Staphylococcus saprophyticus, Pasteurella multocida, Eikenella
 CC corrodens, Streptococcus pyogenes, Moraxella catarrhalis, Legionella
 CC pneumophila, Mycobacterium tuberculosis, Mycobacterium avium,
 CC Mycobacterium intracellulare, Mycobacterium kansasii or Mycobacterium
 CC gordonae.

SQ Sequence 50 BP; 12 A; 11 C; 19 G; 8 T; 0 U; 0 Other;

Query Match 85.0%; Score 20.4; DB 12; Length 50;
 Best Local Similarity 95.5%; Pred. No. 6.2;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTTT 22
 |||||
 Db 2 CAAGTCGAACGGAAGGCCTT 23

RESULT 37
 AEB98762
 ID AEB98762 standard; DNA; 209 BP.
 XX
 AC AEB98762;
 XX
 DT 06-OCT-2005 (first entry)
 XX
 DE Mycobacterium avium partial 16S rDNA sequence, SEQ ID 4.
 XX
 KW microorganism detection; mycobacterium infection; antibacterial; ds.
 XX
 OS Mycobacterium avium.
 XX
 PN JP2005204582-A.
 XX
 PD 04-AUG-2005.
 XX
 PF 23-JAN-2004; 2004JP-00015195.
 XX
 PR 23-JAN-2004; 2004JP-00015195.
 XX
 PA (ASAH) ASahi KASEI KK.
 XX
 PI Oda N;
 XX
 DR WPI; 2005-526965/54.
 XX
 PT New single-stranded oligonucleotide, useful for amplifying the nucleic
 PT acid of Mycobacterium avium, Mycobacterium intracellulare, and
 PT Mycobacterium kansasii.

XX
 PS
 XX

Example 1; SEQ ID NO 4; 14pp; Japanese.

CC The invention relates to a novel single-stranded oligonucleotide used in
 CC a detection method of an atypical mycobacteria group. The invention
 CC further includes: amplifying the nucleic acid of Mycobacterium avium by a
 CC loop-mediated isothermal amplification (LAMP) method; amplifying the
 CC nucleic acid of M. intracellulare by a LAMP method; amplifying the
 CC nucleic acid of M. kansasii by a LAMP method; and a kit for detecting the
 CC nucleic acid of M. avium by a LAMP method; detecting the nucleic acid of
 CC M. intracellulare by a LAMP method; or detecting the nucleic acid of M.
 CC kansasii by a LAMP method. The single-stranded oligonucleotide is useful
 CC in medical applications. This polynucleotide represents a Mycobacterium
 CC avium partial 16S rDNA sequence amplified by the LAMP method of the
 CC invention.

SQ Sequence 209 BP; 48 A; 48 C; 70 G; 43 T; 0 U; 0 Other;

Query Match 85.0%; Score 20.4; DB 14; Length 209;
 Best Local Similarity 95.5%; Pred. No. 7.3;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTTT 22
 |||||
 Db 40 CAAGTCGAACGGAAGGCCTT 61

RESULT 38
 ABT23571
 ID ABT23571 standard; DNA; 560 BP.

XX
 AC ABT23571;
 XX
 DT 22-MAY-2003 (first entry)
 XX
 DE Stabilising reagent method related oligo SEQ ID No 23.
 XX
 KW Stabilising reaction reagent; PCR; primer; RNaseH; long-term storage;
 KW specific amplification; pathogenic microorganism; chimeric;
 KW genetic engineering; clinical medicine; ss.
 XX
 OS Mycobacterium avium.

PN WO2002101042-A1.
 XX
 PD 19-DEC-2002.
 XX
 PF 12-JUN-2002; 2002WO-JP005832.
 XX
 PR 12-JUN-2001; 2001JP-00177737.
 XX
 PR 20-AUG-2001; 2001JP-00249689.
 XX
 PA (TAKI) TAKARA BIO INC.
 XX
 PI Sagawa H, Uemori T, Mukai H, Yamamoto J, Tomono J, Kobayashi E;
 PI Enoki T, Asada K, Kato I;
 XX
 DR WPI; 2003-148805/14.

Method for stabilizing and storing reaction reagents for specific
 PT amplification and detection of nucleic acids particularly in e.g.
 PT identifying pathogenic microorganisms or viruses in sample.

Example 15; Page 109; 177pp; Japanese.

CC The invention relates to a novel stabilising reaction reagent for use in
 CC the amplification and/or detection of a target nucleic acid comprising:
 CC preparing a reaction mixture with e.g. a nucleic acid as template, at
 CC least 1 primer and RNaseH; and incubation of the reaction mixture for a
 CC defined period of time to form a reaction product during the
 CC amplification of such target nucleic acid. The method is useful for
 CC stabilising and long-term storage of reaction reagents for highly
 CC sensitive and specific amplification and detection of nucleic acids

CC particularly in identifying pathogenic microorganisms or viruses in a
CC sample using chimeric oligonucleotide primers, which is useful in genetic
CC engineering and clinical medicine. This polynucleotide sequence
CC represents an oligo relating to the novel stabilising reaction reagent
CC method of the invention

XX
SQ Sequence 560 BP; 117 A; 134 C; 198 G; 111 T; 0 U; 0 Other;
Query Match 85.0%; Score 20.4; DB 10; Length 560;
Best Local Similarity 95.5%; Pred. No. 8.1;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCCTTT 22
Db 31 CAAGTCGAACGGAAGGCCTCT 52

RESULT 39

AEA22411
ID AEA22411 standard; DNA; 1421 BP.

XX AEA22411;
XX
XX 25-AUG-2005 (first entry)
XX Mycobacterium lentiflavum 16S rRNA sequence SEQ ID NO:12.
XX DE microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
XX KW Mycobacterium lentiflavum.
XX OS Mycobacterium lentiflavum.

XX US2005130168-A1.

XX 16-JUN-2005.

XX 31-OCT-2003; 2003US-00697802.

XX 31-OCT-2003; 2003US-00697802.

XX (HANX//) HAN X.
XX (PHAM//) PHAM A S.

XX Han X, Pham AS;

XX WPI; 2005-424597/43.

XX Determining a bacterium species comprises providing oligonucleotide
XX primer set comprising SEQ-FOR and SEQ-REV in a complementary fashion.

XX Disclosure; SEQ ID NO 12; 74pp; English.

XX The invention relates to a method (M1) for determining a bacterium
XX species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
XX extracting a genomic nucleotide from the bacterium to provide a
XX nucleotide template; (c) annealing a region of a nucleotide template to a
XX specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
XX complementary fashion, the primer set designed to provide a product
XX having a predetermined size dictated by a complementary primer set; (d)
XX amplifying the region of the nucleotide template to produce the product;
XX and (e) determining a species of a bacterium in a nucleotide sequence of
XX the product. Also described is an alternative method (M2) for determining
XX a bacterium species comprising: (a) providing a specimen or a sample
XX having a template; (b) providing a pair of primers selected from: (i) a
XX first forward primer having consecutive bases of an AFB-f comprising any
XX of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
XX or variations and a first reverse primer having consecutive bases of an
XX AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
XX or their fragments or variations, (ii) a second forward primer having
XX consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
XX bp (AEA22489-AEA22516) or their fragments or variations and a second
XX reverse primer having consecutive bases of an UB-r comprising any of the
XX 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
XX variations, or (iii) a first forward primer having consecutive bases of

CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
CC second reverse primer having consecutive bases of an UB-r of AEA22517-
CC AEA22544 or their fragments or variations; (c) the specimen; and (d)
CC comparing the product from the specimen with a nucleotide sequence from a
CC database to determine the bacterium species present in the specimen. The
CC methods are useful for determining a bacterium species. The present
CC sequence represents a Mycobacterium lentiflavum 16S rRNA nucleotide
CC sequence, which is used in the exemplification of the present invention.

XX Sequence 1421 BP; 306 A; 344 C; 487 G; 284 T; 0 U; 0 Other;

Query Match 85.0%; Score 20.4; DB 14; Length 1421;
Best Local Similarity 95.5%; Pred. No. 8.9;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22

Db 21 CAAGTCGAACGGAAGGCCTCT 42

RESULT 40

ADK66476
ID ADK66476 standard; RNA; 1431 BP.

XX ADK66476;

XX 06-MAY-2004 (first entry)

XX Corynebacterium 16S rRNA sequence.

XX ss; 16S rRNA; microorganism detection; clinical sample;
XX pharmaceutical composition.

XX Corynebacterium sp.

XX WO2004009839-A2.

XX 29-JAN-2004.

XX 16-JUL-2003; 2003WO-EP007717.

XX 18-JUL-2002; 2002DE-01032776.

XX 14-FEB-2003; 2003DE-01007732.

XX (HENK) HENKEL KGAA.

XX (VERM-) VERMICON AG.

XX Saettler A, Jassey C, Scholtyssek R, Maischein V, Nieveler S;
XX Weiss A, Trebesius K, Beimfohr C, Ludwig W, Bamberg RR, Schleifer K;
XX Muellner S, Adomat C, Bergmaier I;

XX WPI; 2004-123402/12.

XX New oligonucleotides for specific detection of microorganisms, useful
XX e.g. for detecting or quantifying microbes on the skin, in foods,
XX clinical samples or water, by in situ hybridization.

XX Disclosure; Page 66-67; 67pp; German.

XX The present invention provides a number of oligonucleotides for the
XX specific detection of microorganisms. The oligonucleotides are used to
XX detect and/or quantify microorganisms, especially on the skin, in foods
XX or the environment (water, soil and air), from waste waters or biofilms,
XX in clinical samples (body fluids or tissues), and in pharmaceutical or
XX cosmetic compositions. The present sequence is a Corynebacterium 16S rRNA
XX sequence.

XX Sequence 1431 BP; 308 A; 327 C; 488 G; 0 T; 307 U; 1 Other;

Query Match 85.0%; Score 20.4; DB 12; Length 1431;

Best Local Similarity 81.8%; Pred. No. 8.9; Indels 0; Gaps 0;

Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;


```

QY 1 CAAGTCGAACGGAAGGCCTTT 22
   ||||:|||||||:|:
Db 31 CAAGUCGAACGGAAGGCCUCU 52

RESULT 41
ADK66445
ID ADK66445 standard; RNA; 1431 BP.
XX
AC ADK66445;
XX
DT 06-MAY-2004 (first entry)
XX
DE Corynebacterium 16S rRNA sequence.
XX
KW ss; 16S rRNA; microorganism detection; skin; acne.
XX
OS Corynebacterium sp.
XX
PN W02004009843-A2.
XX
PD 29-JAN-2004.
XX
PF 16-JUL-2003; 2003WO-EP007718.
XX
PR 18-JUL-2002; 2002DE-01032775.
XX
PR 14-FEB-2003; 2003DE-01006616.
XX
PA (HENK ) HENKEL KGAA.
XX
PI Saettler A, Jassoy C, Scholtyssek R, Maischein V, Nieweler S;
PI Weiss A, Trebesius K, Beimehr C, Ludwig W, Bamberg RR, Schleifer K;
PI Mueller S, Adomat C, Bergmaier I;
XX
DR WPI; 2004-123405/12.
XX
PT Kit for detection of microorganisms on skin, useful e.g. for diagnosis of
PT infection, comprises specific oligonucleotides for in situ hybridization.
XX
PS Disclosure; Page 62-63; 63pp; German.
XX
CC The present invention relates to a kit for detecting microorganisms that
CC contains at least one oligonucleotide specific for at least one species,
CC or group of species, that is present on the skin. The kit is used to
CC detect and/or quantify microorganisms that are present on the skin; e.g.
CC for early diagnosis of secondary infection in cases of acne. The present
CC sequence is a Corynebacterium 16S rRNA sequence.
XX
SQ Sequence 1431 BP; 308 A; 327 C; 488 G; 0 T; 307 U; 1 Other;

Query Match 85.0%; Score 20.4; DB 12; Length 1431;
Best Local Similarity 81.8%; Pred. No. 8.9;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTTT 22
   ||||:|||||||:|:
Db 31 CAAGUCGAACGGAAGGCCUCU 52

RESULT 42
AAQ37639
ID AAQ37639 standard; rRNA; 1449 BP.
XX
AC AAQ37639;
XX
DT 25-MAR-2003 (revised)
DT 18-JUN-1993 (first entry)
XX
DE Mycobacterium genavense 16S rRNA.
XX
KW Detection; rapid; immunosuppressed patients; AIDS; ss.
XX
OS Mycobacterium genavense.

QY 1 CAAGTCGAACGGAAGGCCTTT 22
   ||||:|||||||:|:
Db 48 CAAGTCGAACGGAAGGCCTCT 69

RESULT 43
AEA22401
ID AEA22401 standard; DNA; 1454 BP.
XX
AC AEA22401;
XX
DT 25-AUG-2005 (first entry)
XX
DE Mycobacterium avium 16S rRNA sequence SEQ ID NO:2.
XX
KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
XX
OS Mycobacterium avium.
XX
PN US2005130168-A1.
XX
PD 16-JUN-2005.
XX
PF 31-OCT-2003; 2003US-00697802.
XX
PR 31-OCT-2003; 2003US-00697802.
XX
PA (HANX/) HAN X.
PA (PHAM/) PHAM A S.
XX
PI Han X, Pham AS;
XX
DR WPI; 2005-424597/43.
XX

XX EP529985-A1.
XX
XX 03-MAR-1993.
XX
XX 21-AUG-1992; 92EP-00307690.
XX
XX 23-AUG-1991; 91GB-00018262.
XX
XX 09-JUL-1992; 92GB-00014601.
XX
XX (PINA/) CHANG PINARES H R.
XX
XX (BOET/) BOETTGER E C.
XX
XX (HIRS/) HIRSCHHEL B J.
XX
XX Chang Pinares HR, Boettger EC, Hirschhel BJ;
XX
XX WPI; 1993-068993/09.
XX
XX New 16S ribosomal RNA sequence of new Mycobacterium genavense - also
XX probes and primers specific for the sequence, for detecting M. genavense
XX infections in AIDS patients.
XX
XX Claim 1; Page 17; 21pp; English.
XX
XX The sequence is that of the 16S rRNA of Mycobacterium genavense sp. nov.
XX from which nucleic acid sequences can be obtd. for use in a method for
XX the reliable and rapid detection and identification of M. genavense,
XX partic. opportunistic M. genavense infections in highly immunosuppressed
XX patients suffering from AIDS. It was isolated by PCR amplification of DNA
XX from liver, spleen, lymph nodes and polymorphonuclear leukocytes (PMNs,
XX buffy coats) from AIDS patients. (Updated on 25-MAR-2003 to correct PN
XX field.)
XX
XX Sequence 1449 BP; 316 A; 345 C; 495 G; 289 T; 0 U; 4 Other;

Query Match 85.0%; Score 20.4; DB 2; Length 1449;
Best Local Similarity 95.5%; Pred. No. 8.9;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTTT 22
   ||||:|||||||:|:
Db 48 CAAGTCGAACGGAAGGCCTCT 69

RESULT 43
AEA22401
ID AEA22401 standard; DNA; 1454 BP.
XX
AC AEA22401;
XX
DT 25-AUG-2005 (first entry)
XX
DE Mycobacterium avium 16S rRNA sequence SEQ ID NO:2.
XX
KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
XX
OS Mycobacterium avium.
XX
PN US2005130168-A1.
XX
PD 16-JUN-2005.
XX
PF 31-OCT-2003; 2003US-00697802.
XX
PR 31-OCT-2003; 2003US-00697802.
XX
PA (HANX/) HAN X.
PA (PHAM/) PHAM A S.
XX
PI Han X, Pham AS;
XX
DR WPI; 2005-424597/43.
XX

```

PT Determining a bacterium species comprises providing oligonucleotide
PT primer set comprising SEQ-FOR and SEQ-REV in a complementary fashion.
XX
XX
XX Disclosure; SEQ ID NO 2; 74pp; English.
XX
XX The invention relates to a method (M1) for determining a bacterium
XX species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
XX extracting a genomic nucleotide from the bacterium to provide a
XX nucleotide template; (c) annealing a region of a nucleotide template to a
XX specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
XX complementary fashion, the primer set designed to provide a product
XX having a predetermined size dictated by a complementary primer set; (d)
XX amplifying the region of the nucleotide template to produce the product;
XX and (e) determining a species of a bacterium in a nucleotide sequence of
XX the product. Also described is an alternative method (M2) for determining
XX a bacterium species comprising: (a) providing a specimen or a sample
XX having a template; (b) providing a pair of primers selected from: (i) a
XX first forward primer having consecutive bases of an AFB-f comprising any
XX of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
XX or variations and a first reverse primer having consecutive bases of an
XX AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
XX or their fragments or variations, (ii) a second forward primer having
XX consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
XX bp (AEA22489-AEA22516) or their fragments or variations and a second
XX reverse primer having consecutive bases of an UB-r comprising any of the
XX 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
XX variations, or (iii) a first forward primer having consecutive bases of
XX an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
XX second reverse primer having consecutive bases of an UB-r of AEA22517-
XX AEA22544 or their fragments or variations; (c) the specimen; and (d)
XX comparing the product from the specimen with a nucleotide sequence from a
XX database to determine the bacterium species present in the specimen. The
XX methods are useful for determining a bacterium species. The present
XX sequence represents a Mycobacterium avium 16S rRNA nucleotide sequence,
XX which is used in the exemplification of the present invention.
XX
XX SQ Sequence 1454 BP; 316 A; 348 C; 494 G; 296 T; 0 U; 0 Other;

Query Match 85.0%; Score 20.4; DB 14; Length 1454;
Best Local Similarity 95.5%; Pred. No. 8.9;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTTT 22
| | | | | | | | | | | | | | | | | | | | | |
Db 31 CAAGTCGAACGGAAGGCCTCT 52
| | | | | | | | | | | | | | | | | | | | | |

RESULT 44
ADB61680
ID ADB61680 standard; DNA; 1465 BP.
XX
XX AC ADB61680;
XX
XX DT 04-DEC-2003 (first entry)
XX
XX DE 16S rRNA of Mycobacterium avium DNA sequence.
XX
XX KW enriching mRNA; high quality bacterial mRNA; bacterial gene expression;
XX poly-A tail; mRNA purification; oligo-dT capture;
XX prokaryote mRNA purification; bridging oligonucleotide; targeting region;
XX capture oligonucleotide; prokaryotic 16S rRNA; prokaryotic 23S rRNA;
XX eukaryotic 17S rRNA; eukaryotic 18S rRNA; eukaryotic 28S rRNA;
XX 28S eukaryotic rRNA bridging oligonucleotide; ds.
XX
XX OS Mycobacterium avium.
XX
XX PN WO2003054162-A2.
XX
XX PD 03-JUL-2003.
XX
XX PF 19-DEC-2002; 2002WO-US041014.
XX
XX PR 20-DEC-2001; 2001US-00029397.

XX
PA (AMBI-) AMBION INC.
XX
PI Murphy GL, Whitley JP;
XX
XX WPI; 2003-663255/62.
DR
XX
XX Depleting or isolating targeted nucleic acids e.g. rRNA, involves using a
PT bridging oligonucleotide comprising bridging region and a targeting
PT region complementary to a targeted nucleic acid, and a capture
PT oligonucleotide.
XX
XX PS Claim 4; Page 168; 208pp; English.
XX
XX This invention relates to a novel method for isolating, depleting or
CC separating a targeted nucleic acid, such as rRNA, from a sample
CC comprising targeted and non-targeted nucleic acids. It effects a way of
CC enriching for non-targeted nucleic acids such as mRNAs. Isolating
CC sufficient quantities of high quality bacterial mRNA is a demanding
CC process which impedes analysis of bacterial gene expression in the
CC presence of host cells. A small percentage of bacterial mRNAs may be poly
CC -A tailed, but these are targeted for degradation and tend to be
CC unstable. As a result, the commonly employed method for mRNA purification
CC with eukaryotic cells, oligo-dT capture, is ineffective. The present
CC invention provides an alternative, more suitable method for mRNA
CC purification from prokaryotes. The method of the invention comprises the
CC incubation of a sample with a bridging oligonucleotide (containing a
CC targeting region) and subsequently incubating with a capture
CC oligonucleotide allowing the isolation of the target from the sample. The
CC method is useful for depleting or isolating targeted nucleic acid, for
CC example rRNA such as prokaryotic 16S or prokaryotic 23S, eukaryotic 17S
CC or 18S or eukaryotic 28S rRNA, from a sample. The rRNA sequence may
CC comprise any one of 64 fully defined sequences as given in the
CC specification. The present sequence is that of a DNA sequence which
CC represents the sequence of 16S rRNA of Mycobacterium avium related to the
CC invention.
XX
XX SQ Sequence 1465 BP; 321 A; 345 C; 496 G; 298 T; 0 U; 5 Other;

Query Match 85.0%; Score 20.4; DB 10; Length 1465;
Best Local Similarity 95.5%; Pred. No. 8.9;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTTT 22
| | | | | | | | | | | | | | | | | | | | | |
Db 21 CAAGTCGAACGGAAGGCCTCT 42
| | | | | | | | | | | | | | | | | | | | | |

RESULT 45
ADR90572
ID ADR90572 standard; DNA; 1472 BP.
XX
XX AC ADR90572;
XX
XX DT 02-DEC-2004 (first entry)
XX
XX DE M avium 16S rRNA gene sequence SeqID1.
XX
XX KW acid-fast bacterium; differentiation; 16S rRNA; M avium complex; MAC;
XX taxonomic-tree analysis; atypical-mycobacteria; gene; ds.
XX
XX OS Mycobacterium avium.
XX
XX FH Key Location/Qualifiers
XX variation 893 /*tag= a
XX variation 1312 /*tag= b
XX variation 1393 /*tag= c
XX
XX PN JP2004254591-A.
XX


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PI Mabilat C, Ruimy R;
XX WPI; 1997-001738/01.
XX
XX Fragments of Corynebacterium 16S RNA - useful as probes and primers for
XX PT identifying Corynebacterium spp.
XX PT
XX PS Claim 1; Fig 1; 60pp; French.
XX
XX Fragments covering 90 % of the sequence of 16S ribosomal RNA were
XX CC amplified from 28 strains of 25 different species of Corynebacterium by
XX CC PCR using primers specific for eubacteria. The amplification products
XX CC were sequenced and the sequences were aligned for comparison. It was
XX CC found that certain regions, i.e. those corresponding to nucleotides 72-
XX CC 100, 195-215, 466-494, 608-631, 838-853, 859-875 and 1013-1033 in the 16S
XX CC ribosomal RNA of C. diphtheriae (refer to features table for the present
XX CC sequence), vary considerably between different species. Probes and
XX CC primers comprising at least 5 nucleotides from one of these species-
XX CC specific sequences, including the present sequence, or their complements,
XX CC are useful to distinguish between different Corynebacterium species. DNA
XX CC versions of the probes and primers are also included
XX
XX SQ Sequence 1391 BP; 309 A; 317 C; 464 G; 1 T; 295 U; 5 Other;

Query Match 83.3%; Score 20; DB 2; Length 1391;
Best Local Similarity 90.0%; Pred. No. 14;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCT 20
Db 30 CAAGUCGAACGGAAGGCCU 49

RESULT 48
ABN86276
ID ABN86276 standard; DNA; 1457 BP.
XX
XX AC ABN86276;
XX
XX DT 08-OCT-2002 (first entry)
XX
XX DE G. polyisoprenivorans P8219 16S rDNA sequence #2.
XX
XX KW Microorganism; environmental; hormone; phthalic acid; alkyl ester; ds.
XX
XX OS Gordonia polyisoprenivorans.
XX
XX PN JP2002142754-A.
XX
XX PD 21-MAY-2002.
XX
XX PF 08-NOV-2000; 2000JP-00341214.
XX
XX PR 08-NOV-2000; 2000JP-00341214.
XX
XX PA (IMBI-) IMB KK.
XX
XX DR WPI; 2002-561124/60.
XX
XX PT A Gordonia sp. microorganism, useful in the eradication of the
XX PT environmental hormone of phthalic acid esters for environmental
XX PT protection.
XX
XX PS Disclosure; Fig 2A-D; 21pp; Japanese.
XX
XX CC The invention relates to a Gordonia sp. microorganism, capable of
XX CC eradication of the environmental hormone of phthalic acid alkyl esters.
XX CC The microorganism is used in the eradication of phthalic acid esters for
XX CC environmental protection. The present sequence represents an alternate G.
XX CC polyisoprenivorans P8219 16S rDNA sequence
XX
XX SQ Sequence 1457 BP; 323 A; 348 C; 493 G; 291 T; 0 U; 2 Other;

Query Match 82.5%; Score 19.8; DB 6; Length 1457;
Best Local Similarity 91.3%; Pred. No. 17;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTTC 23
Db 41 CAAGTCGAACGGAAGGCCCTGC 63

RESULT 50
AAS59540/c
ID AAS59540 standard; DNA; 2743 BP.
XX
XX AC AAS59540;
XX
XX XX 13-FEB-2002 (first entry)
XX
XX DE Propionibacterium acnes immunogenic protein encoding DNA #35.
XX
XX KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
XX KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
XX KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
XX KW dermatological; osteopathic; neuroprotectant; ds.
XX

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OS Propionibacterium acnes.
PN WO200181581-A2.
XX
XX PD 01-NOV-2001.
XX
XX PF 20-APR-2001; 2001WO-US012865.
XX
XX PR 21-APR-2000; 2000US-0199047P.
XX
XX PR 02-JUN-2000; 2000US-0208841P.
XX
XX PR 07-JUL-2000; 2000US-0216747P.
XX
XX PA (CORI-) CORIXA CORP.
XX
XX PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
XX PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
XX DR WPI; 2001-616774/71.
XX
XX PT Propionibacterium acnes polypeptides and nucleic acids useful for
XX PT vaccinating against and diagnosing infections, especially useful for
XX PT treating acne vulgaris.
XX
XX PS Claim 1; SEQ ID NO 35; 1069pp; English.
XX
XX CC Sequences AAS59506-AAS59804 represent DNA molecules encoding
XX CC Propionibacterium acnes immunogenic polypeptides. The proteins and their
XX CC associated DNA sequences are used in the treatment, prevention and
XX CC diagnosis of medical conditions caused by P. acnes. The disorders include
XX CC SAPHO syndrome (synovitis, acne, pustulosis, hyperostosis and
XX CC osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in
XX CC infections of bone, joints and the central nervous system, however it is
XX CC particularly involved in the inflammatory lesions associated with acne
XX CC vulgaris. A method for detecting the presence or absence of P. acnes in a
XX CC patient comprises contacting a sample with a binding agent that binds to
XX CC the proteins of the invention and determining the amount of bound protein
XX CC in the sample. The polypeptides may be used as antigens in the production
XX CC of antibodies specific for P. acnes proteins. These antibodies can be
XX CC used to downregulate expression and activity of P. acnes polypeptides and
XX CC therefore treat P. acnes infections. The antibodies may also be used as
XX CC diagnostic agents for determining P. acnes presence, for example, by
XX CC enzyme linked immunosorbent assay (ELISA). This sequence encodes the
XX CC polypeptides shown in AAU47822-AAU47846. Note: The sequence data for this
XX CC patent did not form part of the printed specification, but was obtained
XX CC in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 2743 BP; 645 A; 999 C; 546 G; 551 T; 0 U; 2 Other;
Query Match 82.5%; Score 19.8; DB 4; Length 2743;
Best Local Similarity 91.3%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCGCTTTC 23
| | | | | | | | | | | | | | | | | | | | |
Db 2592 CAAGTCGAACGGAAGGCGCTTGC 2570
| | | | | | | | | | | | | | | | | | | | |

RESULT 51
ID ACF64469/c
XX
XX AC ACF64469;
XX
XX DT 17-OCT-2003 (first entry)
XX
XX PT Propionibacterium acnes DNA contig sequence #35.
XX
XX DE Acne vulgaris; antiseborrheic; dermatological; antibacterial;
XX KW immunostimulant; immune response; vaccine; ds.
XX
XX OS Propionibacterium acnes.
XX

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PN WO2003033515-A1.
XX
XX PD 24-APR-2003.
XX
XX PF 11-OCT-2002; 2002WO-US032727.
XX
XX PR 15-OCT-2001; 2001US-00978825.
XX
XX PA (CORI-) CORIXA CORP.
XX
XX PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
XX PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
XX PI Barth B, Vallieue-Douglas J;
XX
XX DR WPI; 2003-381789/36.
XX
XX PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
XX PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
XX PT or for stimulating an immune response specific for a P. acnes protein.
XX
XX PS Claim 1; SEQ ID NO 35; 1481pp; English.
XX
XX CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
XX CC encoding a Propionibacterium acnes protein. The invention also relates to
XX CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
XX CC immunogenic fragments of P. acnes polypeptides. The invention
XX CC additionally encompasses expression vectors and host cells comprising a
XX CC polynucleotide of the invention; antibodies against polypeptides of the
XX CC invention; fusion proteins comprising a polypeptide of the invention; a
XX CC method for stimulating an immune response specific for a P. acnes
XX CC polypeptide and an isolated T cell population comprising T cells prepared
XX CC via this method; a vaccine composition (comprising P. acnes polypeptides,
XX CC polynucleotides, antibodies, fusion proteins, T cell populations, or
XX CC antigen-presenting cells that express the polypeptide); a method and kit
XX CC for detecting or determining the presence or absence of P. acnes in a
XX CC patient; and a method for inhibiting the development of P. acnes in a
XX CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
XX CC proteins, T cell populations or antigen-presenting cells that express the
XX CC polypeptides are useful for diagnosing, preventing or treating acne
XX CC vulgaris, or for stimulating an immune response specific for a P. acnes
XX CC protein. The polynucleotides can also be used as probes or primers for
XX CC nucleic acid hybridisation. The vaccine composition is useful for the
XX CC stimulation of an immune response against P. acnes, or for treating acne,
XX CC and the kit is useful for performing a diagnostic assay. The present
XX CC sequence represents a P. acnes DNA contig which is specifically claimed
XX CC in the invention. Note: The sequence data for this patent did not form
XX CC part of the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 2743 BP; 645 A; 999 C; 546 G; 551 T; 0 U; 2 Other;
Query Match 82.5%; Score 19.8; DB 8; Length 2743;
Best Local Similarity 91.3%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCGCTTTC 23
| | | | | | | | | | | | | | | | | | | | |
Db 2592 CAAGTCGAACGGAAGGCGCTTGC 2570
| | | | | | | | | | | | | | | | | | | | |

RESULT 52
AAAX99198
ID AAAX99198 standard; DNA; 50 BP.
XX
XX AC AAAX99198;
XX
XX DT 28-SEP-1999 (first entry)
XX
XX DE M. smegmatis 16S rRNA gene fragment.
XX
XX KW Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA; ss.
XX KW shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.
XX

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[illegible]

```
CC microorganism: (I) or its mutant, which can cleave urethane bonds. (I) is
CC useful for decomposing urethane compounds which involves contacting (I)
CC with urethane compound. The urethane compound is a raw material of
CC polyurethane or is polyurethane. (I) is useful in plastic disposal and
CC recycling of urethane compounds by decomposing urethane compounds. The
CC present sequence is a 16S rDNA sequence from the microorganism of the
CC invention.
XX
SQ Sequence 535 BP; 118 A; 131 C; 191 G; 95 T; 0 U; 0 Other;

Query Match      80.0%; Score 19.2; DB 13; Length 535;
Best Local Similarity 87.5%; Pred. No. 31;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAAGTCGACGGAAGGCCCTTCG 24
Db 52 CAAGTCGAGCGGTAAAGGCCCTTCG 75

RESULT 55
ADF56670
ID ADF56670 standard; DNA; 1437 BP.
XX
AC ADF56670;
XX
DT 12-FEB-2004 (first entry)
XX
DE YS-44442 16S rDNA, SEQ ID 1.
XX
KW Pravastatin; HMG-CoA reductase inhibitor;
KW 3-hydroxy-3-methyl glutaryl-CoA reductase inhibitor; 16S rDNA; ds.
XX Saccharothrix sp.
OS
PN JP2003250532-A.
XX
XX 09-SEP-2003.
XX
PF 22-FEB-2002; 2002JP-00046750.
XX
PR 22-FEB-2002; 2002JP-00046750.
XX
PA (YUNG-) YUNG SHIN PHARM IND CO LTD.
XX
DR WPI; 2004-046768/05.
XX
PT Microorganisms Saccharothrix genus YS-44442 and YS-45494 and their
PT mutants useful for producing pravastatin.
XX
PS Example 1; SEQ ID NO 1; 18pp; Japanese.
XX
CC The present invention relates to microorganisms (I) Saccharothrix genus
CC YS-44442 and YS-45494 strains and their mutants. Also claimed is a method
CC (M1) for producing pravastatin by using (I) and isolating (M2) 3-hydroxy-
CC 3-methyl glutaryl (HMG)-CoA reductase inhibitors.
XX
SQ Sequence 1437 BP; 320 A; 362 C; 495 G; 260 T; 0 U; 0 Other;

Query Match      80.0%; Score 19.2; DB 12; Length 1437;
Best Local Similarity 87.5%; Pred. No. 34;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAAGTCGACGGAAGGCCCTTCG 24
Db 31 CAAGTCGAGCGGTAAAGGCCCTTCG 54

RESULT 56
ADG64519
ID ADG64519 standard; DNA; 1437 BP.
XX
AC ADG64519;
XX
```

```
DT 11-MAR-2004 (first entry)
XX
DE Saccharothrix strain YS-44442 16S rDNA sequence.
XX
KW Microorganism; Saccharothrix; YS-44442; YS-45494;
KW 3-hydroxy-3-methylglutaryl-CoA reductase inhibitor; HMG-CoA reductase;
KW pravastatin; fermentation; compactin; lovastatin;
KW blood cholesterol level; antilipemic; 16S rDNA; ds.
XX
OS Saccharothrix sp.
XX
PN US2003199047-A1.
XX
PD 23-OCT-2003.
XX
PF 27-FEB-2002; 2002US-00085871.
XX
PR 27-FEB-2002; 2002US-00085871.
XX
PA (LEEF/) LEE F.
PA (LEEM/) LEE M.
PA (HONG/) HONG A C.
PA (CHIU/) CHIU S.
XX
PI Lee F, Lee M, Hong AC, Chiu S;
XX
DR WPI; 2004-041353/04.
XX
PT Novel microorganism strains YS-44442 and YS-45494 of Saccharothrix,
PT useful for producing pravastatin.
XX
PS Example 1; SEQ ID NO 1; 16pp; English.
XX
CC The present invention relates to the isolation of novel microorganism
CC strains of Saccharothrix designated YS-44442 and YS-45494. Also disclosed
CC is a method for isolating 3-hydroxy-3-methylglutaryl (HMG)-CoA reductase
CC inhibitors such as pravastatin. The Saccharothrix strains YS-44442 and YS
CC -45494 are useful for producing pravastatin. The method involves
CC cultivating the strains at a suitable condition to generate a
CC fermentation broth, feeding compactin into the broth, fermenting the
CC broth for a period of time to convert the compactin to pravastatin, and
CC isolating the pravastatin from the broth. The fermentation broth is
CC cultivated for less than 2 days, preferably for 18 hours. The
CC fermentation broth is derived from a seed culture of the microorganism
CC which is cultivated at a suitable condition for 18-48 hours before
CC inoculation into the broth. The broth is fermented for less than 5 days,
CC preferably 3 days, most preferably less than 24 hours. The method of the
CC invention is useful for isolating HMG-CoA reductase inhibitor such as
CC pravastatin, compactin or lovastatin, preferably pravastatin. The
CC pravastatin or HMG-CoA reductase inhibitors are useful for reducing blood
CC cholesterol levels. The present sequence represents Saccharothrix strain
CC YS-44442 16S rDNA sequence.
XX
SQ Sequence 1437 BP; 320 A; 362 C; 495 G; 260 T; 0 U; 0 Other;

Query Match      80.0%; Score 19.2; DB 12; Length 1437;
Best Local Similarity 87.5%; Pred. No. 34;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAAGTCGACGGAAGGCCCTTCG 24
Db 31 CAAGTCGAGCGGTAAAGGCCCTTCG 54

RESULT 57
ADY86147
ID ADY86147 standard; DNA; 1437 BP.
XX
AC ADY86147;
XX
DT 02-JUN-2005 (first entry)
XX
DE Saccharothrix YS-44442 16S rDNA, SEQ ID NO: 1.
```

XX Microorganism; fermentation; hypercholesterolemia; 16s rDNA; antilipemic;
 KW metabolic disorder; ds.
 OS Saccharothrix; YS-44442.
 XX
 FN US2005064566-A1.
 XX
 XX 24-MAR-2005.
 XX
 XX 03-DEC-2003; 2003US-00727643.
 XX
 PR 27-FEB-2002; 2002US-00085871.
 XX
 PA (LEEF/) LEE F.
 PA (LEEM/) LEE M.
 PA (HONG/) HONG A. C.
 PA (CHIU/) CHIU S.
 XX
 PI Lee F, Lee M, Hong AC, Chiu S;
 XX
 XX WPI; 2005-252680/26.
 XX
 PT Isolation of pravastatin, used to treat hypercholesterolemia, comprises
 PT adding ammonium sulfate into a first solution to form precipitate,
 PT isolating and dissolving the precipitate to form a second solution and
 PT followed by extracting.
 XX
 PS Example 1; SEQ ID NO 1; 19pp; English.
 XX
 CC The present invention relates to two new microorganism strains of
 CC Saccharothrix, designated as YS-44442 and YS-45494. The invention also
 CC provides a method of isolating pravastatin from Saccharothrix sp and an
 CC improved process for isolation of 3-hydroxy-3-methylglutaryl-Coenzyme A
 CC (HMG CoA) reductase inhibitor. The invention is useful for the
 CC preparation of pravastatin which is useful in the treatment of
 CC hypercholesterolemia. The present sequence is the Saccharothrix YS-44442
 CC 16s rDNA.
 XX
 SQ Sequence 1437 BP; 320 A; 362 C; 495 G; 260 T; 0 U; 0 Other;
 Query Match 80.0%; Score 19.2; DB 14; Length 1437;
 Best Local Similarity 87.5%; Pred. No. 34;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CAAGTCGAACGGAAGGCTTTTCG 24
 ||||| ||||| ||||| ||||| |||||
 Db 31 CAAGTCGAGCGTAAGGCTTTTCG 54
 ||||| ||||| ||||| ||||| |||||
 RESULT 58
 ADC61232
 ID ADC61232 standard; DNA; 1439 BP.
 XX
 AC ADC61232;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Baeyer-Villiger enzyme 16s rDNA gene from Rhodococcus erythropolis AN12.
 XX
 KW Baeyer-Villiger; BV; monooxygenase; ketone substrate; lactone; ester;
 KW 16s rDNA; ds.
 XX
 XX Rhodococcus erythropolis.
 OS
 FN WO2003020890-A2.
 XX
 XX 13-MAR-2003.
 PD
 XX 29-AUG-2002; 2002WO-US027549.
 PF
 XX 29-AUG-2001; 2001US-0315546P.
 PR
 XX

PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Bramucci MG, Brzosowicz PC, Kostichka KN, Nagarajan V;
 PI Rouviere PE, Thomas SM;
 XX
 XX WPI; 2003-313085/30.
 DR
 XX
 PT Novel nucleic acid fragment useful for converting ketone substrates to
 PT the corresponding lactone or ester, is isolated from Rhodococcus,
 PT Arthrobacter or Acidovorax, encoding Baeyer-Villiger monooxygenase
 PT polypeptide.
 XX
 XX Claim 54; SEQ ID NO 6; 225pp; English.
 PS
 XX
 CC The invention relates to a novel isolated nucleic acid fragment
 CC comprising a fragment encoding a Baeyer-Villiger (BV) monooxygenase
 CC polypeptide having a sequence of 542, 541, 439, 518, 462, 531, 493, 539,
 CC 649, 494, 499, 545, 532 or 538 amino acids defined in the specification;
 CC a nucleic acid molecule that hybridises with the above sequence under the
 CC hybridisation conditions; or their complements. The BV monooxygenase
 CC fragment is useful for obtaining a nucleic acid fragment encoding a BV
 CC monooxygenase polypeptide, by probing a genomic library with the
 CC fragment, identifying a DNA clone that hybridises with the fragment, and
 CC sequencing the genomic fragment that comprises the above identified
 CC clone, where the sequenced genomic fragment encodes a BV monooxygenase
 CC polypeptide. The genes and their products are useful for converting
 CC suitable ketone substrates to the corresponding lactone or ester. This
 CC polynucleotide sequence represents the 16s rDNA gene from Arthrobacter
 CC sp. BP2 relating to the Baeyer-Villiger enzymes of the invention.
 XX
 SQ Sequence 1439 BP; 333 A; 357 C; 465 G; 283 T; 0 U; 1 Other;
 Query Match 80.0%; Score 19.2; DB 10; Length 1439;
 Best Local Similarity 87.5%; Pred. No. 34;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CAAGTCGAACGGAAGGCTTTTCG 24
 ||||| ||||| ||||| ||||| |||||
 Db 32 CAATTCGAGCGTAAGGCTTTTCG 55
 ||||| ||||| ||||| ||||| |||||
 RESULT 59
 ADF56671
 ID ADF56671 standard; DNA; 1471 BP.
 XX
 AC ADF56671;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE YS-45494 16S rDNA, SEQ ID 2.
 XX
 KW Pravastatin; HMG-CoA reductase inhibitor;
 KW 3-hydroxy-3-methyl glutaryl-CoA reductase inhibitor; 16S rDNA; ds.
 XX
 OS Saccharothrix sp.
 XX
 FN JP2003250532-A.
 XX
 PD 09-SEP-2003.
 XX
 XX 22-FEB-2002; 2002JP-00046750.
 PF
 XX 22-FEB-2002; 2002JP-00046750.
 PR
 XX (YUNG-) YUNG SHIN PHARM IND CO LTD.
 PA
 XX WPI; 2004-046768/05.
 DR
 XX Microorganisms Saccharothrix genus YS-44442 and YS-45494 and their
 PT mutants useful for producing pravastatin.
 PT
 XX Example 1; SEQ ID NO 2; 19pp; Japanese.
 PS
 XX

RESULT 62

OS	Lechevallieria aerocolonigenes.
XX	
PN	US2004180960-A1.
AC	
XX	
PD	16-SEP-2004.
XX	
PF	13-JAN-2004; 2004US-00756683.
XX	
PR	13-MAR-2003; 2003KR-00015628.
PR	13-MAR-2003; 2003KR-00015629.
XX	
PA	(HWAN/) HWANG B K.
PA	(LEEJ/) LEE J Y.
XX	
PI	Hwang BK, Lee JY;
XX	
DR	WPI; 2004-661528/64.
DR	EMBL; AY196703.
XX	
PT	New antibiotic compound, thiobutacin, is used to treat plant disease e.g. phytophthora blight and to control plant diseases caused by pathogens e.g. Phytophthora capsici and Botrytis cinerea.
PT	
XX	
PS	Example 2; SEQ ID NO 1; 17pp; English.
XX	
CC	The invention relates to an antibiotic compound thiobutacin and antifungal and antioomycete compositions comprising thiobutacin.
CC	Thiobutacin is used to treat plant disease such as phytophthora blight and to control plant diseases caused by pathogens e.g. Phytophthora capsici and Botrytis cinerea. The present sequence is the Lechevallieria aerocolonigenes strain VK-A9 16S ribosomal DNA (rDNA). L. aerocolonigenes strain VK-A9 has strong antifungal and antimicrobial activity and it can inhibit the growth of Phytophthora capsici.
CC	
XX	
SQ	Sequence 1488 BP; 339 A; 369 C; 508 G; 272 T; 0 U; 0 Other;
Query Match	80.0%; Score 19.2; DB 13; Length 1488;
Best Local Similarity	87.5%; Pred.No. 34;
Matches	21; Conservative 0; Mismatches 3; Indels 0; Gaps 0
Qy	1 CAAGTCGACGGAAAGGCCTTTCG 24
Db	43 CAAGTCGACGGTAAGGCCCTTTCG 66
RESULT 64	
ADWI2667	
ID	ADWI2667 standard; DNA; 1514 BP.
XX	
AC	ADWI2667;
XX	
DT	07-APR-2005 (first entry)
XX	
DE	Rhodococcus opacus 16S rDNA, SEQ ID NO:2.
XX	
KW	Stereoselective synthesis; enantiomeric enrichment;
KW	beta-amino acid synthesis; cell culture; 16S ribosomal RNA; 16S rRNA; ds.
XX	
OS	Rhodococcus opacus.
XX	
PN	US2005009151-A1.
XX	
PD	13-JAN-2005.
XX	
PF	22-JUN-2004; 2004US-00875161.
XX	
PR	10-JUL-2003; 2003US-0486032P.
PR	02-SEP-2003; 2003US-0496622P.
XX	
PA	(PHAA) PHARMACIA CORP.
PA	Chase M, Clayton R, Landis B, Banerjee A;
XX	

AED47485	
ID	AED47485 standard; DNA; 1477 BP.
XX	
AC	AED47485;
XX	
DT	15-DEC-2005 (first entry)
XX	
DE	Nocardia sp. TP-A0674 16S ribosomal DNA, SEQ ID 1.
XX	
KW	Analgesic; Nootropic; Antiparkinsonian; Antiasthmatic; Respiratory-Gen.; Uropathic; binding inhibitor; muscarinic acetylcholine receptor;
KW	analgesic; Parkinsons disease; asthma;
KW	chronic obstructive pulmonary disease; bladder disease;
KW	micturition disorder; 16S ribosomal RNA; 16S rRNA; gene; ds.
XX	
OS	Nocardia sp.
XX	
PN	JP2005289890-A.
XX	
PD	20-OCT-2005.
XX	
PF	31-MAR-2004; 2004JP-00107929.
XX	
PR	31-MAR-2004; 2004JP-00107929.
XX	
PA	(YOSH) YOSHITOMI PHARM IND KK.
XX	
PI	Furumai T, Igarashi Y, Onaka H, Ikeda Y, Nonaka H;
XX	
DR	WPI; 2005-738172/76.
XX	
PT	Binding inhibitor of muscarinic acetylcholine receptor subtype 4 or 3 useful for treating diseases e.g. asthma, contains chelate having TPU 0052A-F compound derived from Nocardia species TP-AO674 and metal ion.
PT	
XX	
PS	Disclosure; SEQ ID NO 1; 22pp; Japanese.
XX	
CC	The invention relates to a novel binding inhibitor of muscarinic acetylcholine receptor subtype 4 or 3, comprising a chelate having a TPU 0052A-F compound or its salt and a metal ion. The invention further comprises a method and a microorganism for producing the novel binding inhibitor. The binding inhibitor and compound are useful as central analgesics and memory improving drugs, for treating Parkinson's disease, asthma, chronic obstructive pulmonary disease, overactive bladder, frequent urination and urinary incontinence. This polynucleotide sequence represents the 16S ribosomal DNA of a Nocardia sp. TP-A0674 microorganism, useful in producing a muscarinic acetylcholine receptor binding inhibitor compound of the invention.
CC	
XX	
SQ	Sequence 1477 BP; 341 A; 357 C; 494 G; 285 T; 0 U; 0 Other;
Query Match	80.0%; Score 19.2; DB 14; Length 1477;
Best Local Similarity	87.5%; Pred.No. 34;
Matches	21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	1 CAAGTCGACGGAAAGGCCTTTCG 24
Db	48 CAAGTCGACGGTAAGGCCCTTTCG 71
RESULT 63	
ADS17269	
ID	ADS17269 standard; DNA; 1488 BP.
XX	
AC	ADS17269;
XX	
DT	02-DEC-2004 (first entry)
XX	
DE	Lechevallieria aerocolonigenes strain VK-A9 16S rDNA.
XX	
KW	Plant protectant; antibiotic; thiobutacin; antifungal; antioomycete;
KW	phytophthora blight; gene; ds; ribosomal DNA; rDNA.
XX	


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XX SQ Sequence 23 BP; 7 A; 7 C; 6 G; 3 T; 0 U; 0 Other;
      Query Match      79.2%; Score 19; DB 10; Length 23;
      Best Local Similarity 100.0%; Pred. No. 27;
      Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CAAGTCGAACGGAAGGCC 19
    |||||
Db 1 CAAGTCGAACGGAAGGCC 19
    |||||

RESULT 67
AEA08233
ID AEA08233 standard; DNA; 23 BP.
AC AEA08233;
XX
XX 14-JUL-2005 (first entry)
DT
XX
DE Mycobacterium xenopi 16S rRNA amplifying non-T7 primer, SEQ ID NO: 27.
XX
DE Microorganism detection; DNA amplification; 16S ribosomal RNA; 16S rRNA;
KW PCR; primer; ss.
KW
XX Mycobacterium xenopi; ATCC 19250.
OS
XX
XX US2005100915-A1.
XX
XX 12-MAY-2005.
PD
XX
XX 18-SEP-2003; 2003US-00665708.
PF
XX
XX 17-DEC-1999; 99US-0172190P.
PR
XX 15-DEC-2000; 2000US-00738274.
PR
XX (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZAT P.
PA (RODR/) RODRIGUE M.
XX
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
PI WPI; 2005-345392/35.
XX
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample, comprises using in vitro nucleic acid
PT amplification and detection of amplified products.
XX
XX Example 3; SEQ ID NO 27; 21pp; English.
XX
XX The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample. The method involves using in
CC vitro nucleic acid amplification and detection of amplified products. The
CC invention is useful for diagnostic detection of pathogenic bacteria such
CC as Mycobacterium species. The present sequence is the Mycobacterium
CC xenopi (ATCC 19250) 16S ribosomal RNA (16S rRNA) amplifying non-T7 PCR
CC primer.
XX
XX Sequence 23 BP; 7 A; 7 C; 6 G; 3 T; 0 U; 0 Other;
      Query Match      79.2%; Score 19; DB 14; Length 23;
      Best Local Similarity 100.0%; Pred. No. 27;
      Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CAAGTCGAACGGAAGGCC 19
    |||||
Db 1 CAAGTCGAACGGAAGGCC 19
    |||||

RESULT 68
AEB98776
ID AEB98776 standard; DNA; 39 BP.
AC AEB98776;
XX
XX 06-OCT-2005 (first entry)
DT
XX
DE Mycobacterium intracellulare identification LAMP primer, SEQ ID 18.
XX
DE Microorganism detection; mycobacterium infection; antibacterial; primer;
KW PCR; ss; LAMP.
KW
XX Mycobacterium intracellulare.
OS Synthetic.
OS
XX JP2005204582-A.
PN
XX
XX 04-AUG-2005.
PD
XX
XX 23-JAN-2004; 2004JP-00015195.
PF
XX 23-JAN-2004; 2004JP-00015195.
PR
XX (ASAH ) ASAH I KASEI KK.
PA
XX Oda N;
PI
XX WPI; 2005-526965/54.
XX
XX New single-stranded oligonucleotide, useful for amplifying the nucleic
PT acid of Mycobacterium avium, Mycobacterium intracellulare, and
PT Mycobacterium kansasii.
XX
XX Claim 2; SEQ ID NO 18; 14pp; Japanese.
XX
XX The invention relates to a novel single-stranded oligonucleotide used in
CC a detection method of an atypical mycobacteria group. The invention
CC further includes: amplifying the nucleic acid of Mycobacterium avium by a
CC loop-mediated isothermal amplification (LAMP) method; amplifying the
CC nucleic acid of M. intracellulare by a LAMP method; amplifying the
CC nucleic acid of M. kansasii by a LAMP method; and a kit for detecting the
CC nucleic acid of M. avium by a LAMP method; detecting the nucleic acid of
CC M. intracellulare by a LAMP method; or detecting the nucleic acid of M.
CC kansasii by a LAMP method. The single-stranded oligonucleotide is useful
CC in medical applications. This oligo sequence represents a loop-mediated
CC isothermal amplification (LAMP) primer used in the exemplification of the
CC invention.
XX
XX Sequence 39 BP; 10 A; 12 C; 10 G; 7 T; 0 U; 0 Other;
      Query Match      79.2%; Score 19; DB 14; Length 39;
      Best Local Similarity 100.0%; Pred. No. 29;
      Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CAAGTCGAACGGAAGGCC 19
    |||||
Db 20 CAAGTCGAACGGAAGGCC 38
    |||||

RESULT 69
ADF94053
ID ADF94053 standard; DNA; 50 BP.
XX
XX ADF94053;
AC
XX
XX 11-MAR-2004 (first entry)
DT
XX
XX Microorganism detection probe, SEQ ID 146.
DE
XX Probe; detection; identification; microorganism; food; drug;
KW 16S rRNA V1 region; 16S rRNA V2 region; 16S rRNA V3 region; ss.
KW
XX Mycobacterium intracellulare.
OS
XX

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PN WO2003106676-A1.
 XX 24-DEC-2003.
 XX 16-JUN-2003; 2003WO-JP007620.
 XX 14-JUN-2002; 2002JP-00174564.
 XX (HISF) HITACHI SOFTWARE ENG CO LTD.
 PA (MITS-) MITSUBISHI KAGAKU BIO-CLINICAL LAB INC.
 XX Hashida J, Ueno S, Muto I, Naruse K, Tamura M, Matsuda K;
 PI Shimadzu M, Kobayashi I, Ishiko H;
 XX WPI; 2004-071565/07.
 XX 20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a
 PT microorganism for specific detection and identification of the
 PT microorganism in foods and drug compositions.
 XX Claim 2; SEQ ID NO 146; 150pp; Japanese.
 PS The present invention relates to probes (ADF93908-ADP94059) for the
 CC specific detection and identification of harmful microorganisms in
 CC samples of foods and drug compositions. The probe sequences are derived
 CC from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism,
 CC or its complementary sequence. Detection and identification of the
 CC microorganism is by amplification of the complete 16S rRNA gene using
 CC primers ADF94060 and ADF94061, labelling the amplification product (a
 CC fluorescence label is preferred), and hybridising to the probe or probes
 CC of the invention. The probes may be immobilised on a DNA chip. The
 CC microorganism is selected from Actinobacillus actinomycetemcomitans,
 CC Acinetobacter calcoaceticus, Haemophilus influenzae, Stenotrophomonas
 CC maltophilia, Proteus mirabilis, Streptococcus pneumoniae, Pseudomonas
 CC aeruginosa, Citrobacter freundii, Veillonella parvula, Providencia
 CC stuartii, Neisseria gonorrhoeae, Streptococcus agalactiae, Morganella
 CC morgani, Bacteroides fragilis, Staphylococcus hominis, Staphylococcus
 CC warneri, Staphylococcus haemolyticus, Enterobacter cloacae, Enterobacter
 CC aerogenes, Staphylococcus epidermidis, Streptococcus constellatus,
 CC Serratia marcescens, Streptococcus anginosus, Escherichia coli,
 CC Klebsiella pneumoniae, Enterococcus faecalis, Enterococcus faecium,
 CC Streptococcus sanguis, Streptococcus mitis, Streptococcus intermedius,
 CC Listeria monocytogenes, Clostridium perfringens, Corynebacterium
 CC aquatum, Streptococcus oralis, Staphylococcus aureus, Neisseria
 CC meningitidis, Campylobacter fetus, Enterococcus gallinarum, Enterococcus
 CC casseliflavus, Aeromonas hydrophila, Salmonella paratyphi, Salmonella
 CC typhi, Streptococcus equisimilis, Streptococcus canis, Klebsiella
 CC oxytoca, Staphylococcus saprophyticus, Pasteurella multocida, Eikenella
 CC corrodens, Streptococcus pyogenes, Moraxella catarrhalis, Legionella
 CC pneumophila, Mycobacterium tuberculosis, Mycobacterium avium,
 CC Mycobacterium intracellulare, Mycobacterium kansasii or Mycobacterium
 CC gordonae.
 XX SQ Sequence 50 BP; 11 A; 12 C; 20 G; 7 T; 0 U; 0 Other;
 Query Match 79.2%; Score 19; DB 12; Length 50;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CAACTCGAACGGAAGGCC 19
 |||||
 Db 2 CAACTCGAACGGAAGGCC 20
 RESULT 70
 ADU66542
 ID ADU66542 standard; DNA; 80 BP.
 XX AC ADU66542;
 XX 27-JAN-2005 (first entry)
 XX Cut base A amplicon fragment.

XX ds, mass spectroscopy; DNA cleavage; DNA sequencing; sequencing.
 KW Unidentified.
 OS WO2004097369-A2.
 XX 11-NOV-2004.
 XX 22-APR-2004; 2004WO-US012520.
 XX 25-APR-2003; 2003US-0466006P.
 XX (SEQU-) SEQUENOM INC.
 XX (BOEC/) BOECKER S.
 XX Boecker S, Van Den Boom D;
 XX WPI; 2005-012656/01.
 XX Obtaining sequence information from target biomolecule, by fragmenting
 PT target biomolecule by partial cleavage, performing mass spectrometry,
 PT extracting information from mass spectra, constructing sequencing graph
 PT and traversing graphs.
 XX Disclosure; SEQ ID NO 11; 133pp; English.
 XX This invention describes a novel method for obtaining sequence
 CC information from a target biomolecule and involves fragmenting the target
 CC biomolecule into several fragments by partial cleavage, performing mass
 CC spectrometry on fragments to produce mass spectra, extracting peak
 CC information from the produced mass spectra, constructing sequencing graph
 CC using the extracted peak information and traversing the sequencing graphs
 CC to reconstruct sequence information of the target biomolecule. The target
 CC biomolecule is nucleic acid molecule such as DNA or RNA, or is a protein
 CC and the compositions of the two fragments are the base compositions or
 CC amino acid compositions. This method preferably involves subjecting the
 CC nucleic acid molecule to partial cleavage reactions with one or more
 CC specific cleavage reagents, thus generating two or more fragments that
 CC are specific cleavage products, determining the molecular weights of the
 CC two or more fragments, determining the possible base compositions of the
 CC two or more fragments, ordering the possible base compositions of the two
 CC or more fragments according to the number of specific cleavage sites that
 CC are not cleaved in each fragment, constructing one or more sequencing
 CC graphs that are a graph theoretical representation of the ordered base
 CC compositions for the two or more fragments, and traversing the one or
 CC more sequencing graph to reconstruct one or more underlying sequence
 CC candidates, where each sequencing graph corresponds to the ordered base
 CC compositions derived from a partial cleavage reaction with one base-
 CC specific cleavage reagent. This method further involves scoring the one
 CC or more underlying sequence candidates and determining the rank order of
 CC fitness, where the scoring is done by statistical analysis or maximum
 CC likelihood statistical analysis. This method determines epigenetic
 CC changes in a target nucleic acid molecule relative to reference nucleic
 CC acid molecule and allows the sequencing of large biomolecules. The
 CC invention also describes a method of producing a candidate sequence of a
 CC biomolecule which involves receiving several sequencing graphs having
 CC several vertices and edges, where each vertex represents a compomer of
 CC the biomolecule and each edge represents a cut base of the sequencing
 CC graph and generating the candidate sequence by traversing several
 CC sequencing graphs. This second method further involves traversing several
 CC sequencing graphs by tracing through each sequencing graph, starting at a
 CC source vertex. The results of each method can be read by a program
 CC product for use in a computer that executes program instructions recorded
 CC in a computer-readable media to produce a candidate sequence of a
 CC biomolecule or to obtain sequence information in a target biomolecule.
 CC The target biomolecule contains a sequence variation, which is a mutation
 CC or a polymorphism. The target is a target nucleic acid molecule from an
 CC organism chosen from eukaryotes, prokaryotes and viruses, preferably a
 CC bacterium. The specific cleavage reagent is an RNase chosen from RNase
 CC T1, RNase U2, RNase PnM, RNase A, chicken liver RNase (RNase CL3) and
 CC cusavitin, or a glycosylase. The sequence variations in the target
 CC biomolecule permit genotyping a subject, forensic analysis, disease

CC diagnosis or disease prognosis. The novel methods are useful for de novo
 CC sequencing, to identify genetic disease or chromosome abnormality,
 CC identifying a predisposition to a disease, or condition including
 CC obesity, atherosclerosis, or cancer, to identify an infection by an
 CC infectious agent, to identify a pathogen, determine haplotypes, analyze
 CC microsatellite sequences, and short tandem repeat (STR) loci, determine
 CC allelic variation and/or frequency, and analyze cellular methylation
 CC patterns. This sequence represents an amplicon used to illustrate the
 CC sequencing technique described in the invention.

XX Sequence 80 BP; 18 A; 20 C; 27 G; 15 T; 0 U; 0 Other;

Query Match 79.2%; Score 19; DB 14; Length 80;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCC 19
 |||||
 Db 51 CAAGTCGAACGGAAGGCC 69

RESULT 71
 AEB98763
 ID AEB98763 standard; DNA; 209 BP.

XX AEB98763;

DT 06-OCT-2005 (first entry)

DE Mycobacterium intracellulare partial 16S rDNA sequence, SEQ ID 5.

XX microorganism detection; mycobacterium infection; antibacterial; ds.

OS Mycobacterium intracellulare.

PN JP2005204582-A.

PD 04-AUG-2005.

PF 23-JAN-2004; 2004JP-00015195.

PR 23-JAN-2004; 2004JP-00015195.

XX (ASAH) ASAH KASEI KK.

PI Oda N;

DR WPI; 2005-526965/54.

XX New single-stranded oligonucleotide, useful for amplifying the nucleic
 PT acid of Mycobacterium avium, Mycobacterium intracellulare, and
 PT Mycobacterium kansasii.

PS Example 1; SEQ ID NO 5; 14pp; Japanese.

XX The invention relates to a novel single-stranded oligonucleotide used in
 CC a detection method of an atypical mycobacteria group. The invention
 CC further includes: amplifying the nucleic acid of Mycobacterium avium by a
 CC loop-mediated isothermal amplification (LAMP) method; amplifying the
 CC nucleic acid of M. intracellulare by a LAMP method; amplifying the
 CC nucleic acid of M. kansasii by a LAMP method; and a kit for detecting the
 CC nucleic acid of M. avium by a LAMP method; detecting the nucleic acid of
 CC M. intracellulare by a LAMP method; or detecting the nucleic acid of M.
 CC kansasii by a LAMP method. The single-stranded oligonucleotide is useful
 CC in medical applications. This polynucleotide represents a Mycobacterium
 CC intracellulare partial 16S rDNA sequence amplified by the LAMP method of
 CC the invention.

XX Sequence 209 BP; 45 A; 47 C; 73 G; 44 T; 0 U; 0 Other;

Query Match 79.2%; Score 19; DB 14; Length 209;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCC 19
 |||||
 Db 40 CAAGTCGAACGGAAGGCC 58

RESULT 72
 ABT23572
 ID ABT23572 standard; DNA; 560 BP.

XX ABT23572;

AC ABT23572;

DT 22-MAY-2003 (first entry)

DE Stabilising reagent method related oligo SEQ ID No 24.

XX Stabilising reaction reagent; PCR; primer; RNaseH; long-term storage;
 KW specific amplification; pathogenic microorganism; chimeric;
 KW genetic engineering; clinical medicine; ss.

XX Mycobacterium avium.

OS WO2002101042-A1.

PN 19-DEC-2002.

PF 12-JUN-2002; 2002WO-JP005832.

PR 12-JUN-2001; 2001JP-00177737.

PR 20-AUG-2001; 2001JP-00249689.

XX (TAKI) TAKARA BIO INC.

XX Sagawa H, Uemori T, Mukai H, Yamamoto J, Tomono J, Kobayashi B;
 PI Enoki T, Asada K, Kato I;

XX WPI; 2003-148805/14.

DR Method for stabilizing and storing reaction reagents for specific
 XX amplification and detection of nucleic acids particularly in e.g.
 PT identifying pathogenic microorganisms or viruses in sample.

PS Example 15; Page 110; 177pp; Japanese.

XX The invention relates to a novel stabilising reaction reagent for use in
 CC the amplification and/or detection of a target nucleic acid comprising:
 CC preparing a reaction mixture with e.g. a nucleic acid as template, at
 CC least 1 primer and RNaseH; and incubation of the reaction mixture for a
 CC defined period of time to form a reaction product during the
 CC amplification of such target nucleic acid. The method is useful for
 CC stabilising and long-term storage of reaction reagents for highly
 CC sensitive and specific amplification and detection of nucleic acids
 CC particularly in identifying pathogenic microorganisms or viruses in a
 CC sample using chimeric oligonucleotide primers, which is useful in genetic
 CC engineering and clinical medicine. This polynucleotide sequence
 CC represents an oligo relating to the novel stabilising reaction reagent
 CC method of the invention

SQ Sequence 560 BP; 117 A; 134 C; 199 G; 110 T; 0 U; 0 Other;

Query Match 79.2%; Score 19; DB 10; Length 560;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCC 19
 |||||
 Db 43 CAAGTCGAACGGAAGGCC 61

RESULT 73
 AEA22410
 ID AEA22410 standard; DNA; 1321 BP.

XX

```

AC AEA22410;
XX
XX 25-AUG-2005 (first entry)
XX
DE Mycobacterium kubicae 16S rRNA sequence SEQ ID NO:11.
XX
XX microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
XX
XX Mycobacterium kubicae.
XX
XX US2005130168-A1.
XX
XX 16-JUN-2005.
XX
XX 31-OCT-2003; 2003US-00697802.
XX
XX 31-OCT-2003; 2003US-00697802.
XX
XX (HANX/) HAN X.
XX (PHAM/) PHAM A. S.
XX
XX Han X, Pham AS;
XX
XX WPI; 2005-424597/43.
XX
XX Determining a bacterium species comprises providing oligonucleotide
XX primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
XX
XX Disclosure; SEQ ID NO 11; 74pp; English.
XX
XX The invention relates to a method (M1) for determining a bacterium
XX species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
XX extracting a genomic nucleotide from the bacterium to provide a
XX nucleotide template; (c) annealing a region of a nucleotide template to a
XX specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
XX complimentary fashion, the primer set designed to provide a product
XX having a predetermined size dictated by a complementary primer set; (d)
XX amplifying the region of the nucleotide template to produce the product;
XX and (e) determining a species of a bacterium in a nucleotide sequence of
XX the product. Also described is an alternative method (M2) for determining
XX a bacterium species comprising: (a) providing a specimen or a sample
XX having a template; (b) providing a pair of primers selected from: (i) a
XX first forward primer having consecutive bases of an AFB-f comprising any
XX of the 36 sequences of 15-21 bp (AEA22417-AEA22452), or their fragments
XX or variations and a first reverse primer having consecutive bases of an
XX AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
XX or their fragments or variations, (ii) a second forward primer having
XX consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
XX bp (AEA22489-AEA22516) or their fragments or variations and a second
XX reverse primer having consecutive bases of an UB-r comprising any of the
XX 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
XX variations, or (iii) a first forward primer having consecutive bases of
XX an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
XX second reverse primer having consecutive bases of an UB-r of AEA22517-
XX AEA22544 or their fragments or variations; (c) the specimen; and (d)
XX comparing the product from the specimen with a nucleotide sequence from a
XX database to determine the bacterium species present in the specimen. The
XX methods are useful for determining a bacterium species. The present
XX sequence represents a Mycobacterium kubicae 16S rRNA nucleotide sequence,
XX which is used in the exemplification of the present invention.
XX
XX Sequence 1321 BP; 287 A; 314 C; 457 G; 263 T; 0 U; 0 Other;
XX
XX Query Match 79.2%; Score 19; DB 14; Length 1321;
XX Best Local Similarity 100.0%; Pred. No. 42;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CAAGTCGAACGGAAGGCC 19
XX |||||
XX 15 CAAGTCGAACGGAAGGCC 33
XX
XX RESULT 74

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AD085868/c
ID AD085868 standard; DNA; 1344 BP.
XX
AC AD085868;
XX
XX 29-JUL-2004 (first entry)
XX
XX Gordonia sp. bacterium 16S rDNA.
XX
XX microorganism; Gordonia genus; gram-positive bacillus; catalase;
XX nitrate reduction; alkali phosphatase; beta-galactosidase;
XX pyrazinamidase; pyrolydonyl allyl amidase; beta-glucuronidase;
XX alpha-glucosidase; urease; gelatin-liquefaction; esculin; glucose;
XX ribose; GR-004 strain; FERM P-18806;
XX cyclic hydrocarbon degradation agent; waste engine oil; 16S rDNA; ds.
XX
XX Gordonia sp.
XX
XX JP2004121068-A.
XX
XX 22-APR-2004.
XX
XX 01-OCT-2002; 2002JP-00288714.
XX
XX 01-OCT-2002; 2002JP-00288714.
XX
XX (SEIT-) GEITO KK.
XX
XX WPI; 2004-322761/30.
XX
XX Novel microorganism of Gordonia genus having biochemical properties
XX positive for catalase, approximately beta-galactosidase, nitrate reduction
XX ability, is useful as cyclic hydrocarbon degradation agent in waste-oil
XX treatment.
XX
XX Claim 2; SEQ ID NO 1; 12pp; Japanese.
XX
XX The invention relates to a novel microorganism belonging to the Gordonia
XX genus, a gram-positive bacillus. The novel microorganism having ability,
XX biochemical properties positive for catalase, nitrate reduction ability,
XX alkali phosphatase, and beta-galactosidase, and negative for
XX pyrazinamidase, pyrolydonyl allyl amidase, beta-glucuronidase, alpha-
XX glucosidase, urease, gelatin-liquefaction ability, and esculin, glucose
XX and ribose utilisation ability. The invention further comprises: a GR-004
XX strain of Gordonia sp. having the accession number FERM P-18806; and a
XX cyclic hydrocarbon degradation agent containing the novel microorganism.
XX The Gordonia genus microorganism is useful for processing a cyclic
XX hydrocarbon-containing substance, which involves using the cyclic
XX hydrocarbon degradation agent, where the cyclic hydrocarbon-containing
XX substance is a waste engine oil. The Gordonia genus microorganism is
XX useful as a cyclic hydrocarbon degradation agent for waste-oil treatment.
XX This polynucleotide sequence represents the Gordonia sp. bacterium 16S
XX rDNA of the invention.
XX
XX Sequence 1344 BP; 276 A; 447 C; 315 G; 306 T; 0 U; 0 Other;
XX
XX Query Match 79.2%; Score 19; DB 12; Length 1344;
XX Best Local Similarity 100.0%; Pred. No. 42;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CAAGTCGAACGGAAGGCC 19
XX |||||
XX 1298 CAAGTCGAACGGAAGGCC 1280
XX
XX RESULT 75
XX AEA22413
XX ID AEA22413 standard; DNA; 1415 BP.
XX
XX AC AEA22413;
XX
XX 25-AUG-2005 (first entry)
XX
XX

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DE Mycobacterium paraffinicum 16S rRNA sequence SEQ ID NO:14.
XX microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
XX
XX
OS Mycobacterium paraffinicum.
XX
XX US2005130168-A1.
XX
XX 16-JUN-2005.
XX
XX 31-OCT-2003; 2003US-00697802.
XX
XX 31-OCT-2003; 2003US-00697802.
XX
XX (HANX//) HAN X.
XX (PHAM//) PHAM A S.
XX
XX Han X, Pham AS;
XX
XX WPI; 2005-424597/43.
XX
XX Determining a bacterium species comprises providing oligonucleotide
XX primer set comprising SEQ-FOR and SEQ-REV in a complementary fashion.
XX
XX Disclosure; SEQ ID NO 14; 74pp; English.
XX
XX The invention relates to a method (M1) for determining a bacterium
XX species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
XX extracting a genomic nucleotide from the bacterium to provide a
XX nucleotide template; (c) annealing a region of a nucleotide template to a
XX specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
XX complementary fashion, the primer set designed to provide a product
XX having a predetermined size dictated by a complementary primer set; (d)
XX amplifying the region of the nucleotide template to produce the product;
XX and (e) determining a species of a bacterium in a nucleotide sequence of
XX the product. Also described is an alternative method (M2) for determining
XX a bacterium species comprising: (a) providing a specimen or a sample
XX having a template; (b) providing a pair of primers selected from: (i) a
XX first forward primer having consecutive bases of an AFB-f comprising any
XX of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
XX or variations; and a first reverse primer having consecutive bases of an
XX AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
XX or their fragments or variations; (ii) a second forward primer having
XX consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
XX bp (AEA22489-AEA22516) or their fragments or variations; and a second
XX reverse primer having consecutive bases of an UB-r comprising any of the
XX 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
XX variations; or (iii) a first forward primer having consecutive bases of
XX an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
XX second reverse primer having consecutive bases of an UB-r of AEA22517-
XX AEA22544 or their fragments or variations; (c) the specimen; and (d)
XX comparing the product from the specimen with a nucleotide sequence from a
XX database to determine the bacterium species present in the specimen. The
XX methods are useful for determining a bacterium species. The present
XX sequence represents a Mycobacterium paraffinicum 16S rRNA nucleotide
XX sequence, which is used in the exemplification of the present invention.
XX
XX Sequence 1415 BP; 307 A; 343 C; 480 G; 285 T; 0 U; 0 Other;
XX
XX Query Match 79.2%; Score 19; DB 14; Length 1415;
XX Best Local Similarity 100.0%; Pred. No. 43;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 CAAGTCGAACGGAAGGCC 19
XX |||||
XX Db 16 CAAGTCGAACGGAAGGCC 34
XX
XX RESULT 76
XX AA222765
XX ID AA222765 standard; DNA; 1460 BP.
XX
XX AC AA222765;

XX 15-MAR-2000 (first entry)
XX Corynebacterium sp. NK-1 16S rRNA gene.
XX
XX Seasoning liquor; flavour; vegetable; pickling; salted rice bran paste;
XX microorganism; gamma-dodecalactone; gamma-dodecalactone; lactic acid;
XX propionic acid; 16S rRNA; pickle; ss.
XX
XX Corynebacterium sp.
XX
XX WO9962347-A1.
XX
XX 09-DEC-1999.
XX
XX 28-MAY-1999; 99WO-JP002854.
XX
XX 29-MAY-1998; 98JP-00162226.
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX
XX Saitoh C, Yashiro A, Tokunaga C, Ozawa K, Yokoi A, Ogata N;
XX Ochiai K, Ando K, Katahira H;
XX
XX WPI; 2000-062809/05.
XX
XX Production of seasoning liquors with the flavor of vegetables pickled in
XX salted rice bran.
XX
XX Disclosure; Page 41-43; 45pp; Japanese.
XX
XX The invention relates to a method of producing seasoning liquors with the
XX flavour of vegetables pickled in salted rice bran paste by culturing a
XX microorganism in a rice bran dispersion to produce gamma-dodecalactone
XX and/or gamma-dodecalactone. The microorganism produces lactic acid,
XX propionic acid, gamma-dodecalactone and/or gamma-dodecalactone. The
XX microorganism is especially a novel strain of Corynebacterium (strain NK-
XX 1, FERM BP-6329) with properties defined in the specification. This
XX sequence represents the 16S rRNA gene from the novel Corynebacterium
XX strain. The seasoning liquor is used for preparing a salted rice bran
XX pickle bed which provides pickles
XX
XX Sequence 1460 BP; 320 A; 342 C; 492 G; 305 T; 0 U; 1 Other;
XX
XX Query Match 79.2%; Score 19; DB 3; Length 1460;
XX Best Local Similarity 100.0%; Pred. No. 43;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 CAAGTCGAACGGAAGGCC 19
XX |||||
XX Db 39 CAAGTCGAACGGAAGGCC 57
XX
XX RESULT 77
XX ID AEA22415
XX ID AEA22415 standard; DNA; 1462 BP.
XX
XX AC AEA22415;
XX
XX 25-AUG-2005 (first entry)
XX
XX Mycobacterium szulgai 16S rRNA sequence SEQ ID NO:16.
XX
XX microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
XX
XX Mycobacterium szulgai.
XX
XX US2005130168-A1.
XX
XX 16-JUN-2005.
XX
XX 31-OCT-2003; 2003US-00697802.
XX
XX


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PR 31-OCT-2003; 2003US-00697802.
XX (HANK/) HAN X.
PA (PHAM/) PHAM A S.
XX
XX Han X, Pham AS;
XX WPI; 2005-424597/43.
XX
PT Determining a bacterium species comprises providing oligonucleotide
PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
XX
XX Disclosure; SEQ ID NO 16; 74pp; English.
XX
XX The invention relates to a method (M1) for determining a bacterium
XX species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
XX extracting a genomic nucleotide from the bacterium to provide a
XX nucleotide template; (c) annealing a region of a nucleotide template to a
XX specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
XX complimentary fashion, the primer set designed to provide a product
XX having a predetermined size dictated by a complimentary primer set; (d)
XX amplifying the region of the nucleotide template to produce the product;
XX and (e) determining a species of a bacterium in a nucleotide sequence of
XX the product. Also described is an alternative method (M2) for determining
XX a bacterium species comprising: (a) providing a specimen or a sample
XX having a template; (b) providing a pair of primers selected from: (i) a
XX first forward primer having consecutive bases of an AFB-f comprising any
XX of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
XX or their fragments or variations; (ii) a second forward primer having
XX consecutive bases of 15-21 bp (AEA22489-AEA22516), or their fragments or
XX variations; or (iii) a first forward primer having consecutive bases of
XX an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
XX second reverse primer having consecutive bases of an UB-r of AEA22517-
XX AEA22544 or their fragments or variations; (c) the specimen; and (d)
XX comparing the product from the specimen with a nucleotide sequence from a
XX database to determine the bacterium species present in the specimen. The
XX methods are useful for determining a bacterium species. The present
XX sequence represents a Mycobacterium szulgai 16S rRNA nucleotide sequence,
XX which is used in the exemplification of the present invention.
XX
XX Query Match 79.2%; Score 19; DB 14; Length 1462;
XX Best Local Similarity 100.0%; Pred. No. 43;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 CAAAGTCGACGGAAGGCC 19
Db 21 CAAAGTCGACGGAAGGCC 39

RESULT 78
AEA22414
ID AEA22414 standard; DNA; 1484 BP.
XX
XX AEA22414;
XX
XX 25-AUG-2005 (first entry)
XX
XX Mycobacterium simiae 16S rRNA sequence SEQ ID NO:15.
XX
XX microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
XX
XX Mycobacterium simiae.
XX
XX US2005130168-A1.
XX
XX 16-JUN-2005.
XX

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XX 31-OCT-2003; 2003US-00697802.
XX (HANK/) HAN X.
XX (PHAM/) PHAM A S.
XX
XX Han X, Pham AS;
XX WPI; 2005-424597/43.
XX
PT Determining a bacterium species comprises providing oligonucleotide
PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
XX
XX Disclosure; SEQ ID NO 15; 74pp; English.
XX
XX The invention relates to a method (M1) for determining a bacterium
XX species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
XX extracting a genomic nucleotide from the bacterium to provide a
XX nucleotide template; (c) annealing a region of a nucleotide template to a
XX specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
XX complimentary fashion, the primer set designed to provide a product
XX having a predetermined size dictated by a complimentary primer set; (d)
XX amplifying the region of the nucleotide template to produce the product;
XX and (e) determining a species of a bacterium in a nucleotide sequence of
XX the product. Also described is an alternative method (M2) for determining
XX a bacterium species comprising: (a) providing a specimen or a sample
XX having a template; (b) providing a pair of primers selected from: (i) a
XX first forward primer having consecutive bases of an AFB-f comprising any
XX of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
XX or variations and a first reverse primer having consecutive bases of an
XX AFB-f comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
XX or their fragments or variations; (ii) a second forward primer having
XX consecutive bases of 15-21 bp (AEA22489-AEA22516), or their fragments or
XX variations; or (iii) a first forward primer having consecutive bases of
XX an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
XX second reverse primer having consecutive bases of an UB-r of AEA22517-
XX AEA22544 or their fragments or variations; (c) the specimen; and (d)
XX comparing the product from the specimen with a nucleotide sequence from a
XX database to determine the bacterium species present in the specimen. The
XX methods are useful for determining a bacterium species. The present
XX sequence represents a Mycobacterium szulgai 16S rRNA nucleotide sequence,
XX which is used in the exemplification of the present invention.
XX
XX Query Match 79.2%; Score 19; DB 14; Length 1484;
XX Best Local Similarity 100.0%; Pred. No. 43;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 CAAAGTCGACGGAAGGCC 19
Db 21 CAAAGTCGACGGAAGGCC 39

RESULT 79
ADM92517
ID ADM92517 standard; DNA; 1517 BP.
XX
XX ADM92517;
XX
XX 03-JUN-2004 (first entry)
XX
XX Gordonia genus Actinomycetes DNA sequence SeqID1.
XX
XX Gordonia genus; Actinomycetes; ammonia; nitrous acid oxidation;
XX purifying fresh water; purifying seawater; ayu fish; flatfish; blowfish;
XX gold fish; ds.
XX

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OS Gordonia.
 XX JP2004081109-A.
 XX
 XX 18-MAR-2004.
 XX
 XX 27-AUG-2002; 2002JP-00247166.
 XX
 XX 27-AUG-2002; 2002JP-00247166.
 XX
 XX (KANM-) KANMONKAI KK.
 XX
 XX WPI; 2004-233309/22.
 XX
 XX Gordonia genus Actinomyces for purifying fresh water and seawater useful
 PT in raising ayu fish, flatfish, blowfish and gold fish, has ammonia
 PT utilizing ability and nitrous acid oxidation ability.
 XX
 XX Disclosure; SEQ ID NO 1; 16pp; Japanese.
 XX
 XX This invention relates to a novel Gordonia genus Actinomyces which has
 CC ammonia utilising ability and nitrous acid oxidation ability. The
 CC invention may be useful for purifying fresh water and seawater, of
 CC particular use in raising ayu fish, flatfish, blowfish and gold fish. The
 CC Gordonia genus actinomyces effectively suppresses concentration of
 CC ammonia and nitrous acid in fresh water and seawater, and provides
 CC purified water that is favourable for raising fishes.
 XX
 XX Sequence 1517 BP; 334 A; 363 C; 515 G; 304 T; 0 U; 1 Other;
 SQ

Query Match 79.2%; Score 19; DB 12; Length 1517;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CAAGTCGAACGGAAGGCC 19
 DB 54 CAAGTCGAACGGAAGGCC 72

RESULT 80
 AD071823
 ID AD071823 standard; DNA; 1517 BP.
 XX
 XX AD071823;
 AC
 XX
 XX 15-JUL-2004 (first entry)
 DT
 XX
 XX DNA of RNA isolated from Gordonia sp. Kanmonkai-1129 SeqID 1.
 DE
 XX astaxanthin; canthaxanthine; microbial; livestock fodder; fish breeding;
 KW ds.
 XX
 XX Gordonia sp.
 OS
 XX JP2004089015-A.
 XX
 XX 25-MAR-2004.
 PD
 XX
 XX 29-AUG-2002; 2002JP-00251165.
 PP
 XX
 XX 29-AUG-2002; 2002JP-00251165.
 PR
 XX
 XX (KANM-) KANMONKAI KK.
 PA
 XX
 XX WPI; 2004-253025/24.
 DR
 XX
 XX Production of astaxanthin and canthaxanthine useful as fodder and feed
 PT for livestock, domestic fowl and fish, involves cultivating Actinomyces
 PT belonging to Gordonia genus.
 XX
 XX Disclosure; SEQ ID NO 1; 13pp; Japanese.
 PS
 XX This invention relates to a novel method for producing astaxanthin and

CC canthaxanthine. Specifically, it refers to the cultivation of Actinomyces
 CC microbial cells belonging to the Gordonia genus using a fresh water or
 CC sea water mineral nutrition containing culture medium. The present
 CC invention describes producing astaxanthin and canthaxanthine for use as a
 CC fodder for livestock and domestic fowl, as well as a feed for fish
 CC breeding. The production method uses natural products and is efficient at
 CC a low cost. This polynucleotide sequence is a DNA copy of RNA isolated
 CC from the Gordonia sp. Kanmonkai-1129 microorganism of the invention.
 XX
 XX Sequence 1517 BP; 334 A; 363 C; 515 G; 304 T; 0 U; 1 Other;
 SQ

Query Match 79.2%; Score 19; DB 12; Length 1517;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CAAGTCGAACGGAAGGCC 19
 DB 54 CAAGTCGAACGGAAGGCC 72

RESULT 81
 AEA22407
 ID AEA22407 standard; DNA; 1527 BP.
 XX
 XX AEA22407;
 AC
 XX
 XX 25-AUG-2005 (first entry)
 DT
 XX
 XX Mycobacterium heckeshornense 16S rRNA sequence SEQ ID NO:8.
 DE
 XX microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
 KW
 XX Mycobacterium heckeshornense.
 OS
 XX US2005130168-A1.
 PN
 XX 16-JUN-2005.
 PD
 XX
 XX 31-OCT-2003; 2003US-00697802.
 PF
 XX
 XX 31-OCT-2003; 2003US-00697802.
 PR
 XX (HANX/) HAN X.
 PA (PHAM/) PHAM A S.
 XX
 XX Han X, Pham AS;
 PI
 XX WPI; 2005-424597/43.
 DR
 XX
 XX Determining a bacterium species comprises providing oligonucleotide
 PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
 PT
 XX Disclosure; SEQ ID NO 8; 74pp; English.
 PS
 XX
 XX The invention relates to a method (M1) for determining a bacterium
 CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
 CC extracting a genomic nucleotide from the bacterium to provide a
 CC nucleotide template; (c) annealing a region of a nucleotide template to a
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
 CC complimentary fashion, the primer set designed to provide a product
 CC having a predetermined size dictated by a complementary primer set; (d)
 CC amplifying the region of the nucleotide template to produce the product;
 CC and (e) determining a species of a bacterium in a nucleotide sequence of
 CC the product. Also described is an alternative method (M2) for determining
 CC a bacterium species comprising: (a) providing a specimen or a sample
 CC having a template; (b) providing a pair of primers selected from: (i) a
 CC first forward primer having consecutive bases of an AFB-f comprising any
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
 CC or variations and a first reverse primer having consecutive bases of an
 CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
 CC or their fragments or variations, (ii) a second forward primer having
 CC consecutive bases of an AFB-f comprising any of the 28 sequences of 15-21
 CC bp (AEA22489-AEA22516) or their fragments or variations and a second

CC reverse primer having consecutive bases of an UB-r comprising any of the
CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
CC variations, or (iii) a first forward primer having consecutive bases of
CC an APB-f of AEA22417-AEA22452 or their fragments or variations and a
CC second reverse primer having consecutive bases of an UB-r of AEA22517-
CC AEA22544 or their fragments or variations; (c) the specimen; and (d)
CC comparing the product from the specimen with a nucleotide sequence from a
CC database to determine the bacterium species present in the specimen. The
CC methods are useful for determining a bacterium species. The present
CC sequence represents a Mycobacterium heckeshornense 16S rRNA nucleotide
CC sequence, which is used in the exemplification of the present invention.
XX
SQ Sequence 1527 BP; 325 A; 365 C; 534 G; 303 T; 0 U; 0 Other;

Query Match 79.2%; Score 19; DB 14; Length 1527;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCC 19
Db 45 CAAGTCGAACGGAAGGCC 63
|||||

RESULT 82
AAD11264
ID AAD11264 standard; DNA; 32 BP.

AC AAD11264;

XX 24-SEP-2001 (first entry)

XX Mycobacterium 16S rRNA amplifying primer #8.

XX Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;

KW Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.

XX Mycobacterium sp.

XX W0200144510-A2.

XX 21-JUN-2001.

XX 17-DEC-1999; 99WO-US030346.

XX 17-DEC-1999; 99WO-US030346.

XX (GENP-) GEN-PROBE INC.

XX (INMR) BIOMERIEUX SA.

PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;

DR WPI; 2001-398170/42.

PT Detecting Mycobacterium species, involves in vitro amplification of 16S
PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using
PT specific primers, and detecting the amplified nucleic acid.

XX Claim 1; Page 35; 44pp; English.

XX The invention relates to a method of detecting Mycobacterium species,
CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture
CC comprising a polymerase, and at least two primers, and then detecting the
CC amplified nucleic acid. The method is relatively simple and useful for
CC detecting the presence of various Mycobacterium species in a biological
CC sample, and thus important for diagnosis of infections resulting from
CC them. The method is especially important for screening opportunistic
CC infections caused by M. tuberculosis or a Mycobacterium other than
CC tuberculosis (MOTT). The present sequence is a PCR primer used for
CC amplifying Mycobacterium 16S rRNA

XX Sequence 32 BP; 10 A; 6 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 78.3%; Score 18.8; DB 4; Length 32;
Best Local Similarity 90.9%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCCTTT 22
Db 2 CAAGTCGAACGGAAGGCTCTCT 23
|||||

RESULT 83
ADG88345
ID ADG88345 standard; DNA; 32 BP.

XX ADG88345;

XX 11-MAR-2004 (first entry)

XX Mycobacterium amplifying PCR primer #14.

XX In vitro amplification; PCR; primer; ss.

XX Mycobacterium sp.

XX US2003165824-A1.

XX 04-SEP-2003.

XX 15-DEC-2000; 2000US-00738274.

XX 17-DEC-1999; 99US-0172190P.

XX (BREN/) BRENTANO S T.

XX (JUCK/) JUCKER M T.

XX (DELG/) DELGADO F D.

XX (CLEU/) CLEUZIAZ P.

XX (RODR/) RODRIGUE M.

PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;

DR WPI; 2003-898044/82.

XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX in a biological sample comprises performing in vitro nucleic acid
XX amplification and detection of amplified products.

XX Claim 1; SEQ ID NO 14; 20pp; English.

XX The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample comprises performing an in vitro
CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
CC detecting the amplified Mycobacterium nucleic acid. The present sequence
CC is Mycobacterium amplifying PCR primer.

XX Sequence 32 BP; 10 A; 6 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 78.3%; Score 18.8; DB 10; Length 32;
Best Local Similarity 90.9%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCCTTT 22
Db 2 CAAGTCGAACGGAAGGCTCTCT 23
|||||

RESULT 84
AEA08220
ID AEA08220 standard; DNA; 32 BP.

XX AEA08220;

XX 14-JUL-2005 (first entry)

XX Mycobacterium tuberculosis 16S rRNA amplifying PCR primer, SEQ ID NO: 14.

XX Microorganism detection; DNA amplification; 16s ribosomal RNA; 16s rRNA;
KW PCR; primer; ss.
XX OS
XX Mycobacterium tuberculosis; ATCC 27294.
XX
XX US2005100915-A1.
XX PD
XX 12-MAY-2005.
XX
XX PF 18-SEP-2003; 2003US-00665708.
XX
XX PR 17-DEC-1999; 99US-0172190P.
XX PR 15-DEC-2000; 2000US-00738274.
XX
XX (BREN/) BRENTANO S T.
XX PA (JUCK/) JUCKER M T.
XX PA (DELG/) DELGADO F D.
XX PA (CLEU/) CLEUZAT P.
XX PA (RODR/) RODRIGUE M.
XX
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2005-345392/35.
XX
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX in a biological sample, comprises using in vitro nucleic acid
XX amplification and detection of amplified products.
XX
XX Example 1; SEQ ID NO 14; 21pp; English.
XX
XX The present invention relates to a method of detecting Mycobacterium
XX species present in a biological sample. The method involves using in
XX vitro nucleic acid amplification and detection of amplified products. The
XX invention is useful for diagnostic detection of pathogenic bacteria such
XX as Mycobacterium species. The present sequence is the Mycobacterium
XX tuberculosis (ATCC 27294) 16S ribosomal RNA (16SrRNA) amplifying PCR
XX primer.
XX
XX Sequence 32 BP; 10 A; 6 C; 10 G; 6 T; 0 U; 0 Other;
SQ
Query Match 78.3%; Score 18.8; DB 14; Length 32;
Best Local Similarity 90.9%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1 CAAGTCGAACGGAAGGCTTT 22
Db 2 CAAGTCGAACGGAAGGCTCT 23
RESULT 85
AAX99199
ID AAX99199 standard; DNA; 50 BP.
XX
XX AC AAX99199;
XX
XX 28-SEP-1999 (first entry)
XX
XX M. kansasii 16S rRNA gene fragment.
XX
XX Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA;
KW shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.
KW
XX Mycobacterium kansasii.
OS
XX WO9935284-A1.
XX
XX 15-JUL-1999.
XX
XX 30-DEC-1997; 97WO-BR000087.
XX
XX 30-DEC-1997; 97WO-BR000087.
XX
XX The invention describes a new method for diagnosis, identification and

PA (UYMI-) UNIV FEDERAL MINAS GERAIS.
XX
XX Peregrino Ferreira PC, Geessien Kroon E;
PI Bernardes Margutti Pinto ME, Aleixo AW;
XX
XX WPI; 1999-444201/37.
DR
XX Detection of mycobacteria by shift mobility assay.
XX
XX Disclosure; Fig 7; 20pp; English.
XX
XX The invention describes a new method for diagnosis, identification and
CC characterisation of Mycobacterium tuberculosis or any other mycobacteria
CC by using polymerase chain reaction (PCR) and shift mobility assay (SMA)
CC in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,
CC DNA amplification and shift mobility assay. The method is based on
CC divergence in sequences found in 16S rRNA to identify mycobacteria
CC species, since a remarkable shift of heteroduplex bands are obtained
CC between single stranded and homoduplex bands in UPAGE. The method is
CC fast, simple and can produce information not easily obtained when
CC compared with other detection methods. The sensitivity of other assays
CC suffer due to the tendency of the denatured PCR product strands to
CC reassociate and exclude oligonucleotide probes, and stearic interference
CC between the bound oligonucleotides and the solid support which impede
CC hybridization to nucleic acids in solution. Sequences AAX99193-237
CC represent 16S rRNA gene regions of some mycobacterial species
XX
SQ Sequence 50 BP; 14 A; 12 C; 14 G; 10 T; 0 U; 0 Other;
Query Match 78.3%; Score 18.8; DB 2; Length 50;
Best Local Similarity 90.9%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1 CAAGTCGAACGGAAGGCTTT 22
Db 10 CAAGTCGAACGGAAGGCTCT 31
RESULT 86
AAX99194
ID AAX99194 standard; DNA; 50 BP.
XX
XX AC AAX99194;
XX
XX 28-SEP-1999 (first entry)
XX
XX M. bovis 16S rRNA gene fragment.
XX
XX Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA;
KW shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.
KW
XX Mycobacterium bovis.
OS
XX WO9935284-A1.
XX
XX 15-JUL-1999.
XX
XX 30-DEC-1997; 97WO-BR000087.
XX
XX 30-DEC-1997; 97WO-BR000087.
XX
XX (UYMI-) UNIV FEDERAL MINAS GERAIS.
XX
XX Peregrino Ferreira PC, Geessien Kroon E;
PI Bernardes Margutti Pinto ME, Aleixo AW;
XX
XX WPI; 1999-444201/37.
DR
XX Detection of mycobacteria by shift mobility assay.
XX
XX Disclosure; Fig 7; 20pp; English.
XX
XX The invention describes a new method for diagnosis, identification and

CC characterisation of Mycobacterium tuberculosis or any other mycobacteria
CC by using polymerase chain reaction (PCR) and shift mobility assay (SMA)
CC in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,
CC DNA amplification and Shift mobility assay. The method is based on
CC divergence in sequences found in 16S rRNA to identify mycobacteria
CC species, since a remarkable shift of heteroduplex bands are obtained
CC between single stranded and homoduplex bands in UPAGE. The method is
CC fast, simple and can produce information not easily obtained when
CC compared with other detection methods. The sensitivity of other assays
CC suffer due to the tendency of the denatured PCR product strands to
CC reassociate and exclude oligonucleotide probes, and stearic interference
CC between the bound oligonucleotides and the solid support which impede
CC hybridization to nucleic acids in solution. Sequences AAX99193-237
CC represent 16S rRNA gene regions of some mycobacterial species
XX
SQ Sequence 50 BP; 15 A; 11 C; 14 G; 10 T; 0 U; 0 Other;

Query Match 78.3%; Score 18.8; DB 2; Length 50;
Best Local Similarity 90.9%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTT 22
Db 10 CAAGTCGAACGGAAGGCTCT 31

RESULT 87
AAX99193
ID AAX99193 standard; DNA; 50 BP.
XX AC
XX AAX99193;
XX AC
DT 28-SEP-1999 (first entry)
XX
DE M. tuberculosis 16S rRNA gene fragment.
XX
XX Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA;
XX shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.
XX
OS Mycobacterium tuberculosis.
XX
XX WO9935284-A1.
XX
XX 15-JUL-1999.
XX
XX 30-DEC-1997; 97WO-BR000087.
XX
XX 30-DEC-1997; 97WO-BR000087.
XX
XX (UYMI-) UNIV FEDERAL MINAS GERAIS.
XX
XX Peregrino Ferreira PC, Geesien Kroon B;
XX Bernardes Margutti Pinto ME, Aleixo AW;
XX
XX WPI; 1999-444201/37.
XX
XX Detection of mycobacteria by shift mobility assay.
XX
XX Disclosure; Fig 7; 20pp; English.
XX
XX The invention describes a new method for diagnosis, identification and
CC characterisation of Mycobacterium tuberculosis or any other mycobacteria
CC by using polymerase chain reaction (PCR) and shift mobility assay (SMA)
CC in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,
CC DNA amplification and Shift mobility assay. The method is based on
CC divergence in sequences found in 16S rRNA to identify mycobacteria
CC species, since a remarkable shift of heteroduplex bands are obtained
CC between single stranded and homoduplex bands in UPAGE. The method is
CC fast, simple and can produce information not easily obtained when
CC compared with other detection methods. The sensitivity of other assays
CC suffer due to the tendency of the denatured PCR product strands to
CC reassociate and exclude oligonucleotide probes, and stearic interference
CC between the bound oligonucleotides and the solid support which impede

CC hybridization to nucleic acids in solution. Sequences AAX99193-237
CC represent 16S rRNA gene regions of some mycobacterial species
XX
SQ Sequence 50 BP; 15 A; 11 C; 14 G; 10 T; 0 U; 0 Other;

Query Match 78.3%; Score 18.8; DB 2; Length 50;
Best Local Similarity 90.9%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTT 22
Db 10 CAAGTCGAACGGAAGGCTCT 31

RESULT 88
ADF94055
ID ADF94055 standard; DNA; 50 BP.
XX AC
XX ADF94055;
XX AC
DT 11-MAR-2004 (first entry)
XX
XX Microorganism detection probe, SEQ ID 148.
DE
XX
XX Probe; detection; identification; microorganism; food; drug;
XX 16S rRNA V1 region; 16S rRNA V2 region; 16S rRNA V3 region; ss.
XX
OS Mycobacterium kansasii.
XX
XX WO2003106676-A1.
XX
XX 24-DEC-2003.
XX
XX 16-JUN-2003; 2003WO-JF007620.
XX
XX 14-JUN-2002; 2002JP-00174564.
XX
XX (HISF) HITACHI SOFTWARE ENG CO LTD.
XX (MITS-) MITSUBISHI KAGAKU BIO-CLINICAL LAB INC.
XX
XX Hashida J, Ueno S, Muto I, Naruse K, Tamura M, Matsuda K;
XX Shimadzu M, Kobayashi I, Ishiko H;
XX WPI; 2004-071565/07.
XX
XX 20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a
PT microorganism for specific detection and identification of the
PT microorganism in foods and drug compositions.
XX
XX Claim 2; SEQ ID NO 148; 150pp; Japanese.
XX
XX The present invention relates to probes (ADF93908-ADF94059) for the
CC specific detection and identification of harmful microorganisms in
CC samples of foods and drug compositions. The probe sequences are derived
CC from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism,
CC or its complementary sequence. Detection and identification of the
CC microorganism is by amplification of the complete 16S rRNA gene using
CC primers ADF94060 and ADF94061, labelling the amplification product (a
CC fluorescence label is preferred), and hybridising to the probe or probes
CC of the invention. The probes may be immobilised on a DNA chip. The
CC microorganism is selected from Actinobacillus actinomycetemcomitans,
CC Haemophilus influenzae, Streptococcus pneumoniae, Stenotrophomonas
CC maltophilia, Proteus mirabilis, Streptococcus pneumoniae, Pseudomonas
CC aeruginosa, Citrobacter freundii, Veillonella parvula, Providencia
CC suararii, Neisseria gonorrhoeae, Streptococcus agalactiae, Morganella
CC morganii, Bacteroides fragilis, Staphylococcus hominis, Staphylococcus
CC warneri, Staphylococcus haemolyticus, Enterobacter cloacae, Enterobacter
CC aerogenes, Staphylococcus epidermidis, Streptococcus constellatus,
CC Serratia marcescens, Streptococcus anginosus, Escherichia coli,
CC Klebsiella pneumoniae, Enterococcus faecalis, Enterococcus faecium,
CC Streptococcus sanguis, Streptococcus mitis, Streptococcus intermedius,
CC Listeria monocytogenes, Clostridium perfringens, Corynebacterium
CC aquatium, Streptococcus oralis, Staphylococcus aureus, Neisseria

CC meningitidis, Campylobacter fetus, Enterococcus gallinarum, Enterococcus
 CC casseliflavus, Aeromonas hydrophila, Salmonella paratyphi, Salmonella
 CC typhi, Streptococcus equisimilis, Streptococcus faecalis, Enterococcus faecium,
 CC oxytoca, Staphylococcus saprophyticus, Pasteurella multocida, Bikenella
 CC corrodens, Streptococcus pyogenes, Moraxella catarrhalis, Legionella
 CC pneumophila, Mycobacterium tuberculosis, Mycobacterium avium,
 CC Mycobacterium intracellulare, Mycobacterium kansasii or Mycobacterium
 CC gordonae.
 XX
 SQ Sequence 50 BP; 13 A; 11 C; 18 G; 8 T; 0 U; 0 Other;
 Query Match 78.3%; Score 18.8; DB 12; Length 50;
 Best Local Similarity 90.9%; Pred. No. 37;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CAAGTCGAACGGAAGGCCTT 22
 Db 2 CAAGTCGAACGGAAGGCTCT 23
 RESULT 89
 ADF94047
 ID ADF94047 standard; DNA; 50 BP.
 XX
 AC ADF94047;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Microorganism detection probe, SEQ ID 140.
 XX
 KW Probe; detection; identification; microorganism; food; drug;
 KW 16S rRNA V1 region; 16S rRNA V2 region; 16S rRNA V3 region; ss.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN WO2003106676-A1.
 XX
 PD 24-DEC-2003.
 XX
 PF 16-JUN-2003; 2003WO-JP007620.
 XX
 PR 14-JUN-2002; 2002JP-00174564.
 XX
 PA (HISF) HITACHI SOFTWARE ENG CO LTD.
 PA (MITS-) MITSUBISHI KAGAKU BIO-CLINICAL LAB INC.
 XX
 PI Hashida J, Ueno S, Muto I, Naruse K, Tamura M, Matsuda K;
 PI Shimadzu M, Kobayashi I, Ishiko H;
 XX
 DR WPI; 2004-071565/07.
 XX
 XX 20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a
 PT microorganism for specific detection and identification of the
 PT microorganism in foods and drug compositions.
 XX
 PS Claim 2; SEQ ID NO 140; 150pp; Japanese.
 XX
 XX The present invention relates to probes (ADF93908-ADF94059) for the
 CC specific detection and identification of harmful microorganisms in
 CC samples of foods and drug compositions. The probe sequences are derived
 CC from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism,
 CC or its complementary sequence. Detection and identification of the
 CC microorganism is by amplification of the complete 16S rRNA gene using
 CC primers ADF94060 and ADF94061, labelling the amplification product (a
 CC fluorescence label is preferred), and hybridising to the probe or probes
 CC of the invention. The probes may be immobilised on a DNA chip. The
 CC microorganism is selected from Actinobacillus actinomycetemcomitans,
 CC Acinetobacter calcoaceticus, Haemophilus influenzae, Stenotrophomonas
 CC maltophilia, Proteus mirabilis, Streptococcus pneumoniae, Pseudomonas
 CC aeruginosa, Citrobacter freundii, Veillonella parvula, Providencia
 CC stuartii, Neisseria gonorrhoeae, Streptococcus agalactiae, Morganella
 CC morganii, Bacteroides fragilis, Staphylococcus hominis, Staphylococcus
 CC warneri, Staphylococcus haemolyticus, Enterobacter cloacae, Enterobacter

CC aerogenes, Staphylococcus epidermidis, Streptococcus constellatus,
 CC Serratia marcescens, Streptococcus anginosus, Escherichia coli,
 CC Klebsiella pneumoniae, Enterococcus faecalis, Enterococcus faecium,
 CC Streptococcus sanguis, Streptococcus mitis, Streptococcus intermedius,
 CC Listeria monocytogenes, Clostridium perfringens, Corynebacterium
 CC aquatium, Streptococcus oralis, Staphylococcus aureus, Neisseria
 CC meningitidis, Campylobacter fetus, Enterococcus gallinarum, Enterococcus
 CC casseliflavus, Aeromonas hydrophila, Salmonella paratyphi, Salmonella
 CC typhi, Streptococcus equisimilis, Streptococcus canis, Klebsiella
 CC oxytoca, Staphylococcus saprophyticus, Pasteurella multocida, Bikenella
 CC corrodens, Streptococcus pyogenes, Moraxella catarrhalis, Legionella
 CC pneumophila, Mycobacterium tuberculosis, Mycobacterium avium,
 CC Mycobacterium intracellulare, Mycobacterium kansasii or Mycobacterium
 CC gordonae.
 XX
 SQ Sequence 50 BP; 13 A; 10 C; 18 G; 9 T; 0 U; 0 Other;
 Query Match 78.3%; Score 18.8; DB 12; Length 50;
 Best Local Similarity 90.9%; Pred. No. 37;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CAAGTCGAACGGAAGGCCTT 22
 Db 2 CAAGTCGAACGGAAGGCTCT 23
 RESULT 90
 AAQ94742
 ID AAQ94742 standard; DNA; 203 BP.
 XX
 AC AAQ94742;
 XX
 DT 26-FEB-1996 (first entry)
 XX
 DE DNA fragment of 16S rRNA gene of M. tuberculosis.
 XX
 KW hybridisation; Mycobacteria; acid-fast; 16S rRNA; ribosomal RNA; probe;
 KW detection; identification; ss.
 XX
 OS Mycobacterium tuberculosis.
 XX
 FH Key Location/Qualifiers
 FT misc_binding /tag= a
 FT /note= "probe binding (see AAQ94743)"
 FT misc_binding 41..60
 FT /tag= b
 FT /note= "probe binding (see AAQ94745)"
 FT misc_binding 92..113
 FT /tag= c
 FT /note= "probe binding (see AAQ94746)"
 FT misc_binding 183..203
 FT /tag= d
 FT /note= "probe binding (see AAQ94744)"
 XX
 PN JP07155200-A.
 XX
 PD 20-JUN-1995.
 XX
 PF 10-DEC-1993; 93JP-00310665.
 XX
 PR 10-DEC-1993; 93JP-00310665.
 XX
 PA (TOYM) TOYOCO KK.
 XX
 DR WPI; 1995-250746/33.
 XX
 XX Novel oligo-nucleotide(s) which hybridise with the 16S rRNA gene of
 PT bacteria - used for detection and identification of acid-fast bacteria,
 PT eg. Mycobacterium.
 XX
 PS Claim 1; Page 10; 13pp; Japanese.
 XX

CC AAQ94743-46 are oligonucleotides used for the detection and
 CC identification of acid-fast bacteria (pref. Mycobacterium) by hybridising
 CC with the base sequence of the 16S rRNA gene of the bacteria. The
 CC oligonucleotides can be represented by all or a part of the 203 base
 CC sequence shown here. Mycobacteria are gram-positive bacteria which grow
 CC very slowly and require a lot of time for culture for detection (longer
 CC than one month). The probes provide a simple, rapid and exact method for
 CC detection and identification of the bacteria. The method can be applied
 CC directly to sputum or blood samples and the result obtd. within one day.
 CC AAQ94747-60 are specific probes for different Mycobacteria species
 XX
 SQ Sequence 203 BP; 44 A; 42 C; 72 G; 45 T; 0 U; 0 Other;

Query Match 78.3%; Score 18.8; DB 2; Length 203;
 Best Local Similarity 90.9%; Pred. No. 43;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22
 |||||
 Db 6 CAAGTCGAACGGAAGGCCTCT 27

RESULT 91

AE98764
 ID AEB98764 standard; DNA; 209 BP.

XX AC AEB98764;

XX DT 06-OCT-2005 (first entry)

XX DE Mycobacterium kansasii partial 16S rDNA sequence, SEQ ID 6.

XX KW microorganism detection; mycobacterium infection; antibacterial; ds.

XX OS Mycobacterium kansasii.

XX PN JP2005204582-A.

XX PD 04-AUG-2005.

XX PF 23-JAN-2004; 2004JP-00015195.

XX PR 23-JAN-2004; 2004JP-00015195.

XX PA (ASAH) ASAH KASEI KK.

XX PI Oda N;

XX DR WPI; 2005-526965/54.

XX PT New single-stranded oligonucleotide, useful for amplifying the nucleic
 PT acid of Mycobacterium avium, Mycobacterium intracellulare, and
 PT Mycobacterium kansasii.

XX PS Example 1; SEQ ID NO 6; 14pp; Japanese.

XX CC The invention relates to a novel single-stranded oligonucleotide used in
 CC a detection method of an atypical mycobacteria group. The invention
 CC further includes: amplifying the nucleic acid of Mycobacterium avium by a
 CC loop-mediated isothermal amplification (LAMP) method; amplifying the
 CC nucleic acid of M. intracellulare by a LAMP method; amplifying the
 CC nucleic acid of M. kansasii by a LAMP method; and a kit for detecting the
 CC nucleic acid of M. avium by a LAMP method; detecting the nucleic acid of
 CC M. intracellulare by a LAMP method; or detecting the nucleic acid of M.
 CC kansasii by a LAMP method. The single-stranded oligonucleotide is useful
 CC in medical applications. This polynucleotide represents a Mycobacterium
 CC kansasii partial 16S rDNA sequence amplified by the LAMP method of the
 CC invention.

XX SQ Sequence 209 BP; 47 A; 49 C; 72 G; 41 T; 0 U; 0 Other;

Query Match 78.3%; Score 18.8; DB 14; Length 209;
 Best Local Similarity 90.9%; Pred. No. 44;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22
 |||||
 Db 40 CAAGTCGAACGGAAGGCCTCT 61

RESULT 92

AE98761

ID AEB98761 standard; DNA; 211 BP.

XX AC AEB98761;

XX DT 06-OCT-2005 (first entry)

XX DE Mycobacterium tuberculosis partial 16S rDNA sequence, SEQ ID 3.

XX KW microorganism detection; mycobacterium infection; antibacterial; ds.

XX OS Mycobacterium tuberculosis.

XX PN JP2005204582-A.

XX PD 04-AUG-2005.

XX PF 23-JAN-2004; 2004JP-00015195.

XX PR 23-JAN-2004; 2004JP-00015195.

XX PA (ASAH) ASAH KASEI KK.

XX PI Oda N;

XX DR WPI; 2005-526965/54.

XX PT New single-stranded oligonucleotide, useful for amplifying the nucleic
 PT acid of Mycobacterium avium, Mycobacterium intracellulare, and
 PT Mycobacterium kansasii.

XX PS Example 1; SEQ ID NO 3; 14pp; Japanese.

XX CC The invention relates to a novel single-stranded oligonucleotide used in
 CC a detection method of an atypical mycobacteria group. The invention
 CC further includes: amplifying the nucleic acid of Mycobacterium avium by a
 CC loop-mediated isothermal amplification (LAMP) method; amplifying the
 CC nucleic acid of M. intracellulare by a LAMP method; amplifying the
 CC nucleic acid of M. kansasii by a LAMP method; and a kit for detecting the
 CC nucleic acid of M. avium by a LAMP method; detecting the nucleic acid of
 CC M. intracellulare by a LAMP method; or detecting the nucleic acid of M.
 CC kansasii by a LAMP method. The single-stranded oligonucleotide is useful
 CC in medical applications. This polynucleotide represents a Mycobacterium
 CC tuberculosis partial 16S rDNA sequence amplified by the LAMP method of
 CC the invention.

XX SQ Sequence 211 BP; 48 A; 45 C; 74 G; 44 T; 0 U; 0 Other;

Query Match 78.3%; Score 18.8; DB 14; Length 211;
 Best Local Similarity 90.9%; Pred. No. 44;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22
 |||||
 Db 40 CAAGTCGAACGGAAGGCCTCT 61

RESULT 93

ADV99481

ID ADV99481 standard; DNA; 349 BP.

XX AC ADV99481;

XX DT 24-FEB-2005 (first entry)

XX

DE Meningitis causing bacteria DNA fragment #9.
 KW ds; antibacterial; antiinflammatory; inflammation; neurological disease;
 KW diagnosis; meningitis; biochip.
 XX
 OS Mycobacterium tuberculosis.
 PN CN1420123-A.
 XX
 PD 28-MAY-2003.
 XX
 XX 16-NOV-2001; 2001CN-00137478.
 XX
 PR 16-NOV-2001; 2001CN-00137478.
 XX
 PA (JING-) JINGQI BIO CHEM SCI & TECH CO LTD.
 XX
 PI Xu B, Jiang Y, Huang X;
 XX WPI; 2004-044307/05.
 XX
 DR A nucleic acid sequence useful for diagnosing pathogenic bacteria for
 PT meningitides.
 PT
 XX Disclosure; Page 18; 24pp; Chinese.
 XX
 CC The invention relates to a nucleic acid sequence group for quickly
 CC diagnosing 20 kinds of pathogenic bacteria for meningitis. Its method
 CC includes comparing the DNA sequences of different pathogenic bacteria,
 CC choosing special fragments, finding out common primer, designing 3
 CC specific probe fragments for each pathogenic bacterium, dotting them on
 CC high-molecular polymer to obtain chip, sampling the DNA of pathogenic
 CC bacterium of patient, labeling, amplification, and reacting with said
 CC chip for visually recognizing the pathogenic bacterium. Its advantages are
 CC high speed and low cost. The present sequence represents a meningitis
 CC causing bacteria DNA fragment.
 XX
 SQ Sequence 349 BP; 75 A; 82 C; 125 G; 67 T; 0 U; 0 Other;
 Query Match 78.3%; Score 18.8; DB 13; Length 349;
 Best Local Similarity 90.9%; Pred. No. 46;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 CAAGTCGAACGGAAGGCCTTT 22
 DB 53 CAAGTCGAACGGAAGGCCTCT 74
 RESULT 94
 AAV24293
 ID AAV24293 standard; DNA; 1271 BP.
 XX
 AC AAV24293;
 XX
 DT 14-SEP-1998 (first entry)
 XX
 DE Mycobacterium tuberculosis 16S ribosomal RNA gene.
 KW Antibacterial; antimycobacterial; oligonucleotide; infection; therapy;
 KW ribosome binding site; Shine-Dalgarno; ribosomal RNA; cystic fibrosis;
 KW tuberculosis; ss.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN WO9814567-A2.
 XX
 PD 09-APR-1998.
 XX
 XX 30-SEP-1997; 97WO-US018094.
 XX
 PR 01-OCT-1996; 96US-0027729P.
 XX
 PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.
 XX

Martin WJ, Wisniewski P;
 WPI; 1998-240079/21.
 Use of oligo:nucleotide(s) corresponding to bacterial 16S rRNA - for
 inhibiting bacterial protein expression and treating bacterial infection.
 Claim 26; Page 60-61; 73pp; English.
 This polynucleotide comprises the 16S ribosomal RNA (rRNA) gene of
 Mycobacterium tuberculosis. The invention relates to methods and
 compositions for the treatment of Gram-negative bacterial infections
 employing novel oligonucleotides as antimicrobial agents. The
 oligonucleotides are targeted to the Shine-Dalgarno (SD) region of
 prokaryotes to inhibit bacterial expression and hence inhibit bacterial
 infection. They preferably comprise 10-35 consecutive bases of the 3' end
 of a bacterial 16S rRNA (see also AAV24291-95). An oligonucleotide may
 also include a transport moiety and may have DNA phosphate modifications
 to increase nuclease resistance, or may be formulated in a liposome. A
 claimed method for treating a bacterial infection of a patient comprises
 administering a liposomal formulation of such an oligonucleotide. The
 oligonucleotides can be used particularly for treating bacterial
 infections in pulmonary diseases such as cystic fibrosis or tuberculosis.
 Since the SD sequence is not present in eukaryotic cells, the
 oligonucleotides provide a pathogen-specific therapeutic method
 Sequence 1271 BP; 260 A; 281 C; 430 G; 300 T; 0 U; 0 Other;
 Query Match 78.3%; Score 18.8; DB 2; Length 1271;
 Best Local Similarity 90.9%; Pred. No. 53;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 CAAGTCGAACGGAAGGCCTTT 22
 DB 443 CAAGTCGAACGGAAGGCCTCT 464
 RESULT 95
 AEA22416
 ID AEA22416 standard; DNA; 1416 BP.
 XX
 AC AEA22416;
 XX
 DT 25-AUG-2005 (first entry)
 XX
 DE Mycobacterium tuberculosis 16S rRNA sequence SEQ ID NO:17.
 KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN US2005130168-A1.
 XX
 PD 16-JUN-2005.
 XX
 XX 31-OCT-2003; 2003US-00697802.
 PF
 XX 31-OCT-2003; 2003US-00697802.
 PR
 XX (HANY/) HAN X.
 PA (PHAM/) PHAM A S.
 XX
 PI Han X, Pham AS;
 XX
 XX WPI; 2005-424597/43.
 DR
 XX Determining a bacterium species comprises providing oligonucleotide
 PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
 XX
 XX Disclosure; SEQ ID NO 17; 74pp; English.
 PS
 XX The invention relates to a method (M1) for determining a bacterium
 CC

CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
 CC extracting a genomic nucleotide from the bacterium to provide a
 CC nucleotide template; (c) annealing a region of a nucleotide template to a
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
 CC complementary fashion, the primer set designed to provide a product
 CC having a predetermined size dictated by a complementary primer set; (d)
 CC amplifying the region of the nucleotide template to produce the product;
 CC and (e) determining a species of a bacterium in a nucleotide sequence of
 CC the product. Also described is an alternative method (M2) for determining
 CC a bacterium species comprising: (a) providing a specimen or a sample
 CC having a template; (b) providing a pair of primers selected from: (i) a
 CC first forward primer having consecutive bases of an AFB-f comprising any
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
 CC or variations and a first reverse primer having consecutive bases of an
 CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
 CC or their fragments or variations, (ii) a second forward primer having
 CC reverse primer having consecutive bases of an UB-r comprising any of the
 CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
 CC variations, or (iii) a first forward primer having consecutive bases of
 CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
 CC second reverse primer having consecutive bases of an UB-r of AEA22517-
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)
 CC comparing the product from the specimen with a nucleotide sequence from a
 CC database to determine the bacterium species present in the specimen. The
 CC methods are useful for determining a bacterium species. The present
 CC sequence represents a Mycobacterium tuberculosis 16S rRNA nucleotide
 CC sequence, which is used in the exemplification of the present invention.

XX
 SQ Sequence 1416 BP; 309 A; 341 C; 481 G; 285 T; 0 U; 0 Other;

Query Match 78.3%; Score 18.8; DB 14; Length 1416;
 Best Local Similarity 90.9%; Pred. No. 53;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CAAGTCGAACGGAAGGCCTTT 22
 |||||
 Db 21 CAAGTCGAACGGAAGGCTCT 42

RESULT 96
 AEA22402
 ID AEA22402 standard; DNA; 1421 BP.
 XX
 AC AEA22402;
 XX
 DT 25-AUG-2005 (first entry)
 XX
 DE Mycobacterium bovis 16S rRNA sequence SEQ ID NO:3.
 XX
 KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
 XX
 OS Mycobacterium bovis.
 XX
 PN US2005130168-A1.
 XX
 PD 16-JUN-2005.
 XX
 XX 31-OCT-2003; 2003US-00697802.
 XX
 XX 31-OCT-2003; 2003US-00697802.
 XX
 PA (HANX/) HAN X.
 PA (PHAM/) PHAM A S.
 XX
 PI Han X, Pham AS;
 XX
 DR WPI; 2005-424597/43.
 XX
 XX Determining a bacterium species comprises providing oligonucleotide
 PT primer set comprising SEQ-FOR and SEQ-REV in a complementary fashion.
 PT
 XX

PS Disclosure; SEQ ID NO 3; 74pp; English.
 XX
 CC The invention relates to a method (M1) for determining a bacterium
 CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
 CC extracting a genomic nucleotide from the bacterium to provide a
 CC nucleotide template; (c) annealing a region of a nucleotide template to a
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
 CC complementary fashion, the primer set designed to provide a product
 CC having a predetermined size dictated by a complementary primer set; (d)
 CC amplifying the region of the nucleotide template to produce the product;
 CC and (e) determining a species of a bacterium in a nucleotide sequence of
 CC the product. Also described is an alternative method (M2) for determining
 CC a bacterium species comprising: (a) providing a specimen or a sample
 CC having a template; (b) providing a pair of primers selected from: (i) a
 CC first forward primer having consecutive bases of an AFB-f comprising any
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
 CC or variations and a first reverse primer having consecutive bases of an
 CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
 CC or their fragments or variations, (ii) a second forward primer having
 CC reverse primer having consecutive bases of an UB-r comprising any of the
 CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
 CC variations, or (iii) a first forward primer having consecutive bases of
 CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
 CC second reverse primer having consecutive bases of an UB-r of AEA22517-
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)
 CC comparing the product from the specimen with a nucleotide sequence from a
 CC database to determine the bacterium species present in the specimen. The
 CC methods are useful for determining a bacterium species. The present
 CC sequence represents a Mycobacterium bovis 16S rRNA nucleotide sequence,
 CC which is used in the exemplification of the present invention.

XX
 SQ Sequence 1421 BP; 310 A; 341 C; 484 G; 286 T; 0 U; 0 Other;

Query Match 78.3%; Score 18.8; DB 14; Length 1421;
 Best Local Similarity 90.9%; Pred. No. 53;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CAAGTCGAACGGAAGGCCTTT 22
 |||||
 Db 21 CAAGTCGAACGGAAGGCTCT 42

RESULT 97
 AEA22409
 ID AEA22409 standard; DNA; 1463 BP.
 XX
 AC AEA22409;
 XX
 DT 25-AUG-2005 (first entry)
 XX
 DE Mycobacterium kansasii 16S rRNA sequence SEQ ID NO:10.
 XX
 KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
 XX
 OS Mycobacterium kansasii.
 XX
 PN US2005130168-A1.
 XX
 PD 16-JUN-2005.
 XX
 XX 31-OCT-2003; 2003US-00697802.
 XX
 XX 31-OCT-2003; 2003US-00697802.
 XX
 PA (HANX/) HAN X.
 PA (PHAM/) PHAM A S.
 XX
 PI Han X, Pham AS;
 XX
 XX WPI; 2005-424597/43.
 XX

PT Determining a bacterium species comprises providing oligonucleotide
 PT primer set comprising SEQ-FOR and SEQ-REV in a complementary fashion.
 XX Disclosure; SEQ ID NO 10; 74pp; English.

XX The invention relates to a method (M1) for determining a bacterium
 CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
 CC extracting a genomic nucleotide from the bacterium to provide a
 CC nucleotide template; (c) annealing a region of a nucleotide template to a
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
 CC complementary fashion, the primer set designed to provide a product
 CC having a predetermined size dictated by a complementary primer set; (d)
 CC amplifying the region of the nucleotide template to produce the product;
 CC and (e) determining a species of a bacterium in a nucleotide sequence of
 CC the product. Also described is an alternative method (M2) for determining
 CC a bacterium species comprising: (a) providing a specimen or a sample
 CC having a template; (b) providing a pair of primers selected from: (i) a
 CC first forward primer having consecutive bases of an AFB-f comprising any
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
 CC or variations and a first reverse primer having consecutive bases of an
 CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
 CC or their fragments or variations; (ii) a second forward primer having
 CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
 CC bp (AEA22489-AEA22516) or their fragments or variations and a second
 CC reverse primer having consecutive bases of an UB-r comprising any of the
 CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
 CC variations; or (iii) a first forward primer having consecutive bases of
 CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
 CC second reverse primer having consecutive bases of an UB-r of AEA22517-
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)
 CC comparing the product from the specimen with a nucleotide sequence from a
 CC database to determine the bacterium species present in the specimen. The
 CC methods are useful for determining a bacterium species. The present
 CC sequence represents a Mycobacterium kansasii 16S rRNA nucleotide
 CC sequence, which is used in the exemplification of the present invention.

XX
 SQ Sequence 1463 BP; 318 A; 354 C; 500 G; 291 T; 0 U; 0 Other;

Query Match 78.3%; Score 18.8; DB 14; Length 1463;
 Best Local Similarity 90.9%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTT 22
 |||||
 Db 20 CAAGTCGAACGGAAGGCTCT 41
 |||||

RESULT 98
 AA235571
 ID AA235571 standard; DNA; 1464 BP.
 XX
 AC AA235571;
 XX
 DT 28-JAN-2000 (first entry)
 XX
 DE Mycobacterium tuberculosis 16S rRNA gene.
 XX
 KW 16S rRNA gene; oligonucleotide primer; amplify; genus specific;
 KW diagnosis; Mycobacterium; ss.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN US5985569-A.
 XX
 PD 16-NOV-1999.
 XX
 PF 26-SEP-1997; 97US-00938858.
 XX
 PR 26-SEP-1997; 97US-00938858.
 XX
 PA (BECT) BECTON DICKINSON & CO.
 XX
 PI Foxall PA, Kumar H;

XX WPI; 2000-012779/01.
 DR
 XX Oligonucleotide primers useful for detecting microorganisms of the genus
 PT Mycobacterium.
 XX
 XX Example; Fig 3; 21pp; English.

XX This sequence is the Mycobacterium tuberculosis 16S rRNA gene. This
 CC sequence is used in an example of a method using oligonucleotide primers
 CC for amplification of a genus specific sequence of the 16S rRNA gene. The
 CC method of the invention consists of using primers AA235572-235586 to
 CC amplify M. tuberculosis DNA and then detecting the amplified nucleic
 CC acids. The oligonucleotides are useful for the detection of species of
 CC medical interest of the genus Mycobacterium. In particular the detection
 CC can be used for human and veterinary diagnosis from samples of biological
 CC fluids or tissue e.g. sputum, bronchial washings, gastric washings,
 CC blood, milk, lymph, skin and soft tissues. Identifying the mycobacterium
 CC using the nucleic acid based diagnostic assay reduces the time required
 CC for an accurate diagnosis as cultivation of the organisms is not required

XX
 SQ Sequence 1464 BP; 321 A; 349 C; 502 G; 292 T; 0 U; 0 Other;

Query Match 78.3%; Score 18.8; DB 3; Length 1464;
 Best Local Similarity 90.9%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTT 22
 |||||
 Db 21 CAAGTCGAACGGAAGGCTCT 42
 |||||

RESULT 99
 AAS11027
 ID AAS11027 standard; DNA; 1464 BP.
 XX
 AC AAS11027;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Mycobacterium tuberculosis 16S ribosomal RNA gene.
 XX
 KW Antisense; bacterial 16S ribosomal RNA; rRNA; bacterial infection; human;
 KW food grain supplement; livestock; poultry; therapeutic; ds.
 XX
 OS Mycobacterium tuberculosis.
 XX
 FN WO200142457-A2.
 XX
 PD 14-JUN-2001.
 XX
 PF 29-NOV-2000; 2000WO-US042391.
 XX
 PR 29-NOV-1999; 99US-0168150P.
 XX
 PA (AVIB-) AVI BIOPHARMA INC.
 XX
 PI Iversen PL;
 XX
 DR WPI; 2001-457295/49.
 XX
 XX Antibacterial compound, useful for treating bacterial infections and as
 PT livestock and poultry food supplement, comprises antisense
 PT oligonucleotides complementary to bacterial 16S and 23S rRNA.
 XX
 PS Disclosure; Page; 62pp; English.
 XX
 CC AAS11021-AAS11034 represent the coding sequences of bacterial 16S
 CC ribosomal RNA (rRNA) genes. The sequences were used to design anti-
 CC bacterial compounds comprising substantially uncharged antisense
 CC oligomers containing 8-40 nucleotide subunits, including a targeting
 CC nucleic acid sequence at least 10 nucleotides in length which is
 CC complementary to a bacterial 16S or 23S rRNA nucleic acid sequence. The

CC antisense oligomers are used for treating a bacterial infection in a
 CC human or a mammalian animal produced by Escherichia coli, Salmonella
 CC typhimurium Pseudomonas aeruginosa, Vibrio cholerae, Neisseria
 CC gonorrhoea, Helicobacter pylori, Bartonella henselae, Haemophilus
 CC influenza, Shigella dysenteriae, Staphylococcus aureus, Mycobacterium
 CC tuberculosis, Streptococcus pneumoniae, Treponema pallidum and Chlamydia
 CC trachomatis. The antibacterial compound may be used as a food grain
 CC supplement in livestock and poultry food composition. Note: The present
 CC sequence is not shown in the specification but has been accessed from
 CC GenBank using the appropriate accession number given in the specification
 XX
 SQ Sequence 1464 BP; 321 A; 349 C; 502 G; 292 T; 0 U; 0 Other;

Query Match 78.3%; Score 18.8; DB 5; Length 1464;
 Best Local Similarity 90.9%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CAAGTCGAACGGAAGGCTCTT 22
 |||||
 Db 21 CAAGTCGAACGGAAGGCTCTT 42
 |||||

RESULT 100
 ADR90574
 ID ADR90574 standard; DNA; 1469 BP.

XX AC ADR90574;
 XX DT 02-DEC-2004 (first entry)
 XX DE M kansasii 16S rRNA gene sequence SeqID3.
 XX KW acid-fast bacterium; differentiation; 16S rRNA; M avium complex; MAC;
 XX KW taxonomic-tree analysis; atypical-mycobacteria; gene; ds.
 XX OS Mycobacterium kansasii.
 XX PN JP2004254591-A.
 XX PD 16-SEP-2004.

XX 26-FEB-2003; 2003JP-00048654.

XX 26-FEB-2003; 2003JP-00048654.

XX (MTP) MITSUBISHI YUKA BCL KK.

XX WPI; 2004-664464/65.

XX Differentiating acid-fast bacterium e.g., Mycobacterium avium complex.
 PT useful for detecting mutant of M.avium complex, and for grouping strains
 PT of M.kansasii, involves detecting mutation in 16S rRNA gene of acid-fast
 PT bacterium.

PS Claim 3; SEQ ID NO 3; 23pp; Japanese.

XX This invention relates to a novel method of differentiating acid-fast
 CC bacterium, which involves detecting a mutation in the 16S rRNA gene of
 CC the acid-fast bacterium. The method is useful for differentiating acid-
 CC fast bacterium such as M avium complex (MAC) or M kansasii, in particular
 CC for detecting mutants of MAC, and for grouping strains of M kansasii. The
 CC method is also useful for carrying out taxonomic-tree analysis of
 CC atypical-mycobacteria and enables detection of MAC accurately and
 CC reliably. The present sequence is that of a Mycobacterium 16S rRNA gene
 CC which may be used in the method of the invention.

XX SQ Sequence 1469 BP; 321 A; 355 C; 502 G; 291 T; 0 U; 0 Other;

Query Match 78.3%; Score 18.8; DB 13; Length 1469;
 Best Local Similarity 90.9%; Pred. No. 54;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CAAGTCGAACGGAAGGCTTT 22

Db 31 CAAGTCGAACGGAAGGCTCTT 52
 |||||

Search completed: May 19, 2006, 04:19:09
 Job time : 284.94 secs

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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 02:24:46 ; Search time 1605.11 Seconds
(without alignments)
836.120 Million cell updates/sec

Title: US-10-665-708-22

Perfect score: 24

Sequence: 1 caagtcgaacggaagcccttcg 24

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

EST:*

- 1: gb_est1:*
- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
- 5: gb_est6:*
- 6: gb_hcc:*
- 7: gb_est2:*
- 8: gb_est7:*
- 9: gb_est8:*
- 10: gb_est9:*
- 11: gb_gss1:*
- 12: gb_gss2:*
- 13: gb_gss3:*
- 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20.8	86.7	657	CN208729	TO9226 G
C 2	19.8	82.5	312	BB241896	BB241896 BB241896
C 3	19.8	82.5	356	CD122074	ME1-0071G
4	19.2	80.0	683	DU818647	OG ABA009
5	19	79.2	650	CN204419	TO94810 G
6	19	79.2	874	C0365133	CN201712 RTKL23 G
7	19	79.2	885	CN201712	TO91780 G
C 8	18.8	78.3	903	CC453191	CN201712 ZMMBGC034
9	18.8	78.3	910	DN561788	92178421
10	18.4	76.7	735	CF882404	tric086xm
11	18.4	76.7	788	CB908942	tric086xm
12	18.2	75.8	327	DY091901	010128BEM
13	18.2	75.8	421	BY457153	BY457153
14	18.2	75.8	452	11 AQ627316	CITBI-E1-
15	18.2	75.8	475	9 DN526979	1271790 M
16	18.2	75.8	540	11 AQ549361	RPCI-11-3
17	18.2	75.8	630	4 CB378019	rq06all.Y
18	18.2	75.8	719	5 CK950118	4075090 B
19	18.2	75.8	835	9 DN283722	1183944 M

93	17.8	74.2	912	10	DR815819	DR815819 ZM BPb004	C 166	17.6	73.3	452	8	CR470938	CR470938
94	17.8	74.2	918	2	BG247267	BG247267 602360162	167	17.6	73.3	462	4	BY599571	BY599571
95	17.8	74.2	945	10	DV062398	DV062398 NEONATAL	C 168	17.6	73.3	465	1	AI235898	AI235898
96	17.8	74.2	995	12	CL029182	CL029182 CH216-28U	169	17.6	73.3	466	7	BB833557	BB833557
97	17.8	74.2	1199	9	DR045951	DR045951 FP-11 G06	170	17.6	73.3	468	1	AI372548	AI372548
98	17.6	73.3	193	1	AA204210	AA204210 mu60h11.r	171	17.6	73.3	473	7	BB283360	BB283360
99	17.6	73.3	233	3	BQ322138	BQ322138 PM3-CT081	172	17.6	73.3	478	10	W54232	W54232
100	17.6	73.3	239	1	BY366949	BY366949 AV266949	173	17.6	73.3	485	1	AA832954	AA832954
101	17.6	73.3	242	3	EUB99169	EUB99169 mai46g11.	174	17.6	73.3	490	4	CB434145	CB434145
102	17.6	73.3	247	1	AV314699	AV314699 AV314699	175	17.6	73.3	490	4	CB437180	CB437180
103	17.6	73.3	247	7	BB015618	BB015618 BB015618	C 176	17.6	73.3	490	4	CB438188	CB438188
104	17.6	73.3	256	1	AV264774	AV264774 AV264774	177	17.6	73.3	496	3	BY579473	BY579473
105	17.6	73.3	257	1	AV140604	AV140604 AV140604	178	17.6	73.3	496	4	BY448707	BY448707
106	17.6	73.3	266	1	AV268640	AV268640 AV268640	C 179	17.6	73.3	499	2	BM121724	BM121724
107	17.6	73.3	270	1	AV074580	AV074580 AV074580	C 180	17.6	73.3	502	9	CX598149	CX598149
108	17.6	73.3	277	1	AV105856	AV105856 AV105856	C 181	17.6	73.3	504	7	AW361919	AW361919
109	17.6	73.3	289	1	AV078336	AV078336 AV078336	C 182	17.6	73.3	504	9	DN363141	DN363141
110	17.6	73.3	282	1	AV351905	AV351905 AV351905	C 183	17.6	73.3	505	2	BM232039	BM232039
111	17.6	73.3	290	3	BQ840493	BQ840493 mah68h07.	C 184	17.6	73.3	507	1	AA000190	AA000190
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113	17.6	73.3	293	1	AV144872	AV144872 AV144872	186	17.6	73.3	513	4	CA282280	CA282280
114	17.6	73.3	293	7	BB516293	BB516293 BB516293	C 187	17.6	73.3	517	4	BX283328	BX283328
115	17.6	73.3	295	7	BB028015	BB028015 BB028015	C 188	17.6	73.3	517	5	CK840680	CK840680
116	17.6	73.3	295	7	BB511052	BB511052 BB511052	C 189	17.6	73.3	524	7	AW435159	AW435159
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118	17.6	73.3	300	1	AV147017	AV147017 AV147017	C 191	17.6	73.3	529	1	AI838320	AI838320
119	17.6	73.3	305	1	AV088825	AV088825 AV088825	C 192	17.6	73.3	529	2	BG012793	BG012793
120	17.6	73.3	305	1	AV258314	AV258314 AV258314	C 193	17.6	73.3	532	7	BF017987	BF017987
121	17.6	73.3	305	4	BY432536	BY432536 BY432536	C 194	17.6	73.3	539	1	BE989007	BE989007
122	17.6	73.3	305	8	CK213854	CK213854 MNS20950	C 195	17.6	73.3	539	7	AA542056	AA542056
123	17.6	73.3	311	1	AV310522	AV310522 AV310522	C 196	17.6	73.3	569	5	CK902574	CK902574
124	17.6	73.3	312	7	BB361078	BB361078 BB361078	C 197	17.6	73.3	569	5	CK902574	CK902574
125	17.6	73.3	319	1	AA374314	AA374314 EST86475	C 198	17.6	73.3	574	2	BM383870	BM383870
126	17.6	73.3	324	1	AV216218	AV216218 AV216218	C 199	17.6	73.3	580	5	CF968672	CF968672
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128	17.6	73.3	336	7	AW014662	AW014662 UI-H-BJ0P	C 201	17.6	73.3	601	3	BM735102	BM735102
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135	17.6	73.3	369	4	BY663759	BY663759 BY663759	C 208	17.6	73.3	680	9	DN116917	DN116917
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139	17.6	73.3	390	2	EG146385	EG146385 mad91b09.	C 212	17.6	73.3	713	2	BG478164	BG478164
140	17.6	73.3	392	4	BY625882	BY625882 BY625882	C 213	17.6	73.3	721	7	BE384503	BE384503
141	17.6	73.3	394	4	CA976745	CA976745 AGENCOURT	C 214	17.6	73.3	725	14	CR921765	CR921765
142	17.6	73.3	395	4	BY626963	BY626963 BY626963	C 215	17.6	73.3	744	9	CX605206	CX605206
143	17.6	73.3	398	4	BY434099	BY434099 BY434099	C 216	17.6	73.3	755	4	EX667075	EX667075
144	17.6	73.3	399	3	BQ104075	BQ104075 ggi205.e	C 217	17.6	73.3	755	2	BG764347	BG764347
145	17.6	73.3	400	4	BY420961	BY420961 BY420961	C 218	17.6	73.3	772	3	BQ716203	BQ716203
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147	17.6	73.3	401	8	CO625353	CO625353 BY625353	C 220	17.6	73.3	790	2	BG767613	BG767613
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150	17.6	73.3	409	7	BE173992	BE173992 QV1-H7057	C 223	17.6	73.3	798	2	BI224442	BI224442
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152	17.6	73.3	421	1	AA655960	AA655960 vs49f08.r	C 225	17.6	73.3	806	2	BI157204	BI157204
153	17.6	73.3	421	1	AI043633	AI043633 UI-R-CO-J	C 230	17.6	73.3	813	9	DR105701	DR105701
154	17.6	73.3	425	5	CJ317470	CJ317470 CJ317470	C 231	17.6	73.3	855	3	BU239599	BU239599
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156	17.6	73.3	417	5	CJ210067	CJ210067 UI-M-PA0-	C 228	17.6	73.3	842	2	BI415736	BI415736
157	17.6	73.3	421	1	AA655960	AA655960 vs49f08.r	C 229	17.6	73.3	848	2	BG769503	BG769503
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161	17.6	73.3	434	5	CJ228806	CJ228806 CJ228806	C 233	17.6	73.3	879	3	BU853415	BU853415
162	17.6	73.3	435	3	BU961211	BU961211 AGENCOURT	C 234	17.6	73.3	882	5	CD793487	CD793487
163	17.6	73.3	443	4	BY452887	BY452887 BY452887	C 235	17.6	73.3	907	2	BI526517	BI526517
164	17.6	73.3	444	4	BY432547	BY432547 BY432547	C 237	17.6	73.3	916	5	CD782407	CD782407
165	17.6	73.3	447	4	CA563760	CA563760 K0317F10-	C 238	17.6	73.3	940	12	CC597932	CC597932

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239 17.6 73.3 942 10 DV043460
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260 17.6 73.3 1723 6 CR594015 full-leng
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266 17.6 73.3 1772 6 CR620296 full-leng
267 17.6 73.3 1807 6 CR859228
268 17.6 73.3 1822 6 AI609775 Sus scrof
269 17.6 73.3 1832 6 CR592602 full-leng
270 17.6 73.3 1886 6 CR605577 full-leng
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289 17.2 71.7 396 5 CJ187723 CJ187723
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291 17.2 71.7 425 7 AW634562 BL48b2.w
292 17.2 71.7 446 5 CK234849 SB010090
293 17.2 71.7 472 2 BG019725 dc67ell.x
294 17.2 71.7 510 3 BP741473 BP741473
295 17.2 71.7 532 2 BM261043 dag33b10.
296 17.2 71.7 538 11 AQ519367 HS 5162.A
297 17.2 71.7 570 3 BQ397715 NISC mc01
298 17.2 71.7 573 2 BG021880 df52506.x
299 17.2 71.7 586 11 AQ2677094 RPCI11-72
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ALIGNMENTS

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RESULT 1
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LOCUS Tor9226 Gametophyte rehydration Library Tortula ruralis cDNA, mRNA
DEFINITION sequence.
ACCESSION CN208729
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VERSION CN208729.1 GI:46905460
KEYWORDS EST.
SOURCE Tortula ruralis
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Dicranidae; Pottiaceae; Tortula.
REFERENCE 1 (bases 1 to 657)
AUTHORS Oliver,M.J., Dowd,S.E., Zaragosa,J., Mauget,S.A. and Payton,P.R.
TITLE The rehydration transcriptome of the desiccation-tolerant bryophyte
Tortula ruralis: transcript classification and analysis
JOURNAL BMC Genomics 5 (1), 89 (2004)
PUBMED 15546486
COMMENT Contact: Oliver Melvin J
Plant Stress Lab
USDA-ARS
3810 4th St, Lubbock, TX 79415, USA
Tel: 806-749-5560
Fax: 806-723-5272
Email: moliver@lbk.ars.usda.gov
PCR Primers
FORWARD: GTTTTCCCACTGCTACGAC
BACKWARD: CAGGAACAGCTATGAC.
FEATURES
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Location/Qualifiers
i. .657
/organism="Tortula ruralis"
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Best Local Similarity 91.7%; Pred. No. 55;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAAGCCCTTTCG 24
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Db 240 CAAGTCGAGCGGAAGGCCCTTCG 263
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LOCUS BB241896.1 312 bp mRNA linear EST 06-JUL-2000
DEFINITION BB241896 RIKEN full-length enriched, 3 days neonate thymus Mus
musculus cDNA clone A630089H08 3', mRNA sequence.
ACCESSION BB241896
VERSION BB241896.1 GI:8934642
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 312)
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,
Hiroane,T., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
Iizawa,M., Kadoya,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,
Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,
Okazaki,K., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K.,
Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A.,
Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watabiki,A.,
Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A.,
Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and
Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Konno,H., et al.)
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
```

The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@isc.riken.jp, URL: <http://genome.gsc.riken.jp/>
 Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoaka, S.,
 Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Thermostabilization and thermoactivation of thermolabile enzymes by
 trehalose and its application for the synthesis of full length
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh, M., Kitsuai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,
 Okazaki, Y. and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for
 further details

FEATURES

Location/Qualifiers
 1. 312
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="A630089H08"
 /tissue_types="thymus"
 /dev_stage="3 days neonate"
 /lab_host="DH10B"
 /clone_lib="RIKEN full-length enriched, 3 days neonate
 thymus"
 /notes="Site 1: SalI; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. cDNA went through one round of normalization
 to Rot = 20.0 and subtraction to Rot = 459.0. Second
 strand cDNA was prepared with the primer adapter of
 sequence [5' GAGAGAGAGATTCGAGTTAATAATTAATCCCCCCCCCCC
 3']. cDNA was cleaved with XhoI and BamHI. Vector: a
 modified pBluescript KS(+) after bulk excision from Lambda
 FLC I."

ORIGIN

Query Match 82.5%; Score 19.8; DB 7; Length 312;
 Best Local Similarity 91.3%; Pred. No. 1.5e+02;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 AAGTCGACGGAAGGCTTTC 24
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 Db 73 AAGTCGACGGAAGGCTTACG 51
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RESULT 3
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 LOCUS
 DEFINITION ME1-0071G-A160-E04-1.B ME1-0071 Schistosoma mansoni cDNA clone
 ME1-0071G-A160-E04.B, mRNA sequence.
 CD122074
 ACCESSION CD122074.1 GI:34660126
 VERSION
 KEYWORDS EST.
 SOURCE Schistosoma mansoni
 ORGANISM Schistosoma mansoni
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 Strigoida; Schistosomatoidea; Schistosomatidae; Schistosoma.
 1 (bases 1 to 356)
 Verjovski-Almeida, S., DeMarco, R., Martins, E.A.L., Guimaraes, P.E.M.,

Ojopi, E.P.B., Paquola, A.C.M., Piazza, J.P., Nishiyama, M.Y. Jr.,
 Kitajima, J.P., Adanson, R.B., Ashton, P.D., Bonaldo, M.F.,
 Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho, P.L.,
 Leite, R.A., Malaquias, L.C.C., Marques, R.C.P., Miyasato, P.A.,
 Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A.,
 Sa, R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T.,
 Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M.,
 Stubal, J.C., Leite, L.C.C. and Dias-Neto, E.
 Transcriptome analysis of the acelomate human parasite Schistosoma
 mansoni
 Nat. Genet. 35 (2), 148-157 (2003)
 12973350
 Other ESTs: ME1-0071G-A160-E04-2.B
 Contact: Dr. Sergio Verjovski-Almeida
 Departamento de Bioquímica
 Instituto de Química - Universidade de São Paulo
 Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 São Paulo - SP,
 Brasil
 Tel: +55-11-3091-2173
 Fax: +55-11-3091-2186
 Email: verjo@ig.usp.br
 This sequence was derived from the FAPESP Schistosoma mansoni EST
 Genome Project. All sequences in the project were assembled and
 annotated. This entry and all the assembled sequences can be seen
 in the following URL: <http://bioinfo.ig.usp.br/schisto/>
 Plate: ME1-0071G-A160 row: 4 column: E.

FEATURES

Location/Qualifiers
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 /notes="Vector: pGEM T-easy"

ORIGIN

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 Best Local Similarity 91.3%; Pred. No. 1.5e+02;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CAAGTCGACGGAAGGCTTTC 23
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 Db 294 CAAGTCGACGGAAGGCTTCG 272
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RESULT 4

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 DEFINITION DU818647 683 bp DNA linear GSS 13-DEC-2005
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 3', genomic survey sequence.
 DU818647
 ACCESSION DU818647.1 GI:83614306
 VERSION
 KEYWORDS GSS.
 SOURCE Oryza granulata
 ORGANISM Oryza granulata
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 683)
 SanMiguel, P., Westerman, R., Kim, H., Yu, Y., Wissotski, M., Yost, D.,
 Stum, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C.,
 Hatfield, J., Soderlund, C., Wing, R. and Jackson, S.A.
 OMAP (Oryza Map Alignment Project) - Purdue University
 Unpublished (2004)
 Contact: Scott A. Jackson
 Jackson Laboratory
 Purdue University
 915 W. State St., West Lafayette, IN 47907, USA
 Tel: 7654963621
 Fax: 7654967255

Email: sjackson@purdue.edu
 Basecalling by phred version 0.020425.c. This sequence was derived from the raw sequence read by clipping with lacy version 1.19s. Bases 111-793 of the raw sequence (length 1048) were retained after clipping.
 Plate: 0092 row: L column: 10
 Seq primer: CAC TCA TTA GGC ACC CCA
 Class: BAC ends.

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 /lab_host="DH10B T1 phage resistant"
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 /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN

Query Match 80.0%; Score 19.2; DB 14; Length 683;
 Best Local Similarity 87.5%; Pred. No. 3.2e+02;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTTTCG 24
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 Db 238 CAAGTCGAGCGTAAGGCGCTTCG 261

RESULT 5
 CN204419
 LOCUS
 DEFINITION Tor4810 Gametophyte rehydration Library Tortula ruralis cDNA, mRNA
 650 bp mRNA linear EST 30-APR-2004
 sequence.
 ACCESSION CN204419
 VERSION CN204419.1 GI:46901150
 KEYWORDS EST.
 SOURCE Tortula ruralis
 ORGANISM Tortula ruralis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 Bryopsida; Dicranidae; Pottiales; Pottiaceae; Tortula.
 1 (bases 1 to 650)
 Oliver, M.J., Dowd, S.E., Zaragosa, J., Mauget, S.A. and Payton, P.R.
 The rehydration transcriptome of the desiccation-tolerant bryophyte
 Tortula ruralis: transcript classification and analysis
 BMC Genomics 5 (1), 89 (2004)
 15546486
 Contact: Oliver Melvin J
 Plant Stress Lab
 USDA-ARS
 3810 4th St, Lubbock, TX 79415, USA
 Tel: 806-749-5560
 Fax: 806-723-5272
 Email: moliver@lbrk.ars.usda.gov
 PCR Primers
 FORWARD: GTTTTCCAGTCACGAC
 BACKWARD: CAGGAACAGCTATGAC.

FEATURES
 source
 1..650
 Location/Qualifiers
 /organism="Tortula ruralis"
 /mol_type="mRNA"
 /db_xref="taxon:38588"
 /clone_lib="Gametophyte rehydration Library"
 /note="Organ: Green Gametophyte; Vector: pSport1; Site_1: SalI; Site_2: NotI"

ORIGIN

Query Match 79.2%; Score 19; DB 8; Length 650;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCC 19
 |||||

Db

RESULT 6
 CO365133
 LOCUS

DEFINITION
 RTK1_23_G09_g1_A029 Roots minus potassium pinus taeda cDNA clone
 874 bp mRNA linear EST 29-JUN-2004
 RTK1_23_G09_A029 5', mRNA sequence.
 ACCESSION CO365133
 VERSION CO365133.1 GI:49446450
 KEYWORDS EST.
 SOURCE Pinus taeda (loblolly pine)

ORGANISM
 Pinus taeda

REFERENCE
 AUTHORS Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Zimmermann, C. and Dean, J.F.D.

TITLE

An EST database from potassium-deficient loblolly pine (Pinus taeda) roots

JOURNAL
 COMMENT

Unpublished (2004)
 Other ESTs: RTK1_23_G09_bi_A029
 Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmpratt@uga.edu

RNA prepared and library constructed by W. Walter Lorenz (School of Forest Resources, University of Georgia); plant material prepared by Craig Zimmermann (School of Forest Resources, University of Georgia) using rooted cuttings provided by the Forest Biology Research Cooperative (FBRC) and the CCLONES project at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.

Seq primer: JENREV (CAGGAACAGCTATGACC).

FEATURES

source

1..874
 Location/Qualifiers
 /organism="Pinus taeda"
 /mol_type="mRNA"
 /strain="3 CCLONES"
 /db_xref="taxon:3352"
 /clone="RTK1_23_G09_A029"
 /lab_host="DH10B-T1 phage-resistant E. coli"
 /clone_lib="Roots minus potassium"
 /note="Organ: Root; Vector: pSL1180; Site_1: EcoRI; Site_2: XhoI; The library was prepared from polyA+ RNA from the roots of 1-year-old loblolly pine (Pinus taeda) cuttings that were rooted and then planted in washed sand. The rooted cuttings were maintained for 117 days (July 2003 harvest) under ambient conditions in a local greenhouse. They were kept on a weekly regimen of 0.5x nutrient-complete Hoagland's solution and supplemented with additional water sufficient to maintain a 15% soil moisture content. For twenty-eight days (28 d) prior to harvesting roots for mRNA preparation, the trees received Hoagland's solution lacking potassium (K) to induce a potassium-deficiency. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts can be excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Query Match 79.2%; Score 19; DB 8; Length 874;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCC 19
 |||||

Db

24 CAAGTCGAACGGAAGGCC 42


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RESULT 7
LOCUS CN201712
DEFINITION Tor1780 Gametophyte rehydration Library Tortula ruralis EST 30-APR-2004
sequence.
ACCESSION CN201712
VERSION 1 GI:46898443
KEYWORDS EST.
SOURCE Tortula ruralis
ORGANISM Tortula ruralis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Dicranidae; Pottiales; Pottiaceae; Tortula.
REFERENCE 1 (bases 1 to 885)
AUTHORS Oliver,M.J., Dowd,S.E., Zaragosa,J., Mauget,S.A. and Payton,P.R.
TITLE The rehydration transcriptome of the desiccation-tolerant bryophyte
Tortula ruralis: transcript classification and analysis
JOURNAL BMC Genomics 5 (1), 89 (2004)
PUBMED 15546486
COMMENT Contact: Oliver Melvin J
Plant Stress Lab
USDA-ARS
3810 4th St, Lubbock, TX 79415, USA
Tel: 806-749-5560
Fax: 806-723-5272
Email: moliver@lbrk.ars.usda.gov
PCR Primers
FORWARD: GTTTCCTCCAGTCAGCAG
BACKWARD: CAGGAACAGCTATGAC.
FEATURES
source
Location/Qualifiers
1..885
/organism="Tortula ruralis"
/mol_type="mRNA"
/db_xref="taxon:38588"
/clone_lib="Gametophyte rehydration Library"
/note="Organ: Green Gametophyte; Vector: pSport1; Site_1:
SalI; Site_2: NotI"
ORIGIN
Query Match 79.2%; Score 19; DB 8; Length 885;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAAGTCGAACGGAAGGCC 19
Db 54 CAAGTCGAACGGAAGGCC 72
RESULT 8
LOCUS CC453191/c
DEFINITION ZMMBBC0347A07f ZMMBBC Zea mays genomic clone ZMMBBC0347A07 5',
genomic survey sequence.
ACCESSION CC453191
VERSION CC453191.1 GI:31000754
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 903)
AUTHORS Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
Rouzaud,K., Fuks,G., Yu,Y., Wing,R. and Messing,J.
TITLE Sequencing of the maize genome at PCR (2003b)
JOURNAL Unpublished (2003)
COMMENT Contact: Bharti,A.K.
Dr. Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
```

```
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: T7
Class: BAC ends
High quality sequence start: 398.
Location/Qualifiers
1..903
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBBC0347A07"
/lab_host="E. coli DH10B"
/clone_lib="ZMMBBC"
/note="Vector: pTABAC1.3; Site_1: BamHI; Site_2: BamHI"
FEATURES
source
Location/Qualifiers
1..903
/organism="Strongylocentrotus purpuratus"
/mol_type="mRNA"
/db_xref="taxon:7668"
/clone="PMCSPR2-102A16"
/tissue_type="embryo"
/cell_type="primary mesenchyme cells"
/lab_host="E.coli"
/clone_lib="Sea Urchin primary mesenchyme cell cDNA
library"
/note="Vector: pSPORT1; Site 1: NotI; Site 2: MluI; oligo
dt priming from poly A+ RNA, directionally cloned"
ORIGIN
Query Match 78.3%; Score 18.8; DB 9; Length 910;
Best Local Similarity 90.9%; Pred. No. 5.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CAAGTCGAACGGAAGGCCTTT 22
Db 75 CAAGTTGATCGGAAGGCCTTT 54
RESULT 9
LOCUS DN561788
DEFINITION DN561788.1 GI:61120827
ACCESSION DN561788
VERSION DN561788.1
KEYWORDS EST.
SOURCE Strongylocentrotus purpuratus
ORGANISM Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoidea;
Strongylocentrotidae; Strongylocentrotus.
REFERENCE 1 (bases 1 to 910)
AUTHORS Zhu,X., Mahairas,G., Illies,M.R., Cameron,R.A., Davidson,E.H. and
Ettensohn,C.A.
TITLE A large scale analysis of mRNAs expressed by primary mesenchyme
cells of the sea urchin embryo
JOURNAL Development 128 (13), 2615-2627 (2001)
PUBMED 11493577
COMMENT Contact: Erica Sodergren
Human Genome Sequencing Center
Baylor College of Medicine
One Baylor Plaza, Houston, TX 77030, USA
Tel: 713-798-7676
Fax: 713-798-6977
Email: ericas@bcm.tmc.edu
NCBI Trace Archive: 48682679
Insert Length: 1750 Std Error: 0.25
Plate: 102 row: A column: 16.
FEATURES
source
Location/Qualifiers
1..910
/organism="Strongylocentrotus purpuratus"
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/clone="PMCSPR2-102A16"
/tissue_type="embryo"
/cell_type="primary mesenchyme cells"
/lab_host="E.coli"
/clone_lib="Sea Urchin primary mesenchyme cell cDNA
library"
/note="Vector: pSPORT1; Site 1: NotI; Site 2: MluI; oligo
dt priming from poly A+ RNA, directionally cloned"
ORIGIN
Query Match 78.3%; Score 18.8; DB 9; Length 910;
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Best Local Similarity 90.9%; Pred. No. 5.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 AGTCGAACGGAAGGCGCTTTCG 24
|||
Db 790 AGGCGACGGAAGGCGCTTTCG 811

RESULT 10
CF882404 735 bp mRNA linear EST 31-OCT-2003
LOCUS
DEFINITION trico86xm16.b1 T.reesei mycelial culture, Version 6 October 2003
ACCESSION Hypocrea jecorina cDNA clone trico86xm16, mRNA sequence.
VERSION CF882404
KEYWORDS EST.
SOURCE CF882404.1 GI:38137086
ORGANISM Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
REFERENCE 1 (bases 1 to 735)
AUTHORS Diener,S.E., Dunn-Coleman,N., Foreman,P., Houfek,T.D.,
Teunissen,P.J.M., van Solingen,P., Dankmeyer,L., Mitchell,T.K.,
Ward,M. and Dean,R.A.
TITLE Characterization of the protein processing and secretion pathways
in a comprehensive set of expressed sequence tags from Trichoderma
reesei
JOURNAL FEMS Microbiol. Lett. 230 (2), 275-282 (2004)
PUBMED 14757250
COMMENT Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph.dean@ncsu.edu
Seq primer: LT-F1 primer.
Location/Qualifiers
1. 735
/organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
/clone="trico86xm16"
/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 6 October
2003"
/note="Vector: PREP3Y; Site_1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."

ORIGIN
Query Match 76.7%; Score 18.4; DB 5; Length 735;
Best Local Similarity 95.0%; Pred. No. 7.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 GTCGAACGGAAGGCGCTTTC 23
|||
Db 58 GTCGACGGAAGGCGCTTTC 77

RESULT 11
CB908942 788 bp mRNA linear EST 02-JUL-2003
LOCUS
DEFINITION trico86xm16 T.reesei mycelial culture, Version 3 april Hypocrea
jecorina cDNA clone trico86xm16, mRNA sequence.
ACCESSION CB908942
VERSION CB908942.1 GI:30123600
KEYWORDS EST.
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

```

```

REFERENCE 1 (bases 1 to 788)
AUTHORS Foreman,P.K., Brown,D.E., Dankmeyer,L., Dean,R., Diener,S.,
Dunn-Coleman,N.S., Goedegebuur,F., Houfek,T.D., England,G.J.,
Kelley,A.S., Meerman,H.J., Mitchell,T., Mitchinson,C.,
Olivares,H.A., Teunissen,P.J., Yao,J. and Ward,M.
TITLE Transcriptional regulation of biomass-degrading enzymes in the
filamentous fungus Trichoderma reesei
JOURNAL J. Biol. Chem. 278 (34), 31988-31997 (2003)
PUBMED 12788920
COMMENT Contact: Pamela K. Foreman
Genencor Intl.
925 Page Mill Road, Palo Alto, CA 94304, USA
Tel: (650) 846-7635
Fax: (650) 621-7817
Email: Pforeman@genencor.com
Seq primer: LT-F1 primer.
Location/Qualifiers
1. 788
/organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
/clone="trico86xm16"
/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 3 april"
/note="Vector: PREP3Y; Site 1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."

ORIGIN
Query Match 76.7%; Score 18.4; DB 4; Length 788;
Best Local Similarity 95.0%; Pred. No. 8e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 GTCGAACGGAAGGCGCTTTC 23
|||
Db 111 GTCGACGGAAGGCGCTTTC 130

RESULT 12
DY091901 327 bp mRNA linear EST 31-JAN-2006
LOCUS
DEFINITION 010128BENMN062222HT BENM Bos taurus CDNA, mRNA sequence.
ACCESSION DY091901
VERSION DY091901.1 GI:86238488
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 327)
AUTHORS McCulloch,A., Wilson,T., Molenaar,A., Grigor,M., Davis,S.,
Glenn,M., Havukkala,I., Watson,J., Crawford,A., Wheeler,T.,
Hagemann,L., Lee,R., Hein,W., Johnstone,P., Magbool,N., McMahon,C.,
McCracken,J., Stelwagen,K., Farr,V., Singh,K., Whitley,J.,
Nicholas,K., Savin,K., Mather,A., McPartlan,H., Whitley,J.,
Wells,M., Bowman,P., Goddard,M., Langford,C., McEwan,J. and
Atkinson,P.
TITLE AgResearch, Genesis and Primary Industry Victoria Bovine EST
project
JOURNAL Unpublished (2006)
COMMENT Contact: Magbool N
AgResearch Ltd.
Invermay Agricultural Centre, Puddle Alley, Private Bag 50034,
Mosgiel, New Zealand
Email: nauman.magbool@agresearch.co.nz.
Location/Qualifiers
1. 327
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="Life Tech Normalised library"

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/clone lib="BEMN"
/note="Vector: pCMV-Sport6; Life Tech Normalised library"

ORIGIN
Query Match      75.8%; Score 18.2; DB 10; Length 327;
Best Local Similarity 87.0%; Pred. No. 9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCCTTTC 23
    ||||| ||||| ||||| ||||| |||||
Db 106 CAAGTCGAACGGAAGGACTGTC 128

RESULT 13
BY457153
LOCUS
DEFINITION
BY457153 RIKEN full-length enriched, 15 days pregnant adult female
amion Mus musculus cDNA clone K630096B19 3', mRNA sequence.
BY457153
VERSION
BY457153.1 GI:26755296
EST.
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
1 (bases 1 to 421)
Okazaki, I., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikado, I., Osato, N., Saito, R., Suzuki, H., Yamana, K.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusica, V.,
Chotia, C., Corbani, L. E., Cousins, S., Dalia, E., Dragan, T. A.,
Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierzki, R. M., King, B. L., Konagaya, A.,
Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W. J., Perte, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,
Vizarado, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
NATURE 420, 563-573 (2002)
12466851
JOURNAL
PUBMED
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Wataniki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
Location/Qualifiers
1. 421
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="K630096B19"
/sex="female"
/tissue_type="amion"
/dev_stage="15 days pregnant adult"
/clone_lib="RIKEN full-length enriched, 15 days pregnant
adult female amion"

FEATURES
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="K630096B19"
/sex="female"
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/clone_lib="RIKEN full-length enriched, 15 days pregnant
adult female amion"

ORIGIN
Query Match      75.8%; Score 18.2; DB 4; Length 421;
Best Local Similarity 87.0%; Pred. No. 9.2e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCCTTTC 23
    ||||| ||||| ||||| ||||| |||||
Db 272 CAAGTCGAGCAGAAAGCTCTTC 294

RESULT 14
AQ627316
LOCUS
DEFINITION
CITBI-E1-2650113.TR CITBI-E1 Homo sapiens genomic clone 2650113,
genomic survey sequence.
ACCESSION
AQ627316 GI:5089708
VERSION
AQ627316.1
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 452)
Zhao, S., Adams, M. D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and
Venter, J. C.
Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
Map Building
Unpublished (1997)
Other GSSs: CITBI-E1-2650113.TF
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers

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1..452
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="2650113"
/sex="male"
/cell_type="sperm"
/clone_lib="CHBI-E1"
/note="Vector: pBelOAc11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"

ORIGIN

Query Match      75.8%; Score 18.2; DB 11; Length 452;
Best Local Similarity 87.0%; Pred. No. 9.3e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTC 23
|||||
Db 192 CAAGTCGACCTGAAGGCGCTTTC 214
|||||

RESULT 15
DN526979      DN526979      475 bp      mRNA      linear      EST 11-MAR-2005
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Bos taurus
Bos taurus (cattle)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE
1 (bases 1 to 475)
Smith,T.P.L., Roberts,A.J., Echtenkamp,S.E., Chitko-McKown,C.G.,
Wray,J.E. and Keefe,J.W.,
A second set of bovine ESTs from pooled-tissue normalized libraries
Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: RLK8046 row: I column: 10
Seq primer: GTAATACGACTCACTATAGGG.

FEATURES
source
Location/Qualifiers
1..475
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DHI08"
/clone_lib="MARC 7BOV"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
Library made with RNA pooled from multiple tissues
including ovary, hindbrain, uterus, and day-30 whole
embryos."

ORIGIN

Query Match      75.8%; Score 18.2; DB 9; Length 475;
Best Local Similarity 87.0%; Pred. No. 9.4e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTC 23
|||||
Db 163 CAAGTCGAACTGAAGGACTGTC 185
|||||

RESULT 16
source
1..540
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7642248"
/db_xref="taxon:9606"
/clone="RPCI-11-371H1"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPC11 Human Male BAC Library"

ORIGIN

Query Match      75.8%; Score 18.2; DB 11; Length 540;
Best Local Similarity 87.0%; Pred. No. 9.5e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTC 23
|||||
Db 172 CAAGTCGACCTGAAGGCGCTTTC 194
|||||

RESULT 17
CB378019
LOCUS
DEFINITION
CB378019      630 bp      mRNA      linear      EST 16-MAY-2003
rQ06all.y1 Heterodera glycines J3 Heterodera glycines cDNA 5'
similar to WP:CE23823 H24K24.4 RNA-binding protein i, mRNA
sequence.
CB378019
CB378019.1 GI:29127315
EST.
Heterodera glycines
Heterodera glycines
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.
1 (bases 1 to 630)
McCartner,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
Wyllie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,

```



```

/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 7BOV"
/notes="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including ovary, hindbrain, uterus, and day-30 whole
embryos."

ORIGIN
Query Match      75.8%; Score 18.2; DB 9; Length 835;
Best Local Similarity 87.0%; Pred. No. 1e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTC 23
    |||||
Db 552 CAAGTCGAACGGAAGGACTGTC 574
    |||||

RESULT 20
CR077081
LOCUS      835 bp      DNA      linear      GSS 05-JUL-2004
DEFINITION Reverse strand read from insert in 3'HPRT insertion targeting and
            chromosome engineering clone MHP284c21, genomic survey sequence.
ACCESSION  CR077081
VERSION     CR077081.1 GI:49810669
KEYWORDS   GSS; genome survey sequence; MICER.
SOURCE     Mus musculus (house mouse)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 835)
AUTHORS   Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
            Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
            Rogers,J. and Bradley,A.
TITLE     Direct Submission
JOURNAL   Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. http://www.sanger.ac.uk/MICER
FEATURES   Location/Qualifiers
            source
            1..835
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /db_xref="taxon:10090"
            /clone_lib="MHP284c21"
            /clone_lib="MHPp"

ORIGIN
Query Match      75.8%; Score 18.2; DB 14; Length 835;
Best Local Similarity 87.0%; Pred. No. 1e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 519 AATTAGAAGGAAGGCGCTTTCG 541
    |||||

RESULT 21
DN282351/c
LOCUS      843 bp      mRNA      linear      EST 02-MAR-2005
DEFINITION DN282351 MARC 7BOV Bos taurus CDNA 3', mRNA sequence.
ACCESSION  DN282351
VERSION     DN282351.1 GI:60450961
KEYWORDS   EST.
SOURCE     Bos taurus (cattle)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE  1 (bases 1 to 843)
AUTHORS   Smith,T.P.L., Roberts,A.J., Echtenkamp,S.E., Chitko-McKown,C.G.,
            Wray,J.E. and Keale,J.W.
TITLE     A second set of bovine ESTs from pooled-tissue normalized libraries
            Unpublished (2003)

```

COMMENT

Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smitht@mail.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
 cross_match v0.990329.

Plate: RLK8014 row: J column: 12

Seq primer: TAGAAGGCACAGTCGAGG.

FEATURES

Location/Qualifiers

1..843

/organism="Bos taurus"

/mol_type="mRNA"

/db_xref="taxon:9913"

/tissue_type="pooled"

/lab_host="DH10B"

/clone_lib="MARC 7BOV"

/notes="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;

Library made with RNA pooled from multiple tissues

including ovary, hindbrain, uterus, and day-30 whole

embryos."

ORIGIN

Query Match 75.8%; Score 18.2; DB 9; Length 843;
 Best Local Similarity 87.0%; Pred. No. 1e+03;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTC 23

|||||

Db 284 CAAGTCGAACGGAAGGACTGTC 262

RESULT 22

DU746898/c

LOCUS

DEFINITION

906 bp DNA linear GSS 27-JAN-2006
 ANSC3551.b2 HF10_10-07-02 uncultured marine microorganism
 HF10_10-07-02 genomic clone HF0010_049G12, genomic survey sequence.

ACCESSION DU746898

VERSION DU746898.1 GI:85756734

KEYWORDS GSS.

SOURCE uncultured marine microorganism HF10_10-07-02

uncultured marine microorganism HF10_10-07-02

unclassified sequences; environmental samples.

REFERENCE 1 (bases 1 to 906)

AUTHORS DeLong,E.F., Preston,C.M., Mincer,T., Rich,V., Hallam,S.J.,

Frigaard,N.U., Martinez,A., Sullivan,M., Edwards,R., Chisholm,S.W.

and Karl,D.M.

Comparative genomics reveals ecological trends in stratified

microbial communities in the ocean's interior

Science (2006) In press

Contact: Susan Lucas, Alex Copeland, Sam Pitluck, Alla Lapidus,

Kerrie Barry, Rijana Glavinadelrio, David Bruce, Paul Richardson

and Edward DeLong

US DOE Joint Genome Institute

US DOE Joint Genome Institute

2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA

Tel: 617-253-5271

Fax: 617-253-2679

Email: PMRichardson@lbl.gov; delong@mit.edu

North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid

DNA library prepared from marine picoplankton in the less than 1.6

um, greater than 0.22 um fraction. Sample Date: 10/7/2002

Coordinates: 22.45 N, 158 W Depth: 10 m Temperature: 26.4 C

Salinity 35.08 psu Oxygen: 204.6 umol/kg

Class: fosmid ends.

Location/Qualifiers

1..906

/organism="uncultured marine microorganism HF10_10-07-02"

/mol_type="genomic DNA"

/db_xref="taxon:361145"

/clone="HF0010_049G12"

FEATURES

source

/cell type="marine picoplankton, less than 1.8 um, greater than 0.22 um fraction"
/clone_lib="HF10.10-07-02"
/notes="vector: pC1FOS; North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid DNA library prepared from marine picoplankton in the less than 1.6 um, greater than 0.22 um fraction. Picoplankton collected at 10 m depth on 10/7/2002. Coordinates: 22.45 N, 158 W. Sample Date: 10/7/2002 Coordinates: 22.45 N, 158 W Depth: 10 m Temperature: 26.4 C Salinity 35.08 psu Oxygen: 204.6 umol/kg"

ORIGIN
Query Match 75.8%; Score 18.2; DB 14; Length 906;
Best Local Similarity 87.0%; Pred. No. 1e+03; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCTTTTCG 24
||||||| | |||||
Db 421 AAGTCGAACGACGAGGCTTTTCG 399
||||||| | |||||

RESULT 23
DQ213078
LOCUS
DEFINITION
Taeniopygia guttata clone 0058P0007D03 gephyrin-like mRNA, complete sequence.
ACCESSION
DQ213078
VERSION
DQ213078.1 GI:76152437
KEYWORDS
HTC.
SOURCE
Taeniopygia guttata (Poephila guttata)
ORGANISM
Taeniopygia guttata
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Passeriformes; Estrildidae; Estrildinae; Taeniopygia.
REFERENCE
1 (bases 1 to 1052)
Wada,K., Howard,J.T., McConnell,P., Lints,T., Rivas,R.V., Whitney,O.B., Horita,H., Patterson,M., White,S., Zhao,S., Sakaguchi,H., Hagiwara,M., Toshiyuki,S., Hirozane-Kishikawa,T., Skene,P., Hayashizaki,Y., Carninci,P. and Jarvis,E.D.
A molecular neuroethological approach for identifying and characterizing a melody of behaviorally regulated genes
Unpublished
JOURNAL
2 (bases 1 to 1052)
Wada,K. and Jarvis,E.D.
AUTHORS
Direct Submission
TITLE
Submitted (21-SEP-2005) Neurobiology, Duke University Medical Center, Box 3209, Durham, NC 27710, USA
JOURNAL
Center, Box 3209, Durham, NC 27710, USA
FEATURES
source
1..1052
/organism="Taeniopygia guttata"
/mol_type="mRNA"
/db_xref="taxon:99729"
/clone="0058P0007D03"
/sex="female"
/tissue types="whole brain"
/clone_lib="normalized (50 mix pooled juveniles + adults)"
/dev_stage="PH88"
/notes="common: zebra finch; authority: Taeniopygia guttata Vieillot (1817); synonym: Poephila guttata"
misc_feature
1..1052
/note="similar to gephyrin"

ORIGIN
Query Match 75.8%; Score 18.2; DB 6; Length 1052;
Best Local Similarity 87.0%; Pred. No. 1e+03; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTTTC 23
||||||| | |||||
Db 193 CAAGTCGAACGACGAGGCTTTTC 215
||||||| | |||||

RESULT 24
CL645653/c
LOCUS
DEFINITION
CH213-99C02.SP6 CH213 Gasterosteus aculeatus genomic clone CH213-99C02 3', genomic survey sequence.
ACCESSION
CL645653
VERSION
CL645653.1 GI:49665077
KEYWORDS
GSS.
SOURCE
Gasterosteus aculeatus (three spined stickleback)
ORGANISM
Gasterosteus aculeatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes; Gasterosteidae; Gasterosteus.
REFERENCE
1 (bases 1 to 1242)
Kingsley,D., Grimwood,J., Dickson,M., Schmutz,J. and Myers,R.M.
Expressed sequence tags from Gasterosteus aculeatus
Unpublished (2004)
JOURNAL
Contact: Grimwood, Jane
Stanford Human Genome Center
Stanford University School of Medicine
975 S California Avenue, Palo Alto, CA 94304, USA
Tel: 650 320 5917
Fax: 650 320 5801
Email: jane@hgsc.stanford.edu
Plasmids: 99
Class: BAC ends
High quality sequence start: 18
High quality sequence stop: 933.
Location/Qualifiers
1..1242
/organism="Gasterosteus aculeatus"
/mol_type="genomic DNA"
/strain="Salmon River"
/db_xref="taxon:69293"
/clone="CH213-99C02"
/sex="Mixed"
/cell type="Blood"
/clone_lib="CH213"
/notes="Vector: pIABAC2.1; Site_1: EcoRI; The sequence of the clone was established as a mapping and sequencing collaboration at the Stanford Genome Evolution Center, funded by the NIH Centers of Excellence in Genomic Science (CEGS) initiative (<http://cegs.stanford.edu>). The clone was isolated from the BAC library CHORI-213 built by Pter devong in collaboration with the Stanford Genome Evolution Center (<http://www.chori.org/bacpac/>). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering_information.html)."

FEATURES
source
1..1242
/organism="Gasterosteus aculeatus"
/mol_type="genomic DNA"
/strain="Salmon River"
/db_xref="taxon:69293"
/clone="CH213-99C02"
/sex="Mixed"
/cell type="Blood"
/clone_lib="CH213"
/notes="Vector: pIABAC2.1; Site_1: EcoRI; The sequence of the clone was established as a mapping and sequencing collaboration at the Stanford Genome Evolution Center, funded by the NIH Centers of Excellence in Genomic Science (CEGS) initiative (<http://cegs.stanford.edu>). The clone was isolated from the BAC library CHORI-213 built by Pter devong in collaboration with the Stanford Genome Evolution Center (<http://www.chori.org/bacpac/>). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering_information.html)."

ORIGIN
Query Match 75.8%; Score 18.2; DB 13; Length 1242;
Best Local Similarity 87.0%; Pred. No. 1e+03; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCTTTTCG 24
||||||| | |||||
Db 517 AAGTCGAACGGAAGGCTTTTCG 495
||||||| | |||||

RESULT 25
BX342644
LOCUS
DEFINITION
BX342644 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED Homo sapiens cDNA clone CS0DL004YB13 5-PRIME, mRNA sequence.
ACCESSION
BX342644
VERSION
BX342644.2 GI:46275066
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE
AUTHORS      1 (bases 1 to 994)
TITLE        Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
JOURNAL      Full-length cDNA libraries and normalization
COMMENT      Unpublished (2001)
              On May 2, 2003 this sequence version replaced gi:30342105.
              Contact: Genoscope
              Genoscope - Centre National de Sequencage
              2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
              Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
              1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
              end enriched, double-strand cDNA was digested with Not I and cloned
              into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
              was normalized. Library was constructed by Life technologies, a
              division of Invitrogen. This sequence belongs to sequence cluster
              6269.r
              For more information about this cluster, see
              http://www.genoscope.cns.fr/cdna?s=CS0DL004CA07QPl&c=6269.r.

FEATURES
source
1..994
    Location/Qualifiers
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="CS0DL004VB13"
        /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
        /cell_lines="RAMOS CELL LINE"
        /note="1st strand cDNA was primed with a NotI-oligo(dT)
        primer. Five prime end enriched, double-strand cDNA was
        digested with Not I and cloned into the Not I and EcoR V
        sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match      75.0%; Score 18; DB 4; Length 994;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
    |||:|||||:|||||:|||||
Db 928 CAARTCGAATTAAAGGMCCTGCG 951

RESULT 26
W10183
LOCUS      W10183
DEFINITION ma3f03.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone
IMAGE:313469 5', mRNA sequence.
W10183
VERSION    W10183.1 GI:1284500
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 223)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI: 204085

REFERENCE
AUTHORS      1 (bases 1 to 994)
TITLE        Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
JOURNAL      Full-length cDNA libraries and normalization
COMMENT      Unpublished (2001)
              On May 2, 2003 this sequence version replaced gi:30342105.
              Contact: Genoscope
              Genoscope - Centre National de Sequencage
              2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
              Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
              1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
              end enriched, double-strand cDNA was digested with Not I and cloned
              into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
              was normalized. Library was constructed by Life technologies, a
              division of Invitrogen. This sequence belongs to sequence cluster
              6269.r
              For more information about this cluster, see
              http://www.genoscope.cns.fr/cdna?s=CS0DL004CA07QPl&c=6269.r.

FEATURES
source
1..994
    Location/Qualifiers
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="CS0DL004VB13"
        /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
        /cell_lines="RAMOS CELL LINE"
        /note="1st strand cDNA was primed with a NotI-oligo(dT)
        primer. Five prime end enriched, double-strand cDNA was
        digested with Not I and cloned into the Not I and EcoR V
        sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match      75.0%; Score 18; DB 4; Length 994;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
    |||:|||||:|||||:|||||
Db 928 CAARTCGAATTAAAGGMCCTGCG 951

RESULT 26
W10183
LOCUS      W10183
DEFINITION ma3f03.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone
IMAGE:313469 5', mRNA sequence.
W10183
VERSION    W10183.1 GI:1284500
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 223)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI: 204085

REFERENCE
AUTHORS      1 (bases 1 to 994)
TITLE        Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
JOURNAL      Full-length cDNA libraries and normalization
COMMENT      Unpublished (2001)
              On May 2, 2003 this sequence version replaced gi:30342105.
              Contact: Genoscope
              Genoscope - Centre National de Sequencage
              2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
              Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
              1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
              end enriched, double-strand cDNA was digested with Not I and cloned
              into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
              was normalized. Library was constructed by Life technologies, a
              division of Invitrogen. This sequence belongs to sequence cluster
              6269.r
              For more information about this cluster, see
              http://www.genoscope.cns.fr/cdna?s=CS0DL004CA07QPl&c=6269.r.

FEATURES
source
1..994
    Location/Qualifiers
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="CS0DL004VB13"
        /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
        /cell_lines="RAMOS CELL LINE"
        /note="1st strand cDNA was primed with a NotI-oligo(dT)
        primer. Five prime end enriched, double-strand cDNA was
        digested with Not I and cloned into the Not I and EcoR V
        sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match      75.0%; Score 18; DB 4; Length 994;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
    |||:|||||:|||||:|||||
Db 928 CAARTCGAATTAAAGGMCCTGCG 951

RESULT 27
AA815626
LOCUS      AA815626
DEFINITION vt03c06.r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone
IMAGE:1161994 5', mRNA sequence.
AA815626
VERSION    AA815626.1 GI:2885222
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 273)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI: 627906

REFERENCE
AUTHORS      1 (bases 1 to 273)
TITLE        The WashU-HHMI Mouse EST Project
JOURNAL      Unpublished (1996)
COMMENT      Contact: Marra M/Mouse EST Project
              WashU-HHMI Mouse EST Project
              Washington University School of MedicineP
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: mouseest@watson.wustl.edu
              This clone is available royalty-free through LLNL ; contact the
              IMAGE Consortium (info@image.llnl.gov) for further information.
              MGI: 627906

Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 259.
Location/Qualifiers
1..273
    /organism="Mus musculus"
    /mol_type="mRNA"
    /strain="C3H"
    /db_xref="taxon:10090"
    /clone="IMAGE:1161994"

FEATURES
source
1..273
    Location/Qualifiers
        /organism="Mus musculus"
        /mol_type="mRNA"
        /db_xref="taxon:10090"
        /clone="IMAGE:313469"
        /dev_stage="19.5 dpc total fetus"
        /lab_host="DRI10B (ampicillin resistant)"
        /clone_lib="Soares mouse p3NMF19.5"
        /note="vector: pT7T3D (Pharmacia) with a modified
        polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
        was primed with a Not I - oligo(dT) primer [5'
        TGTTACCAATCTGAAGTGGAGGCGCGCATTTTTTTTTTTT 3'],
        double-stranded cDNA was size selected, ligated to Eco RI
        adapters (Pharmacia), digested with Not I and cloned into
        the Not I and Eco RI sites of a modified pT7T3 vector
        (Pharmacia). Library went through one round of
        normalization to a Cot = 5. Library constructed by Bento
        Soares and M.Patima Bonaldo. RNA was kindly provided by
        Dr. Minoru Ko (Wayne State University)."
```



```

/cell_line="C2C12"
/lab_host="DH10B"
/clone_lib="Barstead mouse myotubes MPLRB5"
/notes="vector: p773D-Paci; Site_1: EcoRI; Site_2: NotI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5',
TGTTACCAATCTGAAGTGGGAGCGCGCGCTTTTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[ANTTCGGATCCTTG], digested with Not I and cloned into the
Not I and Eco RI sites of the modified p773 vector.
Library constructed by Bob Barstead. The C2C12 cell line
(available from ATCC, catalog # CRL-1772) differentiates
rapidly, forming contractile myotubes and producing
characteristic muscle proteins."

```

ORIGIN

Query Match 74.2%; Score 17.8; DB 1; Length 273;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAGGCCTT 21
|||||
Db 216 CAAAGTCGAACGGAAGGACTT 236
|||||

RESULT 28
LOCUS BG147420 337 bp mRNA linear EST 01-FEB-2001
DEFINITION mac03g07.y1 Soares mouse 3NbMS Mus musculus cDNA clone
IMAGE:3998796 5' similar to TR:088546 O88546 COP9 COMPLEX SUBUNIT
7A. i. mRNA sequence.

ACCESSION BG147420.1 GI:12650828
VERSION BG147420.1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 337)
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:1496524
Seq primer: -40RP from Gibco
High quality sequence stop: 326.
FEATURES
source Location/Qualifiers
1. .337
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3998796"
/sex="male"
/tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares mouse 3NbMS"
/notes="vector: p773D-Paci; Site_1: Not I; Site_2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5',
TGTTACCAATCTGAAGTGGGAGCGCGCGCTTTTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p773 vector. RNA
provided by Dr. Bertrand Jordan. Library went through
three rounds of normalization, and was constructed by
Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 74.2%; Score 17.8; DB 2; Length 337;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAGGCCTT 21
|||||
Db 207 CAAAGTCGAACGGAAGGACTT 227
|||||

RESULT 29
LOCUS CB705072 347 bp mRNA linear EST 10-APR-2003

DEFINITION AMGNNUC.SRPB2-00218-D5-A srpb2 (10220) Rattus norvegicus cDNA clone
srpb2-00218-d5 5', mRNA sequence.

ACCESSION CB705072
VERSION CB705072.1 GI:29762220
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 347)
AUTHORS Amgen EST Program.
TITLE Amgen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00218 row: d column: 5.

FEATURES
source Location/Qualifiers
1. .347
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="srpb2-00218-d5"
/tissue_type="prostate tissue"
/clone_lib="srpb2 (10220)"
/notes="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; rat
prostate normalized double selected poly(A+) mRNA size
fraction > 1 kb"

ORIGIN

Query Match 74.2%; Score 17.8; DB 4; Length 347;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAGGCCTT 21
|||||
Db 95 CAAAGTCGAACGGAAGGACTT 115
|||||

RESULT 30
LOCUS W65078 357 bp mRNA linear EST 10-JUN-1996

DEFINITION me01d06.r1 Soares mouse embryo NBME13.5 14.5 Mus musculus cDNA
clone IMAGE:386219 5', mRNA sequence.

ACCESSION W65078
VERSION W65078.1 GI:1372728
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 357)
AUTHORS Marra,M., Hallier L., Allen M., Bowles M., Dietrich N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

TITLE
JOURNAL
COMMENT
 Waterston, R.
 The WashU-HHMI Mouse EST Project
 Unpublished (1996)
 Contact: Marra M/Mouse EST Project
 WashU-HHMI Mouse EST Project
 Washington University School of MedicineP
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (infoimage.llnl.gov) for further information.
 MGI:238051
 Seq primer: mob.REGA+ET
 High quality sequence stop: 327.
FEATURES
 source
 1..357
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:386219"
 /sex="unknown"
 /tissue_type="embryo"
 /dev_stage="13.5-14.5dpc total fetus"
 /lab_host="DH10B"
 /clone_lib="Soares mouse embryo NME13.5 14.5"
 /note="vector: pT7T3D-PacI; Site 1: Not 1; Site 2: Eco RI;
 1st strand cDNA was primed with a Not I - oligo(dT) primer
 [5'
 TGTTACCAATCTGAAGTGGGAGCGCGCGGAAATTTTTTTTTTTTTTTTTTTT
 T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
 State Univ., from 2]; double-stranded cDNA was ligated to
 Eco RI adaptors (Pharmacia), digested with Not I and
 cloned into the Not I and Eco RI sites of the modified
 pT7T3 vector. Library went through one round of
 normalization, and was constructed by Bento Soares and
 M.Fatima Bonaldo. "

ORIGIN

Query Match 74.2%; Score 17.8; DB 10; Length 357;
 Best Local Similarity 90.5%; Pred. No. 1.4e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCCTT 21
 |||||
Db 183 CAAGTCGAACGGAAGGCCTT 203

RESULT 31
CF425395/c
LOCUS
DEFINITION
 CF425395 384 bp mRNA linear EST 03-SEP-2003
 lads5je02.y1 Gastric Epithelial Progenitor Mus musculus cDNA 5'
 similar to TR:088546 O88546 COP9 COMPLEX SUBUNIT 7A. ;, mRNA
 sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
 Tidwell, R., Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J.,
 Wylie, T., Tsaising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennet, J.,
 Ronko, I., Tsagarisvilli, R., Belaygorod, L., Grow, A., Maguire, L.,
 Waterston, R. and Wilson, R.
 WashU Stem cell EST Project
 Unpublished (2002)
TITLE
JOURNAL
COMMENT
 Contact: Jeff Gordon and Mike Lovett
 WashU, Human Genetics Division

Washington University School of Medicine
 1st strand of cDNA was synthesized with reverse transcriptase and
 oligo(dT) beads, then cDNA was amplified by PCR using modified
 SMART primers. The final cDNA was cloned in pAMP1 vector in
 annealing reaction with Uracil DNA Glycosylase (UDG). Library
 constructed by Y.Korshunova and M. Lovett. Library materials
 provided by Mills JC & Gordon JI.
 Putative full length read
 vector to vector length is
 Possible reversed clone: similarity on wrong strand
 Seq primer: -40RP from Gibco.

FEATURES

source

1..384
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /tissue_type="Gastric Epithelial Progenitor"
 /dev_stage="adult"
 /lab_host="DH5alpha"
 /clone_lib="Gastric Epithelial Progenitor"
 /note="vector: pAMP1; This library was created from
 laser-captured isthmal cells from tox176 transgenic mice.
 1st strand of cDNA was synthesized with reverse
 transcriptase and oligo(dT) beads, then cDNA was amplified
 by PCR using modified SMART primers. The final cDNA was
 cloned in pAMP1 vector in annealing reaction with Uracil
 DNA Glycosylase (UDG). Library constructed by Y.Korshunova
 and M. Lovett. Library materials provided by Mills JC &
 Gordon JI."

ORIGIN

Query Match 74.2%; Score 17.8; DB 5; Length 384;
 Best Local Similarity 90.5%; Pred. No. 1.4e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCCTT 21
 |||||
Db 90 CAAGTCGAACGGAAGGCCTT 70

RESULT 32

AL363886
LOCUS
DEFINITION
 AL363886 ICRFP 522 and 523 Mus musculus cDNA clone V9719B01 5',
 mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
 Eickhoff, H., Schuchhardt, J., Ivanov, I., Meier-Ewert, S., O'Brien, J.,
 Malik, A., Tandon, N., Wolski, E., Rohlf, E., Nyarsik, L.,
 Reinhardt, R., Nietfeld, W. and Lehrach, H.
 Tissue gene expression analysis using arrayed normalized cDNA
 libraries
 Genome Res. (2000) In press
 Contact: MPING
 Abt. Lehrach
 Max Planck Institut Fuer Molekulare Genetik
 Innesstrasse 73, Berlin, 14195 Germany
 The cDNA libraries ICRFP 522 and 523 were normalized with
 oligonucleotide fingerprinting, resulting in a unique subset of
 5376 cDNA clones.
FEATURES
 source
 1..400
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"

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/clones="V9719B01"
/tissue_type="embryo"
/dev_stage="9 and 12 pc embryo"
/clone_lib="ICRFp 522 and 523"

ORIGIN

Query Match
Best Local Similarity 74.2%; Score 17.8; DB 1; Length 400;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
    |||||
Db 350 CAAGTCGAACGGAAGGACTT 370

RESULT 33
AI050353
LOCUS
DEFINITION ub29f09.r1 Soares thymus 2NBMT Mus musculus cDNA clone
            419 bp mRNA linear EST 09-JUL-1998
IMAGE:1379177 5', mRNA sequence.
ACCESSION AI050353
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 419)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
        Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
        Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
        Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
        Waterston,R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
        WashU-HMI Mouse EST Project
        Washington University School of MedicineP
        4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
        Tel: 314 286 1800
        Fax: 314 286 1810
        Email: mouseest@watson.wustl.edu
        This clone is available royalty-free through LLNL; contact the
        IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:901645
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 418.
FEATURES
    source
    1..419
        Location/Qualifiers
            /organism="Mus musculus"
            /mol_type="mRNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="IMAGE:1379177"
            /sex="male"
            /tissue_type="Thymus"
            /dev_stage="4 weeks"
            /lab_host="DH10B"
            /clone_lib="Soares thymus 2NBMT"
            /note="Vector: pT7T3D-PacI; Site 1: Not I; Site 2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5',
TGTACCAATCTGAAGTGGAGCGCGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M.Fatima Bonaldo."

ORIGIN

Query Match
Best Local Similarity 74.2%; Score 17.8; DB 1; Length 419;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
    |||||
Db 350 CAAGTCGAACGGAAGGACTT 370

RESULT 34
AI713707
LOCUS
DEFINITION Rattus norvegicus (Norway rat)
            420 bp mRNA linear EST 08-JUN-1999
IMAGE:1379177 5', mRNA sequence.
ACCESSION AI713707
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE 1 (bases 1 to 420)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
        discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
COMMENT Contact: Soares, MB
        Coordinated Laboratory for Computational Genomics
        University of Iowa
        375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
        Tel: 319 335 8250
        Fax: 319 335 9565
        Email: Bento-soares@uiowa.edu
        Oligo-dT track not found, Not I site shown in beginning of sequence
        is likely internal to the message. cDNA Library Preparation: M.B.
        Soares Lab Clone distribution: clones will be available through
        Research Genetics (www.resgen.com)
        Seq primer: M13 Forward
        POLYA=No.
FEATURES
    source
    1..420
        Location/Qualifiers
            /organism="Rattus norvegicus"
            /mol_type="mRNA"
            /strain="Sprague-Dawley"
            /db_xref="taxon:10116"
            /clone="UI-R-AG1-aao-b-08-0-UI"
            /dev_stage="adult"
            /lab_host="DH10B (Life Technologies)"
            /clone_lib="UI-R-AG1"
            /note="Vector: pT7T3D-PacI; Site 1: Not I; Site 2: Eco RI;
The UI-R-AG1 library is a normalized library constructed
from 13 dpc rat ventricle. The tag is a string of 6
nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6:
791-806, 1996. Tissue provided by Jim Lin, Department of
Biology, University of Iowa.
TAG TISSUE=atrium at 16.5 dpc
TAG LIB=UI-R-AG1
TAG_SEQ=GATTC"

ORIGIN

Query Match
Best Local Similarity 74.2%; Score 17.8; DB 1; Length 420;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
    |||||
Db 143 CAAGTCGAACGGAAGGACTT 163

RESULT 35

```

```

Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
    |||||
Db 367 CAAGTCGAACGGAAGGACTT 387

RESULT 34
AI713707
LOCUS
DEFINITION Rattus norvegicus (Norway rat)
            420 bp mRNA linear EST 08-JUN-1999
IMAGE:1379177 5', mRNA sequence.
ACCESSION AI713707
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE 1 (bases 1 to 420)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
        discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
COMMENT Contact: Soares, MB
        Coordinated Laboratory for Computational Genomics
        University of Iowa
        375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
        Tel: 319 335 8250
        Fax: 319 335 9565
        Email: Bento-soares@uiowa.edu
        Oligo-dT track not found, Not I site shown in beginning of sequence
        is likely internal to the message. cDNA Library Preparation: M.B.
        Soares Lab Clone distribution: clones will be available through
        Research Genetics (www.resgen.com)
        Seq primer: M13 Forward
        POLYA=No.
FEATURES
    source
    1..420
        Location/Qualifiers
            /organism="Rattus norvegicus"
            /mol_type="mRNA"
            /strain="Sprague-Dawley"
            /db_xref="taxon:10116"
            /clone="UI-R-AG1-aao-b-08-0-UI"
            /dev_stage="adult"
            /lab_host="DH10B (Life Technologies)"
            /clone_lib="UI-R-AG1"
            /note="Vector: pT7T3D-PacI; Site 1: Not I; Site 2: Eco RI;
The UI-R-AG1 library is a normalized library constructed
from 13 dpc rat ventricle. The tag is a string of 6
nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6:
791-806, 1996. Tissue provided by Jim Lin, Department of
Biology, University of Iowa.
TAG TISSUE=atrium at 16.5 dpc
TAG LIB=UI-R-AG1
TAG_SEQ=GATTC"

ORIGIN

Query Match
Best Local Similarity 74.2%; Score 17.8; DB 1; Length 420;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
    |||||
Db 143 CAAGTCGAACGGAAGGACTT 163

RESULT 35

```

AA818546
LOCUS
DEFINITION UI-R-A0-aw-f-05-0-UI.s1 424 bp mRNA linear EST 03-JUL-1999
UI-R-A0-aw-f-05-0-UI 3' similar to gb|L02529|RATPRZRH Rattus
norvegicus Drosophila polarity gene (fizzled) homologue mRNA,
complete cds, mRNA sequence.
ACCESSION AA818546
VERSION AA818546.1 GI:4228339
SOURCE EST.
ORGANISM Rattus norvegicus (Norway rat)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 424)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
PUBMED 889548
COMMENT On Feb 17, 1998 this sequence version replaced gi:2889285.
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@iowa.edu
Oligo-dT track not found, Not 1 site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.
Fatima Bonaldo, Ph.D. Clone distribution: clones will be available
through Research Genetics This clone is also available through the
I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE
ID=1776549
Seq primer: M13 Forward
POLYA=No.
FEATURES
source
1..424
Location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clones="UI-R-A0-aw-f-05-0-UI"
/dev_stages="adult"
/lab_host="DH10B (Life Technologies)"
/clone_libs="UI-R-A0"
/notes="Vector: pT73D-PacI; Site 1: Not 1; Site 2: Eco RI;
This library consists of a mixture of individually tagged
normalized libraries constructed from rat placenta, adult
lung, brain, liver, kidney, heart, spleen, ovary, and
muscle. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dT track which allows
identification of the library of origin of a clone within
the mixture."
ORIGIN
Query Match 74.2%; Score 17.8; DB 1; Length 424;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCCTT 21
|||||
Db 143 CAAGTCGAACGGAAGGCCTT 163
|||||
RESULT 36
BU743860
LOCUS
DEFINITION mai49f01.y1 McCarrey Eddy round spermatid Mus musculus cDNA clone
IMAGE:6449520 5', mRNA sequence.
ACCESSION BU743860
VERSION BU743860.1 GI:23691980
KEYWORDS EST.

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 444)
AUTHORS McCarrey,J., Eddy,M., Marra,M., Hillier,L., Clifton,S., Pape,D.,
Martin,J., Wylie,T., Dante,M., Bowers,Y., Theising,B., Gibbons,M.,
Ritter,E., Tsagareishvili,R., Ronko,I., Maguire,L., Kennedy,S.,
Bennett,J., Waterston,R. and Wilson,R.
TITLE NIEHS Mouse
JOURNAL Unpublished (2002)
COMMENT Contact: McCarrey/Eddy NIEHS Mouse
NIEHS Mouse
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:2093832
Seq primer: -40RP from Gibco
High quality sequence stop: 422.
Location/Qualifiers
1..444
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CD-1"
/db_xref="taxon:10090"
/clones="IMAGE:6449520"
/sex="male"
/tissue_type="round spermatids, pooled from multiple mice"
/dev_stages="60 day"
/lab_host="DH10B (phage-resistant)"
/clone_libs="McCarrey Eddy round spermatid"
/notes="Organ: testis; Vector: pBluescript SK+
(Stratagene); Site 1: XhoII; Site 2: ECORI; cDNA oligo
dt-primed [5'-(GA)10-ACTAGTCGAGTTTTTTTTTT-3'] and
directionally cloned using 5' linkers 5'-AATTCGGACGAG-3'
and 5'-CTCGTCCG-3'. Size selection of 400bp material
gives average insert size ranging from 1-2 kb. Library was
mass excised (from lambda-UnizAP-XR) and resulting
single-stranded phagemids were prepped and tranformed
into DH10B. Library contains 98.5% recombinants.
References: J. Androl. 20:635-639 and Gene 25:263-269.
Library constructed and donated by J. McCarrey, Ph.D.
(Southwest Foundation for Biomedical Research, Dept. of
Genetics); excision done by E.M. Eddy, Ph.D. (National
Institutes of Health, National Institute of Environmental
Health Sciences). Original lambda-based library is
available through ATCC, catalog #63423."
ORIGIN
Query Match 74.2%; Score 17.8; DB 3; Length 444;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCCTT 21
|||||
Db 12 CAAGTCGAACGGAAGGCCTT 32
|||||
RESULT 37
W47680
LOCUS
DEFINITION mc89h02.r1 Soares mouse embryo NM01315 14.5 Mus musculus cDNA
clone IMAGE:355731 5', mRNA sequence.
ACCESSION W47680
VERSION W47680.1 GI:1537643
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 446)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1332776.
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:227531
Seq primer: -28W13 rev2 from Amersham
High quality sequence stop: 400.
Location/Qualifiers
1. .446
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:355731"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/clone_lib="Soares mouse embryo NMEL13.5 14.5"
/notes="Vector: pT7T3D-Paci; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTACCAATCTGAAGTGGAGCGCGCGGAAATTTTTTTTTTTTTTTTTT T 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo. "

ORIGIN
Query Match 74.2%; Score 17.8; DB 10; Length 446;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGACGGAAGGCCTT 21
|||||
Db 80 CAAGTCGACGGAAGGCATT 100
|||||

RESULT 38
AI593186
LOCUS
DEFINITION
AI593186 vt03c06.y1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone
IMAGE:1161994 5', mRNA sequence.
AI593186
VERSION
KEYWORDS
SOURCE
AI593186.1 GI:4602234
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 473)

AUTHORS
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,B., Kohn,S., Shin,I., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:627906
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the correct orientation)
Seq primer: -40RP from Gibco
High quality sequence stop: 466.
Location/Qualifiers
1. .473
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C3H"
/db_xref="taxon:10090"
/clone="IMAGE:1161994"
/cell_line="C2C12"
/lab_host="DH10B"
/notes="Vector: pT7T3D-Paci; Site 1: EcoRI; Site 2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTACGAATCTGAAGTGGAGCGCGGCCTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead. The C2C12 cell line (available from ATCC, catalog # CRL-1772) differentiates rapidly, forming contractile myotubes and producing characteristic muscle proteins. "

ORIGIN
Query Match 74.2%; Score 17.8; DB 1; Length 473;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGACGGAAGGCCTT 21
|||||
Db 293 CAAGTCGACGGAAGGCATT 313
|||||

RESULT 39
CN692701
LOCUS
DEFINITION
CN692701 E0326F01-5 NIA Mouse E10.5 whole embryo cDNA library (Long) Mus musculus cDNA clone NIA:E0326F01 IMAGE:30861468 5', mRNA sequence.
CN692701
VERSION
KEYWORDS
SOURCE
CN692701.1 GI:47461449
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 492)
Sharov,A.A., Piao,Y., Matoba,R., Dudekula,D.B., Qian,Y., VanBuren,V., Falco,G., Martin,P.R., Stagg,C.A., Bassey,U.C., Wang,Y., Carter,M.G., Hamatani,T., Aiba,K., Akutsu,H., Sharova,L., Tanaka,T.S., Kimber,W.L., Yoshikawa,T., Jaradat,S.A., Pantano,S., Nagaraja,R., Boheler,K.R., Raub,D., Hodges,R.J., Longo,D.L., Schlessinger,D., Keller,J., Klotz,E., Kelsoe,G., Umezawa,A.,

Vescovi, A.L., Rossant, J., Kunath, T., Hogan, B.L., Curci, A., D'Urso, M., Kelso, J., Hide, W. and Ko, M.S.
Transcriptome analysis of mouse stem cells and early embryos
PLOS Biol. 1 (3), 410-419 (2003)
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: E0326 row: F column: 01
Seq primer: M13 Reverse
High quality sequence stop: 492
POLYA=No.

FEATURES
source
1. .492
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/db_xref="nlaEST:E0326F01-5"
/clones="NTA:E0326F01 IMAGE:30861468"
/tissue_type="whole embryo including extraembryonic tissues at 10 5-days postcoitum"
/dev_stage="E10.5"
/lab_host="DH10B"
/clone_lib="NIA Mouse E10.5 whole embryo cDNA library (Long)"
/note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cdna). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 8 embryos at 10.5-days postcoitum. Double-stranded cDNAs were synthesized with an oligo(dT) primer [Invitrogen]:
5'-pGACTAGTCTAGATCGAGCGGCCCTTTT-3' from
2ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lona-linker Li-SalI, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer SalI-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 3.4Kb. The library was constructed by Yulan Piao."

ORIGIN

Query Match 74.2%; Score 17.8; DB 8; Length 492;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
|||||

Db 107 CAAGTCGAACGGAAGGCCTT 127
|||||

RESULT 40

AA014214/c
LOCUS
DEFINITION
mh18910.r1 Soares mouse placenta 4NBMP13.5 14.5 Mus musculus cDNA
clone IMAGE:442914 5', mRNA sequence.

AA014214

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 500)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HHMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HHMI Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MG1:268250

Seq primer: mob.REGA+ET

High quality sequence stop: 477.

FEATURES

source

1. .500

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="IMAGE:442914"

/sex="unknown"

/tissue_type="placenta"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="Soares mouse placenta 4NBMP13.5 14.5"

/note="Organ: Placenta; Vector: pT7T3D-PacI; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I

- oligo(dT) primer [5,

TGTTACCAATCTGAAGTGGGCGCGCGGAATTTTTTTTTTTTTTTTTTTT

T 3']; double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT7T3 vector. Library

went through one round of normalization, and was

constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 74.2%; Score 17.8; DB 1; Length 500;

Best Local Similarity 90.5%; Pred. No. 1.5e+03;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
|||||

Db 122 CAAGTCGAACGGAAGGCCTT 102
|||||

RESULT 41

LOCUS

DEFINITION

AA509546
vh50c08.r1 Soares mammary gland_NbMNG Mus musculus cDNA clone

IMAGE:890414 5', mRNA sequence.

AA509546

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus
(house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 502)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.

The WashU-HHMI Mouse EST Project

JOURNAL
COMMENT

Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:518374
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 469.

FEATURES
source

1..502
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAG8:890414"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares mammary gland NbMMG"

/note="Organ: mammary gland; Vector: pT7T3D-PacI; Site 1:
Not I; Site 2: Eco RI; 1st strand cDNA was primed with a
Not I - oligo(dT) primer [5'
TGTTCACAACTCGAAGTGGAGCGCCGCAATGGTTTTTTTTTTTTTTTTT
T 3'] ; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."

ORIGIN

Query Match 74.2%; Score 17.8; DB 1; Length 502;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAGGCCTT 21
|||||
Db 58 CAAAGTCGAACGGAAGGACTT 78

RESULT 42
CG036380/c

LOCUS
DEFINITION
PULV37TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTa0612H02,
genomic survey sequence.

ACCESSION
CG036380
VERSION
CG036380.1 GI:33908536
KEYWORDS
GSS.

SOURCE
Zea mays

Zea mays
Zea mays

ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
AUTHORS
1 (bases 1 to 502)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Reenick,A., Frazer,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennerzen,J.

TITLE
Maize Genomics Consortium
JOURNAL
Unpublished (2003)
COMMENT
Other GSSs: PULV37TB
Contact: Cathy Whitelaw
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF

FEATURES
source

Class: sheared ends.
Location/Qualifiers
1..502
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTa0612H02"
/clone_lib="ZM 0.6 1.0 KB"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
Cor selected genomic DNA library"

ORIGIN

Query Match 74.2%; Score 17.8; DB 12; Length 502;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAGGCCTT 21
|||||
Db 431 CAAAGTCGAACGGAAGGCCTT 411

RESULT 43
BE863637

LOCUS
DEFINITION
UI-M-BH0-ake-d-02-0-UI.r1 NIH BMAP_M_S1 Mus musculus cDNA clone
UI-M-BH0-ake-d-02-0-UI 5', mRNA sequence.

ACCESSION
BE863637
VERSION
BE863637.1 GI:10383879
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
1 (bases 1 to 527)
Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL
Genome Res. 6 (9), 791-806 (1996)
PUBMED
8889548

COMMENT
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643 USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov

cDNA Library Preparation: M.B. Soares Lab Clone distribution:
CDNA Library Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It
should be noted that Bento Soares is generating a small number of
additional specialized non-redundant arrays of BMAP cDNAs whose
availability will be considered under appropriate and limited
collaborative arrangements
Seq primer: M13 Reverse.

FEATURES
source

Location/Qualifiers
1..527
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BH0-ake-d-02-0-UI"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NIH_BMAP_M_S1"

/notes="Vector: pT7T3D-PacI; Site 1: Not I; Site 2: Eco RI;
The NIH BMAP M_S1 library is a subtracted library derived
from a mixture of normalized libraries from ten regions of
the mouse brain (cerebellum, brain stems, olfactory bulbs,
hypothalamus, cortex, amygdala, basal ganglia, pineal
gland, striatum, hippocampus). The driver used for
subtraction consisted of a pool of 20,000 cDNA clones
obtained from non-normalized and normalized libraries of

these ten regions of the mouse brain."

Query Match 74.2%; Score 17.8; DB 7; Length 527;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
|||||
Db 83 CAAGTCGAACGGAAGGCCTT 103
|||||

RESULT 44
BQ569727 532 bp mRNA linear EST 19-JUN-2002
LOCUS gi135c11.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
DEFINITION clone gi135c11 5', mRNA sequence.

ACCESSION BQ569727
VERSION BQ569727.1 GI:21473044
KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 532)
AUTHORS Kachar, B.
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
JOURNAL Unpublished (2002)
COMMENT Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kacharb@nidcd.nih.gov
Plate: 135 row: c column: 11
Seq primer: M13RPI reverse primer (ABI).

FEATURES
source
1..532
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/clones="gi135c11"
/sex="male and female"
/dev_stage="Post natal day 5 to 13"
/clone_libs="Mouse Organ of Corti cDNA pBluescript"
/notes="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary

DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and fractionated with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exassist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

ORIGIN

Query Match 74.2%; Score 17.8; DB 3; Length 532;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
|||||
Db 334 CAAGTCGAACGGAAGGCCTT 354
|||||

RESULT 45
BF022607/c

LOCUS BF022607 542 bp mRNA linear EST 29-DEC-2000
DEFINITION uy51d11.y1 NCI CGAP Lu30 Mus musculus cDNA clone IMAGE:3663093 5' similar to TR:088546 O88546 COP9 COMPLEX SUBUNIT 7A. ;, mRNA sequence.

ACCESSION BF022607.1 GI:10753940

VERSION BF022607

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 542)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

COMMENT Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: cgaps-x@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at:

image.llnl.gov/image/html/iresources.shtml

MGI:1423861

Query Match	74.2%;	Score 17.8;	DB 11;	Length 566;
Best Local Similarity	90.5%;	Pred. No. 1.5e+03;		

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
||||| ||||| ||||| |||||
Db 417 CAAGTCGAGCGGAAGGCCTT 397

RESULT 48

CN692527

LOCUS

DEFINITION E0324C02-5 NIA Mouse E10.5 whole embryo cDNA library (Long) Mus
musculus cDNA clone NIA:E0324C02 IMAGE:30861241 5', mRNA sequence.

ACCESSION

CN692527

VERSION

CN692527.1

KEYWORDS

EST.

SOURCE

ORGANISM

Mus musculus

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1..571

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="niaEST:E0324C02-5"

/db_xref="taxon:10090"

/clone="NIA:E0324C02 IMAGE:30861241"

/tissue_type="whole embryo including extraembryonic

tissues at 10.5-days postcoitum"

/dev_stages="E10.5"

/lab_host="DH10B"

/clone_lib="NIA Mouse E10.5 whole embryo cDNA library

(Long)"

/note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI;

Site 2: NotI; Mouse cDNA project by the Laboratory of

Genetics, National Institute on Aging (NIA), Intramural

Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).

This is a long-transcript enriched cDNA library (Ref.

Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total

RNAs were extracted from a pool of 8 embryos at 10.5-days

postcoitum. Double-stranded cDNAs were synthesized with an

Oligo(dT) primer [Invitrogen:

5'-PGACTAGTTCGATCGAGCGCCCTTTTCTTTT-3'] from

2ug of total RNA, treated with T4 DNA polymerase, and

purified by ethanol-precipitation. The cDNAs were ligated

to lona-linker LL-Sal4, purified by phenol/chloroform, and

separated from free linkers by Centricon 100. Then, the

cDNAs were amplified by long-range high fidelity PCR using

Ex Taq polymerase (Takara) with a primer Sal4-S. The

products were purified by phenol/chloroform and Centricon

100. The cDNAs were digested with SalI and NotI enzymes

and cloned into SalI/NotI site of pCMV-SPORT6 plasmid

ORIGIN

Query Match 74.2%; Score 17.8; DB 8; Length 571;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21

||||| ||||| ||||| ||||| |||||

Db 107 CAAGTCGAACGGAAGGCCTT 127

RESULT 49

BE288370/c

LOCUS

DEFINITION

601094841F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3489299 5',

mRNA sequence.

ACCESSION

BE288370

VERSION

BE288370.1

KEYWORDS

EST.

SOURCE

ORGANISM

Mus musculus

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgaabs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LUAM8530 row: a column: 12

High quality sequence stop: 577.

FEATURES

source

Location/Qualifiers

1..577

/organism="Mus musculus"

/mol_type="mRNA"

/strain="mix FVB/N, C57BL/6J"

/db_xref="taxon:10090"

/clone="IMAGE:3489299"

/tissue_type="tumor, gross tissue"

/dev_stages="7 months"

/lab_host="DH10B"

/clone_lib="NCI_CGAP Mam5"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Library constructed by Life Technologies. Investigators

providing samples: Lothar Hennighausen/Robin Humphreys,

NIH"

ORIGIN

Query Match 74.2%; Score 17.8; DB 7; Length 577;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21

||||| ||||| ||||| ||||| |||||

Db 202 CAAGTCGAACGGAAGGCCTT 182

RESULT 50

DN215604/c

LOCUS

DN215604

600 bp

mRNA

linear

EST 28-FEB-2005

MEST971_D01.T7-1 UCA-ZmSAM-XZ2 Zea mays cDNA, mRNA sequence.
 DN215604
 VERSION DN215604.1 GI:60348631
 EST.
 KEYWORDS
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 600)
 AUTHORS Chen,H.D., Zhang,X., Zhou,R.L., Arias L,A.C., Shendelman,J.M.,
 Zazubovits,N., Boreuk,L.A., Emrich,S.J., Ashlock,D.A., Scanlon,M.J.,
 and Schnable,P.S.
 TITLE Expressed Sequence Tags from B73 Maize Shoot Apical Meristems
 JOURNAL Unpublished (2004)
 COMMENT Contact: Patrick S. Schnable
 Schnable Laboratory
 Iowa State University
 2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA
 Tel: 515-294-0975
 Fax: 515-294-5256
 Email: schnable@iastate.edu.

```

FEATURES
    source
        Location/Qualifiers
            1..600
                /organism="Zea mays"
                /mol_type="mRNA"
                /cultivar="inbred B73"
                /db_xref="taxon:4577"
                /tissue_type="Vegetative Shoot Apical Meristem (SAM) and
                leaf primordia staged P1-P4"
                /lab_host="XLI-Blue"
                /clone_lib="UGA-ZmSAM-X22"
                /note="Organ: Shoot apex; Vector: Uni-Zap XR; Site 1:
                EcoRI; Site 2: XhoI; This library was constructed by
                Xiaolan Zhang. Vegetative Shoot Apical Meristem (SAM) and
                leaf primordia staged P1-P4 from 14-17 day-after
                germination seedlings were quickly dissected into dry ice
                under a light microscope. Total RNA was isolated using
                Trizol and mRNA was purified with Dynal Oligo-DT25.
                ds-cDNA molecules were generated as follows. First-strand
                cDNA was prepared from oligo-dT selected mRNA by priming
                with an XhoI oligo-dT primer
                (5'-GAGAGAGAGAGAGAGAACTAGTCTCAGTGTGTTTTTTTTTTTTT)
                The resulting DNA:RNA hybrid was treated with RNase H and
                used as a template for DNA PolI-catalyzed second strand
                synthesis. After the addition of EcoRI adaptors, the
                ds-cDNAs were digested with XhoI and size-selected to be
                >600 bp. The resulting molecules were directionally cloned
                into the EcoRI and XhoI sites of the Uni-Zap XR vector.
                The lambda library was packaged with Gigapack III Gold
                packaging extract and was mass excised by XLI-Blue cells
                and ExAssist helper phage. Excised phagemids were titered
                in SOLR cells and plated onto LB-ampicillin agar plates.
                Base calling was conducted using Phred. Trimming was
                performed using Lucy with the following criteria:
                (-minimum 200 -error 0.01 0.01 -bracket 10 0.01). A low
                complexity filter was applied and additional trimming was
                conducted to remove E. coli, vector, and organelle
                contamination. After processing ~30% of the sequences
                contained a minimum of 10 Ts at the beginning of the
                sequence. For reasons that are not understood many of the
                clones in this library lack an XhoI site at their 3'
                ends."

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ORIGIN

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Query Match      74.2%; Score 17.8; DB 9; Length 600;
Best Local Similarity 90.5%; Pred.No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAAGGCCTT 21
   ||||| ||||| |||||
Db 550 CAAGTGGAAAGAAAGGCCTT 530

```

[illegible]FEATURES
SOURCE

/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/issue_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"
/dev_stage="varies by tissue"
/lab_host="DH10B T1 phage resistant"
/clone_lib="ZM BFB"
/notes="Vector: pCMV-SPORT 6.1; Site_1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (<http://www.genome.arizona.edu/orders/>)."

ORIGIN

Query Match	74.2%	Score 17.8;	DB 10;	Length 602;
Best Local Similarity	90.5%;	Pred. No. 1.5e+03;		
Matches 19;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1	CAAGTCGACGGAAGGCCTT	21	
Db	583	CAAGTGAACGAAAAGCCTT	563	

```

RESULT 52
CA934753/c
LOCUS
DEFINITION MTU5TS.P23.C06 Aspen stem cDNA Library Populus tremuloides cDNA,
              609 bp mRNA linear EST 30-DEC-2002
              mRNA sequence.
ACCESSION CA934753
VERSION CA934753.1 GI:27423233
KEYWORDS EST.
SOURCE Populus tremuloides (quaking aspen)
ORGANISM Populus tremuloides
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
           rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.
REFERENCE 1 (bases 1 to 609)
AUTHORS Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and
         Tsai,C.-J.
TITLE Expressed sequence tags from Aspen
JOURNAL Unpublished (2003)
COMMENT Contact: Tsai C-J
         Michigan Technological University, School of Forest Resources &
         Environmental Science
         1400 Townsend Drive, Houghton, MI 49931-1295, USA
         Tel: 906 487 2914
         Fax: 906 487 2915
         Email: chtsai@mtu.edu.

FEATURES             Location/Qualifiers
     source           1..609
                     /organism="Populus tremuloides"
                     /mol_type="mRNA"
                     /db_xref="taxon:3693"
                     /clone_lib="Aspen stem cDNA Library"
                     /note="Torgan: stem"

ORIGIN
Query Match       74.2%; Score 17.8; DB 4; Length 609;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCTTT 22
    ||||| ||||| ||||| ||||| |||||
Db 274 AAGTCGTTCCGAAGAGGCCTTT 254

RESULT 53
AW914801
LOCUS
DEFINITION EST346105 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
              RG1BH48 5' end, mRNA sequence.
ACCESSION AW914801
VERSION AW914801.1 GI:8080481
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
           Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 613)
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
         Kerlavage,A.R. and Adams,M.D.
TITLE Rat Genome Project: Generation of a Rat EST (RST) Catalog & Rat
JOURNAL Unpublished (1998)
COMMENT Contact: Lee, NH
         The Institute for Genomic Research
         9712, Medical Center Drive, Rockville, MD 20850, USA
         Tel: (301)-838-3529
         Fax: (301)-838-0208
         Email: nhlee@tigr.org
         This clone is available through the ATCC, contact the ATCC
         tel#703-365-2700 for further information
         Seq primer: M13 Reverse.

```

```

FEATURES             Location/Qualifiers
     source           1..613
                     /organism="Rattus sp."
                     /mol_type="mRNA"
                     /db_xref="taxon:10118"
                     /clone="RG1BH48"
                     /clone_lib="Normalized rat ovary, Bento Soares"
                     /note="Organ: ovary; Vector: pT73Pac; Site_1: EcoRI;
                     Site_2: NotI"

ORIGIN
Query Match       74.2%; Score 17.8; DB 7; Length 613;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
    ||||| ||||| ||||| ||||| |||||
Db 61 CAAGTCGAACGGAAGGCCTT 81

RESULT 54
BI648126
LOCUS
DEFINITION BI648126 622 bp mRNA linear EST 12-SEP-2001
              60327844F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5318818 5',
              mRNA sequence.
ACCESSION BI648126
VERSION BI648126.1 GI:15562362
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
           Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 622)
AUTHORS NIH-MGC,http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
         Contact: Robert Strausberg, Ph.D.
         Email: cgapbs-remail.nih.gov
         Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
         cDNA Library Preparation: Life Technologies, Inc.
         cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
         DNA Sequencing by: Incyte Genomics, Inc.
         Clone distribution: MGC clone distribution information can be
         found through the I.M.A.G.E. Consortium/LLNL at:
         http://image.llnl.gov
         Plate: LLAM11808 Row: g Column: 11
         High quality sequence stop: 605.

FEATURES             Location/Qualifiers
     source           1..622
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129,C57BL/6J,FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5318818"
                     /tissue_type="tumor, gross tissue"
                     /dev_stage="10 months"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Mam3"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
                     Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigators
                     providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
                     Reference for transgenic model: Xu et al., Nature Genetics
                     22, 37-43 (1999)."
```

ORIGIN

```

Query Match       74.2%; Score 17.8; DB 2; Length 622;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
    ||||| ||||| ||||| ||||| |||||

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```

Db      433 CAAGTCGAAGTGAAGGACTT 453

RESULT 55
CX734384/c
LOCUS
DEFINITION j01e11.y1 Mouse whole eye, equalized: ja/jb/jc Mus musculus cDNA
            635 bp mRNA linear EST 24-JAN-2005
            Clone j01e11 5', mRNA sequence.
ACCESSION CX734384
VERSION    CX734384.1 GI:58061220
KEYWORDS  EST.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 635)
AUTHORS   Wistow,G. and Tomarev,S.
TITLE     Expressed sequence tag analysis of mouse whole eye
JOURNAL   Unpublished (2004)
COMMENT   Contact: Wistow G
            Section on Molecular Structure and Function
            National Eye Institute
            6/331, NIH, Bethesda, MD 20892-2740, USA
            Tel: 301 402 3452
            Fax: 301 496 0078
            Email: graeme@helix.nih.gov
            Plate: 01 row: e column: 11
            Seq primer: M13RP1 reverse primer (ABI).
FEATURES
            source
            1..635
                /organism="Mus musculus"
                /mol_type="mRNA"
                /strain="C57BL6J"
                /db_xref="taxon:10090"
                /clone="j01e11"
                /tissue_type="Whole eye"
                /dev_stage="Adult"
                /lab_host="EMDH10B"
                /clone_lib="Mouse Whole eye, equalized: ja/jb/jc"
                /notes="Organ: Eye; Vector: pSport1; Approximately 1mg
                total RNA was extracted from 100 adult mouse whole eyes. A
                directionally cloned cDNA library in the pSPORT1 vector
                (Invitrogen) was constructed at Bioserve Biotechnology
                (Laurel MD) essentially following the protocols of the
                SuperScript Plasmid System full details of which are
                contained in the manufacturer's instruction manual
                (http://www.lifetech.com/). First strand synthesis was
                carried out using a Not I primer-adaptor
                [5'-pGACTAGTTCTAGATCGAGCGCGCC(T)15-3']. cDNA was
                cloned in Not I/Sal I sites. EST analysis was performed on
                the unamplified library at the NIH Intramural Sequencing
                Center (NISC)."
```

```

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 641)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-i@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11334 row: 9 column: 17
            High quality sequence stop: 640.
FEATURES
            source
            1..641
                /organism="Mus musculus"
                /mol_type="mRNA"
                /strain="FVB/N"
                /db_xref="taxon:10090"
                /clone="IMAGE:5136040"
                /lab_host="DHI0B (T1 phage-resistant)"
                /clone_lib="NCI CGAP_Li9"
                /notes="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
                Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                Average insert size 1.9 kb. Constructed by Life
                Technologies. Note: this is a NCI CGAP Library."
```

ORIGIN

```

Query Match      74.2%; Score 17.8; DB 2; Length 641;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

QY      1 CAAGTCGAACGGAAGGCCTT 21
        |||||
Db      206 CAAGTCGAACGGAAGGACTT 226
        |||||
```

RESULT 57

```

CF897511
LOCUS
DEFINITION CF897511 641 bp mRNA linear EST 04-NOV-2003
            A0226B05-5 NIA Mouse Embryonic Germ Cell cDNA Library (long,
            subtracted) Mus musculus cDNA clone NIA:A0226B05 IMAGE:30730864 5',
            mRNA sequence.
ACCESSION CF897511
VERSION    CF897511.1 GI:38164560
KEYWORDS  EST.
SOURCE    Mus musculus (house mouse)
```

ORGANISM

```

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 641)
AUTHORS   Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
TITLE     Construction of long-transcript enriched cDNA libraries from
            submicrogram amounts of total RNAs by a universal PCR amplification
            method
            Genome Res. 11 (9), 1553-1558 (2001)
```

JOURNAL

PUBMED

COMMENT

```

11544199
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgscun.grc.nia.nih.gov
Plate: A0226 row: B column: 05
Seq primer: M13 Reverse
High quality sequence stop: 641
POLYA=No.
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RESULT 56

BI331633

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DEFINITION BI331633 641 bp mRNA linear EST 30-JUL-2001
            602983168F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5136040 5',
            mRNA sequence.
ACCESSION BI331633
VERSION    BI331633.1 GI:15016290
KEYWORDS  EST.
SOURCE    Mus musculus (house mouse)
```

FEATURES

Location/Qualifiers

```

1. .641
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL6"
/db_xref="niaEST:A0226B05-5"
/db_xref="taxon:10090"
/clone="NIA:A0226B05 IMAGE:30730864"
/sex="male"
/dev_stage="embryonic day 8"
/lab_host="DH10B"
/clone_lib="NIA Mouse Embryonic Germ Cell cDNA Library
(long, subtracted)"
/notes="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI;
Site 2: NotI; Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://lgsun-grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). EG
cells were obtained from Dr. Brigid L.M. Hogan and RNA was
prepared by Dr. Mark G. Carter (NIH/NIA-IRP). EG cells
were cultured at 37. C. 5% CO2 in DMEM supplemented with
15% ES cell-qualified FBS, 0.1mM non-essential amino
acids, 2 mM glutamine, penicillin/streptomycin, 1 mM
sodium pyruvate, 0.1 mM beta-mercaptoethanol, and 10^-7
units of LIF per liter. Double-stranded cDNAs were
synthesized with an Oligo(dT) primer [Invitrogen:
5'-pGACTAGTCTAGATCGGAGCGCGCCCTTTTTTT-3'] from
2.5 ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to lona-linker Li-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were double digested with NotI and SalI enzymes,
then purified by phenol/chloroform and centrifuged 100. The
cDNA mixture was subjected to a special subtraction
procedure by Dr. Kazuhiro Kondo at AIGIN Cosmos. Then the
subtracted cDNAs were cloned into SalI/NotI site of
pCMV-SPORT6 plasmid vector. The DH10B E. coli host was
transformed with the ligation mixture by the standard
chemical method. The average insert size is about 2.2kb.
The library was constructed by Yulan Piao and Kazuhiro
Kondo."

```

ORIGIN

```

Query Match      74.2%; Score 17.8; DB 5; Length 641;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      1  CAAGTCGAACGGAAGGCCTT 21
|||||  |||||  |||||  |||||  |||||
Db      468 CAAGTCGAACGGAAGGCCTT 498

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RESULT 58

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DV169729/c
LOCUS      DV169729      643 bp      mRNA      linear      EST 04-OCT-2005
DEFINITION ZM_BF00168P08.f_ZM_BFB Zea mays cDNA 3', mRNA sequence.
ACCESSION  DV169729
VERSION     DV169729.1 GI:76923942
KEYWORDS   EST.
SOURCE     Zea mays
ORGANISM   Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 643)
REFERENCE  Kim,H., Collura,K., Wisotski,M., Smart,D., Kudrna,D., Muller,C.,
AUTHORS   Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
TITLE     Zea Full-length cDNA Project
JOURNAL   Unpublished (2005)
COMMENT   Contact: Yeisoo Yu

```

Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9585
Fax: 520 621 1259
Email: yeisoo@genome.arizona.edu
Plate: 0168 row: P column: 08.
Location/Qualifiers

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1. .643
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="mixed (silks, husks, ears, pollen, shoot
tips, leaf, root tips, whole seed, embryo)"
/dev_stage="varies by tissue"
/lab_host="DH10B T1 phage resistant"
/clone_lib="ZM_BFB"

```

FEATURES

```

/notes="Vector: pCMV-SPORT 6.1; Site_1: EcoRV; Site_2:
NotI; Zea Full length cDNA library (3530 library)
created by Invitrogen from multiple tissues; Organ: silks,
husks, ears, pollen, shoot tips, leaf, root tips, whole
seed, embryo. This is a Gateway compatible vector.
permuting clone movement to new vector backbones for
expression in diverse host cells using recombination
rather than restriction enzymes. poly(A) + mRNA was
prepared by Invitrogen, and equimolar amounts of RNA from
each of the 12 tissue samples were mixed together for
selection of mRNA with a 5' cap. After synthesis of cDNA,
a normalization step was conducted against the mixture of
RNA sources. Tissues prepared: 1. just emerging silks; 2.
inner husks from ears of sample #1; 3. 20 day aleurone; 4.
immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to
2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from
15 day old seedlings; all leaves with an expanded or
partially expanded sheath were removed; 8. mature leaf
tissue; 9. 0.5 cm long root tips from 15 day old
seedlings; 10. 10 day whole seed; 11. 12 day endosperm and
embryo; 12. 17 day endosperm and embryo. All of the
sequenced clones in Zea Full-length cDNA Project will be
archived at the University of Arizona. Clones, high
density filters and amplified library can be ordered from
the University of Arizona
(http://www.genome.arizona.edu/orders/)."

```

ORIGIN

```

Query Match      74.2%; Score 17.8; DB 10; Length 643;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      1  CAAGTCGAACGGAAGGCCTT 21
|||||  |||||  |||||  |||||  |||||
Db      535 CAAGTCGAACGGAAGGCCTT 515

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RESULT 59

```

BF237353
LOCUS      BF237353      647 bp      mRNA      linear      EST 14-NOV-2000
DEFINITION 602035026F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:4160215 5',
mRNA sequence.
ACCESSION  BF237353
VERSION     BF237353.1 GI:11151271
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 647)
REFERENCE  NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS   National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE     Unpublished (1999)
JOURNAL
COMMENT    Contact: Robert Strausberg, Ph.D.

```

Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM9439 row: d column: 08
High quality sequence stop: 647.
Location/Qualifiers

FEATURES

source
1. .647
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4160215"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP L19"
/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI CGAP Library."

ORIGIN

Query Match 74.2%; Score 17.8; DB 7; Length 647;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCCTT 21
|||||
Db 530 CAACTCGAACGGAAGGCATT 550

RESULT 60

CF898433 651 bp mRNA linear EST 04-NOV-2003
LOCUS CF898433
DEFINITION A0239B05-5 NIA Mouse Embryonic Germ Cell cDNA Library (long,
subtracted) Mus musculus cDNA clone NIA:A0239B05 IMAGE:30732112 5',
mRNA sequence.

ACCESSION CF898433.1 GI:38165482
VERSION CF898433.1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 651)
Pao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
Construction of long-transcript enriched cDNA libraries from
submicrogram amounts of total RNAs by a universal PCR amplification
method

JOURNAL Genome Res. 11 (9), 1553-1558 (2001)
PUBMED 11544199

COMMENT

Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdnaglsun.grc.nia.nih.gov
Plate: A0239 row: B column: 05
Seq primer: M13 Reverse
High quality sequence stop: 651
POLYA-No.

FEATURES

source
1. .651
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="NIA:A0239B05 IMAGE:30732112"
/sex="male"

/dev stage="embryonic day 8"
/lab_host="DH10B"
/clone_lib="NIA Mouse Embryonic Germ Cell cDNA Library
(long, subtracted)"
/note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI;
Site 2: NotI; Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). EG
cells were obtained from Dr. Brigid L.M. Hogan and RNA was
prepared by Dr. Mark G. Carter (NIH/NIA-IRP). EG cells
were cultured at 37. C. 5% CO2 in DMEM supplemented with
15% ES cell-qualified FBS, 0.1mM non-essential amino
acids, 2 mM glutamine, penicillin/streptomycin, 1 mM
sodium pyruvate, 0.1 mM beta-mercaptoethanol, and 10^-7
units of LIF per liter. Double-stranded cDNAs were
synthesized with an Oligo(dT) primer [Invitrogen:
5'-pGACTAGTTCAGTCGAGCGCGCCCTTTT-TTTT-3'] from
2.5 ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to lone-linker LL-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were double digested with NotI and SalI enzymes,
then purified by phenol/chloroform and Centricon 100. The
cDNA mixture was subjected to a special subtraction
procedure by Dr.Kazuhiro Kondo at Aisin Cosmos. Then the
subtracted cDNAs were cloned into SalI/NotI site of
pCMV-SPORT6 plasmid vector. The DH10B E. coli host was
transformed with the ligation mixture by the standard
chemical method. The average insert size is about 2.2kb.
The library was constructed by Yulan Piao and Kazuhiro
Kondo."

ORIGIN

Query Match 74.2%; Score 17.8; DB 5; Length 651;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCCTT 21
|||||
Db 468 CAACTCGAACGGAAGGCATT 488

RESULT 61

DV023955/c 680 bp mRNA linear EST 26-SEP-2005
LOCUS ZM_BFB0143008.f ZM_BFB Zea mays cDNA 3', mRNA sequence.
DEFINITION DV023955
ACCESSION DV023955
VERSION DV023955.1 GI:76284387
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 680)
Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
Maize Full-length cDNA Project
Unpublished (2005)
Contact: Yeisoo Yu
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9585
Fax: 520 621 1259
Email: yeisoo@genome.arizona.edu
Plate: 0143 row: O column: 08.
Location/Qualifiers

FEATURES

source
1. .680


```

/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"
/dev_stage="varies by tissue"
/lab_host="DH10B T1 phage resistant"
/clone_lib="ZM BFB"
/notes="Vector: pCWV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (http://www.genome.arizona.edu/orders/)."

```

ORIGIN

```

Query Match      74.2%; Score 17.8; DB 10; Length 680;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCCTT 21
    ||||| ||||| ||||| |||||
Db 513 CAAGTGGAAACGAAAGGCCCTT 493

```

```

RESULT 62
CN525338
LOCUS      CN525338      682 bp      mRNA      linear      EST 29-APR-2004
DEFINITION UI-M-HKO-cmw-p-08-0-UI.r1 NIH_BMAP_HKO Mus musculus cDNA clone
IMAGE:30623887 5', mRNA sequence.

ACCESSION  CN525338
VERSION     CN525338.1 GI:46852991
KEYWORDS   EST.

SOURCE      Mus musculus (house mouse)

ORGANISM    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE   1 (bases 1 to 682)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Dr. Jim Lin University of Iowa
            cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
            DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/mousefl.html
            This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)

```

```

Seq primer: pYX-5.
Location/Qualifiers
1..682
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30623887"
/tissue_type="Upper Head"
/dev_stage="9.5 and 10.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_HKO"
/notes="Organ: Head; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGACTCGAAT. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."
```

ORIGIN

```

Query Match      74.2%; Score 17.8; DB 8; Length 682;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCCTT 21
    ||||| ||||| ||||| |||||
Db 148 CAAGTCGAACGGAAGGCCCTT 168

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```

RESULT 63
DT945027/c
LOCUS      DT945027      685 bp      mRNA      linear      EST 21-SEP-2005
DEFINITION ZM_BFB0132B03.f ZM_BFB Zea mays cDNA 3', mRNA sequence.
ACCESSION  DT945027
VERSION     DT945027.1 GI:76017857
KEYWORDS   EST.

SOURCE      Zea mays
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE   1 (bases 1 to 685)
AUTHORS     Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
Rao,K., Haller,K., Wing,R., Soderlund,C., Wallbot,V. and Yu,Y.
TITLE       Maize Full-length cDNA Project
JOURNAL     Unpublished (2005)
COMMENT     Contact: Yeisoo Yu
            Arizona Genomics Institute
            The University of Arizona
            Forbes Building Room 303, Tucson, AZ 85721-0036, USA
            Tel: 520 626 9585
            Fax: 520 621 1259
            Email: yeisoo@genome.arizona.edu
            Plate: 0132 row: B column: 03.
            Location/Qualifiers
            1..685
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            /mol_type="mRNA"
            /cultivar="B73"
            /db_xref="taxon:4577"
            /tissue_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"
            /dev_stage="varies by tissue"
            /lab_host="DH10B T1 phage resistant"
            /clone_lib="ZM_BFB"

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FEATURES

source

1..685

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="B73"

/db_xref="taxon:4577"

/tissue_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"

/dev_stage="varies by tissue"

/lab_host="DH10B T1 phage resistant"

/clone_lib="ZM_BFB"


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FEATURES
  source
    Seq primer: pYX-5.
    Location/Qualifiers
      1..635
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        /mol_type="mRNA"
        /strain="C57BL/6"
        /db_xref="taxon:10090"
        /clone="IMAGE:30681540"
        /tissue_type="whole eye"

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(http://www.genome.arizona.edu/orders/)."

ORIGIN

Query Match 74.2%; Score 17.8; DB 2; Length 700;
 Best Local Similarity 90.5%; Pred. No. 1.5e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAGGCCTT 21
 ||||| ||||| ||||| ||||| |||||
 Db 363 CAAAGTCGAACGGAAGGACTT 383

RESULT 66

DV541234/c

LOCUS DV541234 710 bp mRNA linear EST 25-OCT-2005
 DEFINITION ZM_BFB0235018.f ZM_BFB Zea mays cDNA 3', mRNA sequence.

ACCESSION DV541234

VERSION DV541234.1 GI:78122850

EST.

KEYWORDS

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

AUTHORS

Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
 Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.

TITLE

Maize Full-length cDNA Project

JOURNAL

Unpublished (2005)

COMMENT

Contact: Yeisoo Yu
 Arizona Genomics Institute
 The University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9585

Fax: 520 621 1259

Email: yeisoo@genome.arizona.edu

Plate: 0235 row: O column: 18.

FEATURES

source

1..710

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="B73"

/db_xref="taxon:4577"

/tissue_type="mixed (silks, husks, ears, pollen, shoot

tips, leaf, root tips, whole seed, embryo)"

/dev_stage="varies by tissue"

/lab_host="DH10B T1 phage resistant"

/clone_lib="ZM BFB"

/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2:

NotI; Maize Full length cDNA library (3530 library)

created by Invitrogen from multiple tissues; Organ: silks,

husks, ears, pollen, shoot tips, leaf, root tips, whole

seed, embryo. This is a Gateway compatible vector,

permitting clone movement to new vector backbones for

expression in diverse host cells using recombination

rather than restriction enzymes. poly(A) + mRNA was

prepared by Invitrogen, and equimolar amounts of RNA from

each of the 12 tissue samples were mixed together for

selection of mRNA with a 5' cap. After synthesis of cDNA,

a normalization step was conducted against the mixture of

RNA sources. Tissues prepared: 1. just emerging silks; 2.

inner husks from ears of sample #1; 3. 20 dap aleurone; 4.

immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to

2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from

15 day old seedlings; all leaves with an expanded or

partially expanded sheath were removed; 8. mature leaf

tissue; 9. 0.5 cm long root tips from 15 day old

seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and

embryo; 12. 17 dap endosperm and embryo. All of the

sequenced clones in Maize Full-length cDNA Project will be

archived at the University of Arizona. Clones, high

density filters and amplified library can be ordered from

the University of Arizona

ORIGIN

Query Match 74.2%; Score 17.8; DB 10; Length 710;
 Best Local Similarity 90.5%; Pred. No. 1.5e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAGGCCTT 21
 ||||| ||||| ||||| ||||| |||||
 Db 565 CAAAGTCGAACGGAAGGCCTT 545

RESULT 67

DT654257/c

LOCUS DT654257 711 bp mRNA linear EST 07-SEP-2005
 DEFINITION ZM_BFB0127110.f ZM_BFB Zea mays cDNA 3', mRNA sequence.

ACCESSION DT654257

VERSION DT654257.1 GI:74246343

EST.

KEYWORDS

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

AUTHORS

Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
 Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.

TITLE

Maize Full-length cDNA Project

JOURNAL

Unpublished (2005)

COMMENT

Contact: Yeisoo Yu
 Arizona Genomics Institute
 The University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9585

Fax: 520 621 1259

Email: yeisoo@genome.arizona.edu

Plate: 0127 row: I column: 10.

FEATURES

source

1..711

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="B73"

/db_xref="taxon:4577"

/tissue_type="mixed (silks, husks, ears, pollen, shoot

tips, leaf, root tips, whole seed, embryo)"

/dev_stage="varies by tissue"

/lab_host="DH10B T1 phage resistant"

/clone_lib="ZM BFB"

/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2:

NotI; Maize Full length cDNA library (3530 library)

created by Invitrogen from multiple tissues; Organ: silks,

husks, ears, pollen, shoot tips, leaf, root tips, whole

seed, embryo. This is a Gateway compatible vector,

permitting clone movement to new vector backbones for

expression in diverse host cells using recombination

rather than restriction enzymes. poly(A) + mRNA was

prepared by Invitrogen, and equimolar amounts of RNA from

each of the 12 tissue samples were mixed together for

selection of mRNA with a 5' cap. After synthesis of cDNA,

a normalization step was conducted against the mixture of

RNA sources. Tissues prepared: 1. just emerging silks; 2.

inner husks from ears of sample #1; 3. 20 dap aleurone; 4.

immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to

2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from

15 day old seedlings; all leaves with an expanded or

partially expanded sheath were removed; 8. mature leaf

tissue; 9. 0.5 cm long root tips from 15 day old

seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and

embryo; 12. 17 dap endosperm and embryo. All of the

sequenced clones in Maize Full-length cDNA Project will be

archived at the University of Arizona. Clones, high

density filters and amplified library can be ordered from

the University of Arizona

(<http://www.genome.arizona.edu/orders/>) "

OPTICIN

```
Query Match          74.2%; Score 17.8; DB 10; Length 714;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 CAAGTCGAACGGAAAGGCCTT 21
|||||
db 513 CAAGTGGAAACGGAAAGGCCTT 493

RESULT	69
BF099995	
LOCUS	
BF099995	
DEFINITION	601752156F1 NCI CGAP Maml Mus musculus cdna clone IMAGE:3980095 5'
LOCUS	716 bp mRNA linear EST 19-OCT-2000

ACCESSION
BF099995
mRNA sequence.

VERSION	KEYWORDS	SOURCE	ORGANISM
BF099999.1	EST.	Mus musculus (house mouse)	Eukaryota; Metazoa; Chordata
GI:10882521		Mus musculus	Mammalia; Eutheria; Euarchont

REFERENCE
1 (bases 1 to 716)
AUTHORS Sciurognathi; Madoidea; Mullidae; Mullinae; Mus.
TITLE NIH-MGC <http://mgc.nci.nih.gov/>.
NATIONAL INSTITUTE OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)

CONTACT: Robert Strausberg, Ph.D.
Email: rgsabers@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at

found through the I.M.A.G.E. Consortium/ BENT at:
http://image.llnl.gov
Plate: L14N9174 row: 0 column: 14

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FEATURES
source
1. .716
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3980005"
/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Maml"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

```

Query Match	74.2%;	Score 17.8;	DB 7;	Length 716;
Best Local Similarity	90.5%;	Pred. No. 1.5e+03;		
Matches 19;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

Qy	1	CAAGTCGAACGGAAGGCCTT	21
Db	513	CAAGTCGAACACTGAAAGGACTT	533

RESULT 70				
BQ445033				
LOCUS	BQ445033	729 bp	mRNA	linear
DEFINITION	UT-M-ERO-bxp-o-13-o-UI.r1 NIH_BMAP_ER0 Mus musculus CDNA clone			EST 29-MAY-2002
	IMAGE:5711460	5',	mRNA sequence.	
ACCESSION	BQ445033			
VERSION	BQ445033.1	GI:21248145		

```

KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM

REFERENCE
TITILE      NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL     National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical College of Wisconsin
            cDNA Library Preparation: Express Genomics
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM15342 row: f column: 19
            High quality sequence stop: 612.

FEATURES
source
1..729
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CS7BL/6"
/db_xref="taxon:10090"
/clones="IMAGE:5711460"
/tissue_type="whole brain"
/dev_stages="embryo 15.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_libs="NIH BMAP ERO"
/note="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is GTCGCTGAAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN
Query Match      74.2%; Score 17.8; DB 3; Length 729;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACCGAAGGCCTT 21
|||||
Db 142 CAAGTCGAACCGAAGGACTT 162

RESULT 71
CO383984
LOCUS      AGNCOURT_26623469 NIH_MGC_253 Rattus norvegicus cDNA clone
DEFINITION IMAGE:7307949 5', mRNA sequence.
ACCESSION  CO383984
VERSION     CO383984.1 GI:49489807
KEYWORDS   EST.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM    Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
1 (bases 1 to 738)

REFERENCE
1 (bases 1 to 738)
AUTHORS    Rattus norvegicus
TITLE       NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL     National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

AUTHORS
TITILE      NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL     National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical College of Wisconsin
            cDNA Library Preparation: Express Genomics
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM15342 row: f column: 19
            High quality sequence stop: 612.

FEATURES
source
1..738
Location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clones="IMAGE:7304949"
/tissue_type="Ovary - Brown Norway Line 3 Age 8 weeks. Tissues were snap-frozen and transferred in -70c. RNase free the entire procedure."
/lab_host="DH10B Tona"
/clone_libs="NIH_MGC_253"
/note="Organ: ovary; Vector: pExpress-1; Site 1: EcoRV; Site 2: NotI; RNA obtained from female animals at 8 wk old. Tissues were snap-frozen and kept at -80C for two days before RNA extraction and purification (Tri-reagent method). cDNA was primed using oligo-dT primer: 5'-pGACTACTTCTAGATCGAGCGCCGCCCTT-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size-selection resulted in an average insert size of 1.5 kb. This primary library is normalized (non-normalized primary library is NIH MGC 252) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH_MGC library."

ORIGIN
Query Match      74.2%; Score 17.8; DB 8; Length 738;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACCGAAGGCCTT 21
|||||
Db 202 CAAGTCGAACCGAAGGACTT 222

RESULT 72
BI414831/c
LOCUS      BI414831
DEFINITION 602990771F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5146936 5', mRNA sequence.
ACCESSION  BI414831
VERSION     BI414831.1 GI:15175754
KEYWORDS   EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 739)

REFERENCE
1 (bases 1 to 739)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE       NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL     National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

```

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11362 row: m column: 17
High quality sequence start: 23
High quality sequence stop: 739.

FEATURES
source

1. 739
/organism="Mus musculus"
/mol_type="mRNA"
/strain="Czech II"
/db_xref="taxon:10090"
/clone="INAGS:5146936"
/tissue_type="pooled lung tumors"
/lab_hosts="DH10B (phage-resistant)"
/clone_lib="NCI_CGAP Lu33"
/notes="Organ: lung; Vector: pT7T3D-PacI; Site 1: NotI;
Site 2: EcoRI; 1st strand cDNA was prepared from mRNA
obtained from pooled lung tumors with a Not I - oligo (dT)
primer [5'.
TGTACCAATCTGAAGTGGAGCGCGCTCTGTTTTTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 74.2%; Score 17.8; DB 2; Length 739;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21

Db 708 CAAGTCGAACGGAAGGACTT 688

RESULT 73
BX855983/c
LOCUS
DEFINITION BX855983 tcay Oncorhynchus mykiss cDNA clone tcay0040b.g.16 5prim,
mRNA sequence.
BX855983
VERSION BX855983.2 GI:42752904
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 740)
Govoroun,M., Guiguen,Y. and Le Gac,F.
Construction and primary characterization of normalized cDNA
libraries in rainbow trout, Oncorhynchus mykiss
Unpublished (2003)
On Dec 16, 2003 this sequence version replaced gi:39952993.
Contact: Guiguen Y
INRA - SCRIBE
Campus de Beaulieu, RENNES cedex, 35042, France
Tel: 02-23.48.50.09
Fax: 02-23.48.50.20
Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0040 row: g column: 16
Seq primer: M13R

FEATURES
source

Location/Qualifiers
1. 740
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"

/db_xref="taxon:8022"
/clone="tcay0040b.g.16"
/tissue_type="adipose tissue, blood, brain,
differentiating gonads, gills, interrenal, intestine,
kidney, liver, muscle, ovary, pituitary, testis"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/clone_lib="tcay"
/note="Vector: pT7T3D-PacI; Rainbow trout multi-tissues -
normalized + 1 subtraction (tcay); Clone distribution:
AGENAE Resource centre. Francois PIUMI,
Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, France, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"

ORIGIN

Query Match 74.2%; Score 17.8; DB 4; Length 740;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21

Db 552 CACGTCGACAGAAAGGCCTT 532

RESULT 74

BY732037

LOCUS

DEFINITION

BY732037 RIKEN full-length enriched, 8 cells embryo Mus musculus

cDNA clone E860117P18 5', mRNA sequence.

BY732037

BY732037.1 GI:27145164

EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidae; Muridae; Murinae; Mus.

1 (bases 1 to 745)

Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,

Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,

Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,

Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,

Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,

Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusica,V.,

Ciothia,C., Corbani,L.E., Cousins,S., Dalia,E., Dragani,T.A.,

Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,

Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,

Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,

Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,

Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,

Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,

Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,

Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,

Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,

Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,

Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,

Uetani,R., Wagner,L., Wahlstedt,C., Wang,Y., Watanabe,Y.,

Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,

Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,

Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,

Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,

Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Inotani,K., Ishii,Y.,

Itoh,M., Kigawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,

Shingawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,

Rogers,J., Birney,E. and Hayashizaki,Y.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

12466851

JOURNAL

PUBLISHED

COMMENT

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,
Fukuda, S., Hashizume, W., Hayaashida, K., Hirozane, T., Hori, F.,
Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
Takeda, F., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.

FEATURES

source
1. .745
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="E860117P18"
/cell_type="8 cells"
/dev_stage="8 cells embryo"
/clone_lib="RIKEN full-length enriched, 3 cells embryo"

ORIGIN

Query Match 74.2%; Score 17.8; DB 4; Length 745;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
|||||
Db 368 CAAGTCGAACGGAAGGACTT 388

RESULT 75

DV942547/c 746 bp mRNA linear EST 05-DEC-2005
LOCUS
DEFINITION
ACCESSION DV942547
VERSION DV942547.1 GI:83278539

KEYWORDS
SOURCE EST.
Zeae may

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 746)
Zhou, R.L., Shendelman, J.M., Borsuk, L.A., Chen, H.D., Chen, Y.R. and
Schnable, P.S.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Resequencing Unigene I EST set
Unpublished (2005)
Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University

2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA
Tel: 515-294-0975
Fax: 515-294-5256
Email: schnable@iastate.edu

Insert Length: 746 Std Error: 0.00.
Location/Qualifiers
1. .746

/organism="Zea mays"
/mol_type="mRNA"
/db_xref="taxon:4577"
/clone_lib="UGI-Reseq"

ORIGIN

Query Match 74.2%; Score 17.8; DB 10; Length 746;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
|||||
Db 613 CAAGTCGAACGGAAGGCCTT 593

RESULT 76

DR794419/c 752 bp mRNA linear EST 27-JUL-2005
LOCUS
DEFINITION ZM BF50015C05.f ZM_BFB Zea mays cDNA 3', mRNA sequence.
ACCESSION DR794419

VERSION DR794419.1 GI:71315610
KEYWORDS
SOURCE EST.
Zeae may

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 752)

Kim, H., Collura, K., Wissotski, M., Smart, D., Kudrna, D., Muller, C.,
Rao, K., Haller, K., Wing, R., Soderlund, C., Walbot, V. and Yu, Y.

Maize Full-length cDNA Project
Unpublished (2005)
Contact: Veisoo Yu
Arizona Genomics Institute

The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9585
Fax: 520 621 1259

Email: veisoo@genome.arizona.edu
Plate: 0015 row: C column: 05.

FEATURES

source
1. .752
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"

/db_xref="taxon:4577"

/tissue_type="mixed (silks, husks, ears, pollen, shoot
tips, leaf, root tips, whole seed, embryo)"
/dev_stage="varies by tissue"

/lab_host="DH10B T1 phage resistant"

/clone_lib="ZM_BPB"

/note="Vector: pCMV-SPORT 6.1; Site: 1: EcoRV; Site 2:
NotI; Maize Full length cDNA library (3530 library)

created by invitrogen from multiple tissues; Organ: silks,
husks, ears, pollen, shoot tips, leaf, root tips, whole
seed, embryo. This is a Gateway compatible vector,
permitting clone movement to new vector backbones for
expression in diverse host cells using recombination
rather than restriction enzymes. poly(A) + mRNA was

prepared by invitrogen, and equimolar amounts of RNA from
each of the 12 tissue samples were mixed together for
selection of mRNA with a 5' cap. After synthesis of cDNA,
a normalization step was conducted against the mixture of
RNA sources. Tissues prepared: 1. just emerging silks; 2.
inner husks from ears of sample #1; 3. 20 day aleurone; 4.
immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to

2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 day whole seed, 11. 12 day endosperm and embryo; 12. 17 day endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (<http://www.genome.arizona.edu/cordero/>).

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Query Match          74.2%; Score 17.8; DB 10; Length 753;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19: Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 CAAGTCGAACGGAAGGCTT 21
510 CAAGTGGAAACGAAAAGGCTT 490
Db

RESULT 78					
DR786717/c					
LOCUS	DR786717	777 bp	mRNA	linear	EST 27-JUL-2005
DEFINITION	ZM BFB0003M18.f ZM BFB Zea mays cDNA 3'				mRNA sequence.

SOURCE	Zea mays
ORGANISM	Zea mays
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. (bases 1 to 777)
AUTHORS	Kim H., Collura, K., Wissotski, M., Smart, D., Kudrna, D., Muller, C., Rao, K., Haller, K., Wing, R., Soderlund, C., Walbot, V. and Yu, Y.
TITLE	Maize Full-length cDNA Project
JOURNAL	Unpublished (2005)
COMMENT	Contact: Yeisoo Yu

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FEATURES
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Location/Qualifiers
1. .777
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/mol_type="mRNA"
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/db_xref="taxon:4577"
/tissue_type="mixed (silks, husks, ears, pollen, shoot
tips, leaf, root tips, whole seed, embryo)"
/dev_stage="varies by tissue"
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/note="vector: pCMV-SPORT 6.1; Site_1: EcoRV, Site_2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 day aleurone; 4. immature tassels, stages from -2 mm to 1-2 cm 5s. 2 mm to

2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona
(http://www.genome.arizona.edu/orders/).

ORIGIN

Query Match 74.2%; Score 17.8; DB 10; Length 777;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
||||| ||||| ||||| ||||| |||||
Db 535 CAAGTGGAAACGAAAGGCCTT 515

RESULT 79

DR954333/c
LOCUS DR954333 777 bp mRNA linear EST 03-AUG-2005
DEFINITION ZM_BFD0046F03.f ZM_BFB Zea mays cDNA 3', mRNA sequence.
ACCESSION DR954333
VERSION DR954333.1 GI:71756396
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 777)
Kim,H., Collura,K., Wisotski,M., Smart,D., Kudrna,D., Muller,C., Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu.Y.
Maize Full-length cDNA Project
Unpublished (2005)
Contact: Veisoo Yu
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9585
Fax: 520 621 1259
Email: veisoo@genome.arizona.edu
Plate: 0046 row: F column: 03.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..777
Location/Qualifiers
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"
/dev_stage="varies by tissue"
/lab_host="DH10B T1 phage resistant"
/clone_lib="ZM BFB"
/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV, Site 2: NotI; Zea Full length cDNA library (3530 library) created by invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A) + mRNA was prepared by invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to

2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona
(http://www.genome.arizona.edu/orders/).

ORIGIN

Query Match 74.2%; Score 17.8; DB 10; Length 777;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
||||| ||||| ||||| ||||| |||||
Db 535 CAAGTGGAAACGAAAGGCCTT 515

RESULT 80

DV164117/c
LOCUS DV164117 780 bp mRNA linear EST 04-OCT-2005
DEFINITION ZM_BFD0160H01.f ZM_BFB Zea mays cDNA 3', mRNA sequence.
ACCESSION DV164117
VERSION DV164117.1 GI:76910962
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 780)
Kim,H., Collura,K., Wisotski,M., Smart,D., Kudrna,D., Muller,C., Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu.Y.
Maize Full-length cDNA Project
Unpublished (2005)
Contact: Veisoo Yu
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9585
Fax: 520 621 1259
Email: veisoo@genome.arizona.edu
Plate: 0160 row: H column: 01.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..780
Location/Qualifiers
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
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/dev_stage="varies by tissue"
/lab_host="DH10B T1 phage resistant"
/clone_lib="ZM BFB"
/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV, Site 2: NotI; Zea Full length cDNA library (3530 library) created by invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A) + mRNA was prepared by invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to

2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 day whole seed; 11. 12 day endosperm and embryo; 12. 17 day endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (<http://www.genome.arizona.edu/orders/>).

ORIGIN

Query Match 74.2%; Score 17.8; DB 10; Length 780;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGAAAGCCCTT 21
||||| ||||| ||||| |||||
Db 510 CAAGTCGAACGAAAGCCCTT 490

RESULT 81
CB953248 808 bp mRNA linear EST 29-APR-2003
LOCUS AGENCOURT 13687210 NIH_MGC_176 Mus musculus cDNA clone
DEFINITION IMAGE:30304304 5', mRNA sequence.
ACCESSION CB953248
VERSION CB953248.1 GI:30209366
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 808)
TITLE NIH-MGC <http://mgi.nci.nih.gov/>.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-rc@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Michael Brownstein Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: NDCM76 row: d column: 09
High quality sequence stop: 477.

FEATURES

source
Location/Qualifiers
1. .808
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/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:30304304"
/lab_host="DH10B (TI-phage-resistant)"
/clone_lib="NIH_MGC_176"
/notes="Organ: kidney; Vector: pDNR-LIB; Site:1: Sfil (ggccattggcc); Site:2: Sfil (ggccgctcgcc); cDNA made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in cloning as follows:
5'-AACGAGGGTATCAACGAGTGGCATTTACGCGCGG-3' and
5'-ATTCAGGCGCGGCGGCGGACATG-dT(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5 kb size fraction. Library created in the laboratory of M. Brownstein (NIMH, NIH). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 74.2%; Score 17.8; DB 4; Length 808;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGAAAGCCCTT 21
||||| ||||| ||||| |||||
Db 394 CAAGTCGAACGAAAGGACTT 414

RESULT 82

LOCUS DR794420 816 bp mRNA linear EST 27-JUL-2005
DEFINITION ZM BFB0015C05.r ZM_BFB Zea mays cDNA 5', mRNA sequence.
ACCESSION DR794420
VERSION DR794420.1 GI:71315611
KEYWORDS EST.

ORGANISM

Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 816)
Kim, H., Collura, K., Wissotski, M., Smart, D., Kudrna, D., Muller, C.,
Rao, K., Haller, K., Wing, R., Soderlund, C., Walbot, V. and Yu, Y.
Maize Full-length cDNA Project
Unpublished (2005)
Contact: Yeisoo Yu
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9585
Fax: 520 621 1259
Email: yeisoo@genome.arizona.edu
Plate: 0015 row: C column: 05.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source
Location/Qualifiers
1. .816
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"
/dev_stage="varies by tissue"
/lab_host="DH10B T1 phage resistant"
/clone_lib="ZM_BFB"
/notes="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 day aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 day whole seed; 11. 12 day endosperm and embryo; 12. 17 day endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (<http://www.genome.arizona.edu/orders/>).

ORIGIN

Query Match 74.2%; Score 17.8; DB 10; Length 816;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 CAACTCGAACGGAAGGCCTT 21
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Db 776 CAACTGGAACGAAAGGCCTT 796

RESULT 83
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LOCUS ZM_BF00160P07.r 820 bp mRNA linear EST 04-OCT-2005
DEFINITION ZM_BF00160P07.r ZM_BFb Zea mays cDNA 5', mRNA sequence.
ACCESSION DV164477
VERSION DV164477.1 GI:76911880
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 820)
Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
Maize Full-length cDNA Project
Unpublished (2005)
Contact: Yeisoo Yu
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9585
Fax: 520 621 1259
Email: yeisoo@genome.arizona.edu
Plate: 0160 row: P column: 07.
Location/Qualifiers
1..820
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
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tips, leaf, root tips, whole seed, embryo)"
/dev_stages="varies by tissue"
/lab_host="DH10B T1 phage resistant"
/clone_lib="ZM_BFb"
/notes="Vector: pCMV-SPORT 6.1; Site_1: EcoRV; Site_2:
NotI; Maize Full length cDNA library (3530 library)
created by Invitrogen from multiple tissues; Organ: silks,
husks, ears, pollen, shoot tips, leaf, root tips, whole
seed, embryo. This is a Gateway compatible vector.
permitting clone movement to new vector backbones for
expression in diverse host cells using recombination
rather than restriction enzymes. poly(A)+ mRNA was
prepared by Invitrogen, and equimolar amounts of RNA from
each of the 12 tissue samples were mixed together for
a selection of mRNA with a 5' cap. After synthesis of cDNA,
a normalization step was conducted against the mixture of
RNA sources. Tissues prepared: 1. just emerging silks; 2.
inner husks from ears of sample #1; 3. 20 dap aleurone; 4.
immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to
2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from
15 day old seedlings; all leaves with an expanded or
partially expanded sheath were removed; 8. mature leaf
tissue; 9. 0.5 cm long root tips from 15 day old
seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and
embryo; 12. 17 dap endosperm and embryo. All of the
sequenced clones in Maize Full-length cDNA Project will be
archived at the University of Arizona. Clones, high
density filters and amplified library can be ordered from
the University of Arizona
(http://www.genome.arizona.edu/orders/)."

ORIGIN
Query Match 74.2%; Score 17.8; DB 10; Length 820;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;


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Qy 1 CAACTCGAACGGAAGGCCTT 21
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Db 776 CAACTGGAACGAAAGGCCTT 796

RESULT 84
DY361640
LOCUS ZO_Ed0007M16.r 824 bp mRNA linear EST 09-FEB-2005
DEFINITION ZO_Ed0007M16.r ZO_Ed Zingiber officinale cDNA clone ZO_Ed0007M16
3', mRNA sequence.
ACCESSION DY361640
VERSION DY361640.1 GI:87094856
KEYWORDS EST.
SOURCE Zingiber officinale
ORGANISM Zingiber officinale
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales;
Zingiberaceae; Zingiber.
1 (bases 1 to 824)
Ma,X.Q., Koo,H.J., Haller,K.P., Soderlund,C.A. and Gang,D.R.
Comparative Analysis of Expressed Sequence Tags from Different
Organs of Ginger and Turmeric. Insights into Specialized Metabolism
in Traditional Medicinal Plants
Unpublished (2006)
Contact: David R. Gang
Department of Plant Sciences
The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 621 7154
Fax: 520 621 7186
Email: gang@ag.arizona.edu
Plate: 0007 row: M column: 16.
Location/Qualifiers
1..824
/organism="Zingiber officinale"
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/cultivar="Yellow Ginger"
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/tissue_type="rhizome"
/lab_host="TJC 121"
/clone_lib="ZO_Ed"
/notes="Vector: pBluescriptRISK-; Site_1: EcoRI; Site_2:
XhoI; Greenhouse, soil grown"

ORIGIN
Query Match 74.2%; Score 17.8; DB 10; Length 824;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGTCGACGGAAGGCCTTTC 23
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Db 337 AGACGAACGGAAGGCCTTTC 357

RESULT 85
DR786718
LOCUS ZM_BF0003M18.r 827 bp mRNA linear EST 27-JUL-2005
DEFINITION ZM_BF0003M18.r ZM_BFb Zea mays cDNA 5', mRNA sequence.
ACCESSION DR786718
VERSION DR786718.1 GI:71301367
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 827)
Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
Maize Full-length cDNA Project
Unpublished (2005)

REFERENCE
AUTHORS
TITLE
JOURNAL

```

```

COMMENT
Contact: Yeisoo Yu
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9585
Fax: 520 621 1259
Email: yeisoo@genome.arizona.edu
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1. .827
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/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="mixed (silks, husks, ears, pollen, shoot
tips, leaf, root tips, whole seed, embryo)"
/dev_stage="varies by tissue"
/lab_host="DH10B T1 phage resistant"
/clone_lib="ZM BFB"
/notes="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2:
NotI; Maize Full length cDNA library (3530 library)
created by Invitrogen from multiple tissues; Organ: silks,
husks, ears, pollen, shoot tips, leaf, root tips, whole
seed, embryo. This is a Gateway compatible vector,
permitting clone movement to new vector backbones for
expression in diverse host cells using recombination
rather than restriction enzymes. poly(A)+ mRNA was
prepared by Invitrogen, and equimolar amounts of RNA from
each of the 12 tissue samples were mixed together for
selection of mRNA with a 5' cap. After synthesis of cDNA,
a normalization step was conducted against the mixture of
RNA sources. Tissues prepared: 1. just emerging silks; 2.
inner husks from ears of sample #1; 3. 20 dap aleurone; 4.
immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to
2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from
15 day old seedlings; all leaves with an expanded or
partially expanded sheath were removed; 8. mature leaf
tissue; 9. 0.5 cm long root tips from 15 day old
seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and
embryo; 12. 17 dap endosperm and embryo. All of the
sequenced clones in Maize Full-length cDNA Project will be
archived at the University of Arizona. Clones, high
density filters and amplified library can be ordered from
the University of Arizona
(http://www.genome.arizona.edu/orders/)."

ORIGIN
Query Match 74.2%; Score 17.8; DB 10; Length 827;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTT 21
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Db 774 CAAGTGGACGAAAGGCCTT 794

RESULT 86
LOCUS DR966931 848 bp mRNA linear EST 03-AUG-2005
DEFINITION ZM BFB0087116.r ZM_BFB Zea mays cDNA 5', mRNA sequence.
ACCESSION DR966931
VERSION DR966931.1 GI:71768994
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 848)
Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
Maize Full-length cDNA Project
Unpublished (2005)
JOURNAL

FEATURES
source
1. .848
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="mixed (silks, husks, ears, pollen, shoot
tips, leaf, root tips, whole seed, embryo)"
/dev_stage="varies by tissue"
/lab_host="DH10B T1 phage resistant"
/clone_lib="ZM BFB"
/notes="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2:
NotI; Maize Full length cDNA library (3530 library)
created by Invitrogen from multiple tissues; Organ: silks,
husks, ears, pollen, shoot tips, leaf, root tips, whole
seed, embryo. This is a Gateway compatible vector,
permitting clone movement to new vector backbones for
expression in diverse host cells using recombination
rather than restriction enzymes. poly(A)+ mRNA was
prepared by Invitrogen, and equimolar amounts of RNA from
each of the 12 tissue samples were mixed together for
selection of mRNA with a 5' cap. After synthesis of cDNA,
a normalization step was conducted against the mixture of
RNA sources. Tissues prepared: 1. just emerging silks; 2.
inner husks from ears of sample #1; 3. 20 dap aleurone; 4.
immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to
2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from
15 day old seedlings; all leaves with an expanded or
partially expanded sheath were removed; 8. mature leaf
tissue; 9. 0.5 cm long root tips from 15 day old
seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and
embryo; 12. 17 dap endosperm and embryo. All of the
sequenced clones in Maize Full-length cDNA Project will be
archived at the University of Arizona. Clones, high
density filters and amplified library can be ordered from
the University of Arizona
(http://www.genome.arizona.edu/orders/)."

ORIGIN
Query Match 74.2%; Score 17.8; DB 10; Length 848;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTT 21
||||| ||||| ||||| |||||
Db 777 CAAGTGGACGAAAGGCCTT 797

RESULT 87
LOCUS BI664538 856 bp mRNA linear EST 12-SEP-2001
DEFINITION 603290164F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5324391 5',
mRNA sequence.
ACCESSION BI664538
VERSION BI664538.1 GI:15578771
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 856)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL

```

```

COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-remail.nih.gov
              Tissue Procurement: Jeffrey Green M.D.
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Inyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: L1AM11822 row: 0 column: 16
              High quality sequence start: 2
              High quality sequence stop: 677.
              Location/Qualifiers
                1..856
                  /organism="Mus musculus"
                  /mol_type="mRNA"
                  /strain="FVB/N"
                  /db_xref="taxon:10090"
                  /clones="IMAGE:5324391"
                  /sex="female, virgin"
                  /tissue_type="infiltrating ductal carcinoma"
                  /dev_stage="5 months"
                  /lab_host="DH10B"
                  /clone_lib="NCI_CGAP_Mam6"
                  /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
                  Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                  Library constructed by Life Technologies. Investigator
                  providing samples: Jeffrey Green, M.D., NIH"

FEATURES     source
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    /organism="Mus musculus"
    /mol_type="mRNA"
    /strain="FVB/N"
    /db_xref="taxon:10090"
    /clones="IMAGE:5324391"
    /sex="female, virgin"
    /tissue_type="infiltrating ductal carcinoma"
    /dev_stage="5 months"
    /lab_host="DH10B"
    /clone_lib="NCI_CGAP_Mam6"
    /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
    Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
    Library constructed by Life Technologies. Investigator
    providing samples: Jeffrey Green, M.D., NIH"

ORIGIN
Query Match      74.2%; Score 17.8; DB 2; Length 856;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
    |||||
Db 331 CAAGTCGAACGGAAGGACTT 351
    |||||

RESULT 89
BU522312
LOCUS      BU522312      874 bp      mRNA      linear      EST 13-SEP-2002
DEFINITION AGENCOURT 10152472 NCI CGAP Mam2 Mus musculus cDNA clone
IMAGE:6528698 5', mRNA sequence.
ACCESSION  BU522312
VERSION     BU522312.1 GI:22829838
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 874)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: L1AM14127 row: j column: 16
            High quality sequence stop: 650.
            Location/Qualifiers
              1..874
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                /mol_type="mRNA"
                /strain="FVB/N-3"
                /db_xref="taxon:10090"
                /clones="IMAGE:6528698"
                /tissue_type="tumor, biopsy sample"
                /dev_stage="5 months"
                /lab_host="DH10B"
                /clone_lib="NCI_CGAP Mam2"
                /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
                Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                Library constructed by Life Technologies. Investigator
                providing samples: Gilbert Smith, NIH"

FEATURES     source
  1..874
    /organism="Mus musculus"
    /mol_type="mRNA"
    /strain="FVB/N-3"
    /db_xref="taxon:10090"
    /clones="IMAGE:6528698"
    /tissue_type="tumor, biopsy sample"
    /dev_stage="5 months"
    /lab_host="DH10B"
    /clone_lib="NCI_CGAP Mam2"
    /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
    Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
    Library constructed by Life Technologies. Investigator
    providing samples: Gilbert Smith, NIH"

ORIGIN
Query Match      74.2%; Score 17.8; DB 2; Length 856;
Best Local Similarity 90.5%; Pred. NO. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
    |||||
Db 530 CAAGTCGAACGGAAGGACTT 550
    |||||

RESULT 88
CF551692
LOCUS      CF551692      862 bp      mRNA      linear      EST 25-SEP-2003
DEFINITION AGENCOURT 15585358 NIH_MGC_222 Mus musculus cDNA clone
IMAGE:30526004 5', mRNA sequence.
ACCESSION  CF551692
VERSION     CF551692.1 GI:34888526
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 862)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhardt, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Naryan Bhat
            cDNA Library Preparation: Express Genomics
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM608 row: a column: 21
            High quality sequence stop: 626.
            Location/Qualifiers
              1..862
                /organism="Mus musculus"

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Query Match 74.2%; Score 17.8; DB 3; Length 874;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTT 21
|||||
Db 550 CAAGTCGAACGGAAGGACTT 570

RESULT 90
DT942318
LOCUS
DEFINITION ZM BFB01271110.1 ZM BFB Zea mays cDNA 5', mRNA linear EST 21-SEP-2005
ACCESSION DT942318
VERSION DT942318.1 GI:76015148
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 891)
Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
Maize Full-length cDNA Project
Unpublished (2005)
JOURNAL
COMMENT Contact: Yeisoo Yu
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9585
Fax: 520 621 1259
Email: yeisoo@genome.arizona.edu
Plate: 0127 row: 1 column: 10.

FEATURES
source
1. .891
Location/Qualifiers
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"
/dev_stage="varies by tissue"
/lab_host="DH10B T1 phage resistant"
/clone_lib="ZM BPB"
/note="Vector: pCMV-SPORT 6.1; Site_1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (<http://www.genome.arizona.edu/orders/>)."

ORIGIN

Query Match 74.2%; Score 17.8; DB 10; Length 891;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTT 21
|||||
Db 794 CAAGTCGAACGGAAGGCCTT 814

RESULT 91
BE367787
LOCUS
DEFINITION BE367787 894 bp mRNA linear EST 21-JUL-2000
601217408F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3586776 5', mRNA sequence.
ACCESSION BE367787
VERSION BE367787.1 GI:9313059
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 894)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapps-f@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM8748 row: 0 column: 01
High quality sequence stop: 679.

FEATURES
source
1. .894
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="Czech II"
/db_xref="taxon:10090"
/clone="IMAGE:3586776"
/tissue_type="spontaneous tumor, metastatic to mammary. Stem cell origin."
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

ORIGIN
Query Match 74.2%; Score 17.8; DB 7; Length 894;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTT 21
|||||
Db 507 CAAGTCGAACGGAAGGACTT 527

RESULT 92
BQ944677
LOCUS
DEFINITION BQ944677 906 bp mRNA linear EST 21-AUG-2002
AGENCOURT_8933003 NCI CGAP_Mam2 Mus musculus cDNA clone IMAGE:6488886 5', mRNA sequence.
ACCESSION BQ944677
VERSION BQ944677.1 GI:22360155
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 906)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov

cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LHAM14036 row: d column: 07
 High quality sequence stop: 639.

FEATURES

Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N-3"
 /db_xref="taxon:10090"
 /clone="IMAGE:648886"
 /tissue_type="tumor, biopsy sample"
 /dev_stage="5 months"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Mam2"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 74.2%; Score 17.8; DB 3; Length 906;
 Best Local Similarity 90.5%; Pred. NO. 1.6e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTT 21
 |||||
 Db 92 CAAGTCGAACGGAAGGCGCTT 112

RESULT 93

DR815819
 LOCUS ZM_BF00046F03.r ZM_BFB Zea mays cDNA 5', mRNA linear EST 28-JUL-2005
 DEFINITION ZM_BF00046F03.r ZM_BFB Zea mays cDNA 5', mRNA sequence.
 ACCESSION DR815819
 VERSION DR815819.1 GI:71434769
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 912)
 AUTHORS Kim, H., Collura, K., Wisotzki, M., Smart, D., Kudrna, D., Muller, C., Rao, K., Haller, K., Wing, R., Soderlund, C., Walbot, V. and Yu, Y.
 TITLE Maize Full-length cDNA Project
 JOURNAL Unpublished (2005)
 COMMENT Contact: Yeisoo Yu
 Arizona Genomics Institute
 The University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA
 Tel: 520 626 9585
 Fax: 520 621 1259
 Email: yeisoo@genome.arizona.edu
 Plate: 0046 row: F column: 03.

FEATURES

Location/Qualifiers
 1..912
 /organism="Zea mays"
 /mol_type="mRNA"

FEATURES

/cultivar="B73"
 /db_xref="taxon:4577"
 /tissue_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"
 /dev_stage="varies by tissue"
 /lab_hosts="DH10B T1 phage resistant"
 /clone_lib="ZM_BFB"
 /note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues: Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A) + mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona
 (<http://www.genome.arizona.edu/orders/>)."

ORIGIN

Query Match 74.2%; Score 17.8; DB 10; Length 912;
 Best Local Similarity 90.5%; Pred. NO. 1.6e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTT 21
 |||||
 Db 775 CAAGTCGAACGGAAGGCGCTT 795

RESULT 94

BG247267
 LOCUS BG247267 918 bp mRNA linear EST 13-FEB-2001
 DEFINITION 602360162F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4488711 5', mRNA sequence.
 ACCESSION BG247267
 VERSION BG247267.1 GI:12757082
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 918)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LHAM10335 row: k column: 16
 High quality sequence stop: 667.
 Location/Qualifiers

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1. .918
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/dev_stage="3 months, virgin"
/lab_host="DH10B"
/clone_lib="NCI-CCAP Mam1"
/notes="Organ: mammary; Vector: PCMV-SPORT6; Site 1: Sali; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

ORIGIN
Query Match 74.2%; Score 17.8; DB 2; Length 918;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTT 21
|||||
Db 531 CAAGTCGAACGGAAGGACTT 551

RESULT 95
DV062398 945 bp mRNA linear EST 27-SEP-2005
LOCUS
DEFINITION
NEONATAL_12_F04.x1 FH NEONATAL Mus musculus cDNA clone
NEONATAL_12_F04 similar to COP9 (constitutive photomorphogenic)
homolog subunit 7a (Arabidopsis thaliana), mRNA sequence.

ACCESSION
DV062398
VERSION
DV062398.1 GI:76389696
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 945)
Nelson,P.S., Pritchard,C., Abbott,D.E. and Clegg,N.
The human (PEDB) and mouse (mPEDB) Prostate Expression Databases
Nucleic Acids Res. 30 (1), 218-220 (2002)
11752298
PUBMED

COMMENT
Contact: Nelson PS
Peter Nelson Lab, Department of Human Biology
Fred Hutchinson Cancer Research Center
1100 Fairview Ave N D4-100, Seattle, WA 98109, USA
Fax: 206 667 2917
Email: pnelson@fhcrc.org
Insert Length: 945 Std Error: 0.00
High quality sequence start: 23
High quality sequence stop: 663.
Location/Qualifiers
1. .945
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="NEONATAL_12_F04"
/sex="Male"
/tissue_type="Equal amounts of pooled ventral prostate, dorsolateral prostate, and coagulating gland (anterior prostate)"
/lab_host="BM25.8"
/clone_lib="FH NEONATAL"
/notes="Organ: prostate; Vector: pTriplex2; Site 1: SfiI; Site 2: SfiI; Library was constructed using Clontechs SMART cDNA library construction kit. 0.1ug of total RNA from pooled 2-day dorsolateral prostate, 0.1ug of total RNA from pooled 2-day ventral prostate, and 0.1ug of total RNA from pooled 2-day coagulating gland (anterior prostate) was combined and used in 1st strand cDNA

source
1. .918
/organism="Mus musculus"
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/strain="FVB/N"
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/dev_stage="3 months, virgin"
/lab_host="DH10B"
/clone_lib="NCI-CCAP Mam1"
/notes="Organ: mammary; Vector: PCMV-SPORT6; Site 1: Sali; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

ORIGIN
Query Match 74.2%; Score 17.8; DB 2; Length 918;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTT 21
|||||
Db 531 CAAGTCGAACGGAAGGACTT 551

RESULT 95
DV062398 945 bp mRNA linear EST 27-SEP-2005
LOCUS
DEFINITION
NEONATAL_12_F04.x1 FH NEONATAL Mus musculus cDNA clone
NEONATAL_12_F04 similar to COP9 (constitutive photomorphogenic)
homolog subunit 7a (Arabidopsis thaliana), mRNA sequence.

ACCESSION
DV062398
VERSION
DV062398.1 GI:76389696
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 945)
Nelson,P.S., Pritchard,C., Abbott,D.E. and Clegg,N.
The human (PEDB) and mouse (mPEDB) Prostate Expression Databases
Nucleic Acids Res. 30 (1), 218-220 (2002)
11752298
PUBMED

COMMENT
Contact: Nelson PS
Peter Nelson Lab, Department of Human Biology
Fred Hutchinson Cancer Research Center
1100 Fairview Ave N D4-100, Seattle, WA 98109, USA
Fax: 206 667 2917
Email: pnelson@fhcrc.org
Insert Length: 945 Std Error: 0.00
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Location/Qualifiers
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/mol_type="mRNA"
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/lab_host="BM25.8"
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/notes="Organ: prostate; Vector: pTriplex2; Site 1: SfiI; Site 2: SfiI; Library was constructed using Clontechs SMART cDNA library construction kit. 0.1ug of total RNA from pooled 2-day dorsolateral prostate, 0.1ug of total RNA from pooled 2-day ventral prostate, and 0.1ug of total RNA from pooled 2-day coagulating gland (anterior prostate) was combined and used in 1st strand cDNA

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synthesis. 2nd strand cDNA was generated by 23 cycles of
PCR, digested with SfiI and ligated into the
lambdaTriplex2 phagemid. Phagemids were converted to
pTriplex2 plasmids in the BM25.8 e-coli strain. Created
from pooled prostate from five two day old male C57BL/6
mice by Colin Pritchard."

ORIGIN
Query Match 74.2%; Score 17.8; DB 10; Length 945;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTT 21
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Db 230 CAAGTCGAACGGAAGGACTT 250

RESULT 96
CL029182 995 bp DNA linear GSS 31-DEC-2003
LOCUS
DEFINITION
CH216-28J13_Sp6.1 CH216 Xenopus tropicalis genomic clone
CH216-28J13, Genomic survey sequence.

ACCESSION
CL029182
VERSION
CL029182.1 GI:40475616
KEYWORDS
GSS.
SOURCE
Xenopus tropicalis (western clawed frog)
ORGANISM
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus; Silurana.

REFERENCE
1 (bases 1 to 995)
Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
Mardis,E. and Wilson,N.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
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Location/Qualifiers
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QY 2 AAGTCGAACGGAAGGCCTT 22
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Db 773 AAGTTGAACAGAAAGGCCTT 793

RESULT 97
DR045951/c
LOCUS
DEFINITION
FP-11_G06.SFQ cDNA library of Phaeosphaeria nodorum grown on wheat
cell walls Phaeosphaeria nodorum cDNA, mRNA sequence.
DR045951 1199 bp mRNA linear EST 02-JUN-2005
ACCESSION
DR045951

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VERSION DR045951.1 GI:66909787
SOURCE EST.
ORGANISM Phaeosphaeria nodorum

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
AUTHORS Pleosporales; Phaeosphaeriaceae; Phaeosphaeria.
1 (bases 1 to 1199)
Bindschedler,L.V., Cooper,R.M., Thomas,S.W., Madrid,M.P. and
Oliver,R.P.
cdna library of Phaeosphaeria nodorum grown on wheat cell walls
CNDA library (2005)
Unpublished (2005)
Contact: Richard Oliver
Australian Centre for Necrotrophic Fungal Pathogens (ACNFP)
Murdoch University
South Street, Murdoch, W.A 6150, Australia
Tel: +0893607404
Email: roliver@murdoch.edu.au.

FEATURES
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DEFINITION mu60h11.r1 Soares mouse lymph node NbMLN Mus musculus cDNA clone
IMAGE:643845 5', mRNA sequence.
ACCESSION AA204210
VERSION AA204210.1 GI:1800807
SOURCE EST.
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 193)
AUTHORS Matra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LiNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MG1:395837
Putative full length read
vector to vector length is 242
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 133.
Location/Qualifiers
1..193
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FEATURES
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1..193
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3'; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. RNA
provided by Dr. Bertrand Jordan. Library constructed and
normalized by Bento Soares and M.Fatima Bonaldo."

ORIGIN
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Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTTCG 24
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Db 85 CAAGTCGAGCAGAAAGTCCTTACG 108

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DEFINITION PM3-CT0817-240501-007-d02 CT0817 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ322138
VERSION BQ322138.1 GI:20931368
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 233)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.P., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM3&t2=PM3-CT0817-
240501-007-d02&t3=2001-05-24&t4=1)
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/clone lib="CT0817"
/note="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN
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Best Local Similarity 83.3%; Pred. No. 1.7e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db     154 CAAGTCGAATGAAGGACTGCTG 177

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DEFINITION AV366949 RIKEN full-length enriched, 16 days embryo lung Mus
            musculus cDNA clone 8430426E07 3', mRNA sequence.
ACCESSION   AV366949
VERSION     AV366949.1 GI:6414596
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Mus.
            1 (bases 1 to 239)
            Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,
            Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.,
            Iehii,Y., Iehikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I.,
            Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,
            Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
            Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K.,
            Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y.,
            Suzuki,H., Suzuki,H., Takahashi,P., Tateno,M., Tomihaga,N.,
            Tanoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A.,
            Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
            RIKEN Mouse ESTs (Konno,H., et al. 1999)
            Unpublished (1999)
            Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center (GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
            Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
            Hayashizaki,Y.
            Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
            Itoh,M., Kitsuai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
            Okazaki,Y. and Hayashizaki,Y.
            Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
            Carninci,P. and Hayashizaki,Y.
            High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
            Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.

FEATURES             Location/Qualifiers
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                        /Organism="Mus musculus"
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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(without alignments)
611.425 Million cell updates/sec

Title: US-10-665-708-22

Perfect score: 24
Sequence: 1 caagtcgaacggaagccttctcg 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

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4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	20.4	85.0	32	3	US-09-738-972-7
7	20	83.3	1475	3	US-08-641-291A-92
8	19.2	80.0	1437	3	US-10-085-871C-1
9	19.2	80.0	1471	3	US-10-085-871C-2
10	19.2	80.0	1488	3	US-10-756-683B-1
11	19	79.2	2483	3	US-09-738-274-27
12	19	79.2	1460	3	US-09-463-618A-1
13	19	79.2	1460	3	US-10-062-777-1
14	18.8	78.3	32	3	US-09-738-274-14
15	18.8	78.3	1464	3	US-08-938-858-1
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18	18.8	78.3	36470	3	US-08-311-731A-123
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23	17.2	71.7	1791	3	US-09-149-476-226

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16.2	67.5	2497	3	US-09-608-285A-51	Sequence 51, Appl
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16.2	67.5	2805	3	US-09-608-285A-50	Sequence 50, Appl
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16	66.7	601	3	US-09-949-016-79652	Sequence 79652, A
16	66.7	1269	3	US-09-949-016-201683	Sequence 201683,
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98	15.8	65.8	4820	3	US-08-961-527-19	Sequence 19, Appl	c 171	15.2	63.3	95223	4	US-09-531-120-188	Sequence 188, App
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ALIGNMENTS

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RESULT 1
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; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc

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; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-22

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Best Local Similarity 100.0%; Pred. No. 0.0095;
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; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
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US-09-738-274-21

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; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe

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; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
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; GENERAL INFORMATION:
; APPLICANT: Essential Therapeutics, Inc.
; TITLE OF INVENTION: New Antibiotics for Microbispora
; FILE REFERENCE: 262/095
; CURRENT APPLICATION NUMBER: US/09/949,230A
; CURRENT FILING DATE: 2001-09-07
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; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972

; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
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; OTHER INFORMATION: primer
US-09-738-972-7

Query Match 85.0%; Score 20.4; DB 3; Length 32;
Best Local Similarity 95.5%; Pred. No. 0.67; Mismatches 1; Indels 0; Gaps 0;
Matches 21; Conservative 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22
| | | | | | | | | | | | | | | | | | | | | |
Db 2 CAAGTCGAACGGAAGGCCTCT 23

RESULT 6
US-09-738-972-14/c
; Sequence 14, Application US/09738972
; Patent No. 6747141
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: AVIUM COMPLEX SPECIES
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: probe
US-09-738-972-14

Query Match 85.0%; Score 20.4; DB 3; Length 32;
Best Local Similarity 95.5%; Pred. No. 0.67; Mismatches 1; Indels 0; Gaps 0;
Matches 21; Conservative 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22
| | | | | | | | | | | | | | | | | | | | | |
Db 31 CAAGTCGAACGGAAGGCCTCT 10

RESULT 7
US-08-641-291A-92
; Sequence 92, Application US/08641291A
; Patent No. 6037122
; GENERAL INFORMATION:
; APPLICANT: MABILAT Claude
; APPLICANT: RUMY Raymond
; TITLE OF INVENTION: NUCLEOTIDE FRAGMENT OF THE 16S RIBOSOMAL RNA OF CORYNEBACTERIUM
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release # 1.0, version # 1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/641,291A
; FILING DATE: 30-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 38273
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1475 base pairs
; TYPE: nucleotide
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: rRNA
; US-08-641-291A-92
```

```
Query Match      83.3%; Score 20; DB 3; Length 1475;
Best Local Similarity 90.0%; Pred. No. 2.4;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 CAAGTCGAACGGAAGGCGCT 20
    |||||:|||||:|||||:
Db 25 CAAGUCGAACGGAAGGCCU 44
```

RESULT 8

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US-10-085-871C-1
; Sequence 1, Application US/10085871C
; Patent No. 6716615
; GENERAL INFORMATION:
; APPLICANT: Lee, Fang-Yu
; APPLICANT: Lee, Ming-Liang
; APPLICANT: Anderson, Hong C.
; APPLICANT: Chiu, Chung-Ching
; TITLE OF INVENTION: New Strains of Saccharothrix, Process for Producing Pravastatin u
; FILE REFERENCE: 004135.P005
; CURRENT APPLICATION NUMBER: US/10/085,871C
; CURRENT FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1437
; TYPE: DNA
; ORGANISM: Saccharothrix 44442
; US-10-085-871C-1
```

```
Query Match      80.0%; Score 19.2; DB 3; Length 1437;
Best Local Similarity 87.5%; Pred. No. 6.1;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
    |||||:|||||:|||||:
Db 31 CAAGTCGAGCGGTAAGGCCCTTCG 54
```

RESULT 9

```
US-10-085-871C-2
; Sequence 2, Application US/10085871C
; Patent No. 6716615
; GENERAL INFORMATION:
; APPLICANT: Lee, Fang-Yu
; APPLICANT: Lee, Ming-Liang
; APPLICANT: Anderson, Hong C.
```

```
; APPLICANT: Chiu, Chung-Ching
; TITLE OF INVENTION: New Strains of Saccharothrix, Process for Producing Pravastatin u
; FILE REFERENCE: 004135.P005
; CURRENT APPLICATION NUMBER: US/10/085,871C
; CURRENT FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1471
; TYPE: DNA
; ORGANISM: Saccharothrix 45494
; US-10-085-871C-2
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Query Match      80.0%; Score 19.2; DB 3; Length 1471;
Best Local Similarity 87.5%; Pred. No. 6.1;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
    |||||:|||||:|||||:
Db 31 CAAGTCGAGCGGTAAGGCCCTTCG 54
```

RESULT 10

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US-10-756-683B-1
; Sequence 1, Application US/10756683B
; Patent No. 7022875
; GENERAL INFORMATION:
; APPLICANT: Hwang, Byung Kook
; APPLICANT: Lee, Jung Yeop
; TITLE OF INVENTION: THIOTRACIN AND ANTIFUNGAL AND ANTIOOMYCETE COMPOSITION FOR
; FILE REFERENCE: 4228-102
; CURRENT APPLICATION NUMBER: US/10/756,683B
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: KR 10-2003-0015628
; PRIOR FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: KR 10-2003-0015629
; PRIOR FILING DATE: 2003-03-13
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1488
; TYPE: DNA
; ORGANISM: Lechevalieria aerocolonigenes
; US-10-756-683B-1
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Query Match      80.0%; Score 19.2; DB 5; Length 1488;
Best Local Similarity 87.5%; Pred. No. 6.1;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
    |||||:|||||:|||||:
Db 43 CAAGTCGAGCGGTAAGGCCCTTCG 66
```

RESULT 11

```
US-09-738-274-27
; Sequence 27, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
```

```
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-27

Query Match          79.2%; Score 19; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCC 19
Db 1 CAAGTCGAACGGAAGGCC 19

RESULT 12
US-09-463-618A-1
; Sequence 1, Application US/09463618A
; Patent No. 6368835
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: A PROCESS FOR PRODUCING A BRAN PICKLES FLAVORING SOLUTION
; FILE REFERENCE: 11142WO
; CURRENT APPLICATION NUMBER: US/09/463.618A
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: H10-166226
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Corynebacterium sp.NK-1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (166)
; OTHER INFORMATION: n is "a" or "g" or "c" or "t".
US-09-463-618A-1

Query Match          79.2%; Score 19; DB 3; Length 1460;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCC 19
Db 39 CAAGTCGAACGGAAGGCC 57

RESULT 13
US-10-062-777-1
; Sequence 1, Application US/10062777
; Patent No. 6589774
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: A PROCESS FOR PRODUCING A BRAN PICKLES FLAVORING SOLUTION
; FILE REFERENCE: 11142WO
; CURRENT APPLICATION NUMBER: US/10/062,777
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/463,618
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Corynebacterium sp.NK-1
; FEATURE:
; NAME/KEY: unsure
; ,

; LOCATION: (166)
; OTHER INFORMATION: n is "a" or "g" or "c" or "t".
US-10-062-777-1

Query Match          79.2%; Score 19; DB 3; Length 1460;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCC 19
Db 39 CAAGTCGAACGGAAGGCC 57

RESULT 14
US-09-738-274-14
; Sequence 14, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02 UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-14

Query Match          78.3%; Score 18.8; DB 3; Length 32;
Best Local Similarity 90.9%; Pred. No. 4.3;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGCCCTTT 22
Db 2 CAAGTCGAACGGAAGGCTCTCT 23

RESULT 15
US-08-938-858-1
; Sequence 1, Application US/08938858
; Patent No. 5985569
; GENERAL INFORMATION:
; APPLICANT: Foxall, Paul A.
; APPLICANT: Kumar, Harish
; TITLE OF INVENTION: Primers for Amplification of a Genus
; TITLE OF INVENTION: Specific Sequence of the Mycobacterium 16S rRNA Gene
; Patent No. 5985569
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Becton Dickinson and Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07417-6800
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
```

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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,858
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fugic, Donna R.
; REGISTRATION NUMBER: 32,135
; REFERENCE/DOCKET NUMBER: P-3490/5510-12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-847-7166
; TELEFAX: 201-848-9228
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1464 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
; US-08-938-858-1

Query Match 78.3%; Score 18.8; DB 2; Length 1464;
Best Local Similarity 90.9%; Pred. No. 9.7;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTT 22
| | | | | | | | | | | | | | | | | |
Db 21 CAAGTCGAACGGAAGGCTCT 42

RESULT 16
US-09-726-774-7
; Sequence 7, Application US/09726774
; Patent No. 6677153
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/09/726,774
; CURRENT FILING DATE: 2000-11-29
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; US-09-726-774-7

Query Match 78.3%; Score 18.8; DB 3; Length 1464;
Best Local Similarity 90.9%; Pred. No. 9.7;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTT 22
| | | | | | | | | | | | | | | | | |
Db 21 CAAGTCGAACGGAAGGCTCT 42

RESULT 17
US-08-311-731A-134/c
; Sequence 134, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESS: WOLF, GREENFIELD & SACKS, P.C.
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
```



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; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36470 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: MYCOBACTERIUM LEPRAE
;
US-08-311-731A-123

Query Match 78.3%; Score 18.8; DB 3; Length 36470;
Best Local Similarity 90.9%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22
Db 36187 CAAGTCGAACGGAAGGCTCT 36166

RESULT 19
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 78.3%; Score 18.8; DB 3; Length 4403765;
Best Local Similarity 90.9%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22
Db 1471428 CAAGTCGAACGGAAGGCTCT 1471449

RESULT 20
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS

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; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 78.3%; Score 18.8; DB 3; Length 4411529;
Best Local Similarity 90.9%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22
Db 1471904 CAAGTCGAACGGAAGGCTCT 1471925

RESULT 21
US-09-738-274-24
; Sequence 24, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-24

Query Match 75.0%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GAACGGAAGGCCTTTCG 24
Db 1 GAACGGAAGGCCTTTCG 18

RESULT 22
US-09-149-476-59
; Sequence 59, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333

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1	EARLIER	FILING DATE:	1997-03-07
2	EARLIER	APPLICATION NUMBER:	60/038,621
3	EARLIER	FILING DATE:	1997-03-07
4	EARLIER	APPLICATION NUMBER:	60/040,626
5	EARLIER	FILING DATE:	1997-03-07
6	EARLIER	APPLICATION NUMBER:	60/040,334
7	EARLIER	FILING DATE:	1997-03-07
8	EARLIER	APPLICATION NUMBER:	60/040,336
9	EARLIER	FILING DATE:	1997-03-07
10	EARLIER	APPLICATION NUMBER:	60/040,163
11	EARLIER	FILING DATE:	1997-03-07
12	EARLIER	APPLICATION NUMBER:	60/047,600
13	EARLIER	FILING DATE:	1997-05-23
14	EARLIER	APPLICATION NUMBER:	60/047,615
15	EARLIER	FILING DATE:	1997-05-23
16	EARLIER	APPLICATION NUMBER:	60/047,597
17	EARLIER	FILING DATE:	1997-05-23
18	EARLIER	APPLICATION NUMBER:	60/047,502
19	EARLIER	FILING DATE:	1997-05-23
20	EARLIER	APPLICATION NUMBER:	60/047,633
21	EARLIER	FILING DATE:	1997-05-23
22	EARLIER	APPLICATION NUMBER:	60/047,583
23	EARLIER	FILING DATE:	1997-05-23
24	EARLIER	APPLICATION NUMBER:	60/047,617
25	EARLIER	FILING DATE:	1997-05-23
26	EARLIER	APPLICATION NUMBER:	60/047,618
27	EARLIER	FILING DATE:	1997-05-23
28	EARLIER	APPLICATION NUMBER:	60/047,503
29	EARLIER	FILING DATE:	1997-05-23
30	EARLIER	APPLICATION NUMBER:	60/047,592
31	EARLIER	FILING DATE:	1997-05-23
32	EARLIER	APPLICATION NUMBER:	60/047,581
33	EARLIER	FILING DATE:	1997-05-23
34	EARLIER	APPLICATION NUMBER:	60/047,584
35	EARLIER	FILING DATE:	1997-05-23
36	EARLIER	APPLICATION NUMBER:	60/047,500
37	EARLIER	FILING DATE:	1997-05-23
38	EARLIER	APPLICATION NUMBER:	60/047,587
39	EARLIER	FILING DATE:	1997-05-23
40	EARLIER	APPLICATION NUMBER:	60/047,492
41	EARLIER	FILING DATE:	1997-05-23
42	EARLIER	APPLICATION NUMBER:	60/047,598
43	EARLIER	FILING DATE:	1997-05-23
44	EARLIER	APPLICATION NUMBER:	60/047,613
45	EARLIER	FILING DATE:	1997-05-23
46	EARLIER	APPLICATION NUMBER:	60/047,582
47	EARLIER	FILING DATE:	1997-05-23
48	EARLIER	APPLICATION NUMBER:	60/047,596
49	EARLIER	FILING DATE:	1997-05-23
50	EARLIER	APPLICATION NUMBER:	60/047,612
51	EARLIER	FILING DATE:	1997-05-23
52	EARLIER	APPLICATION NUMBER:	60/047,632
53	EARLIER	FILING DATE:	1997-05-23
54	EARLIER	APPLICATION NUMBER:	60/047,601
55	EARLIER	FILING DATE:	1997-05-23
56	EARLIER	APPLICATION NUMBER:	60/043,580
57	EARLIER	FILING DATE:	1997-04-11
58	EARLIER	APPLICATION NUMBER:	60/043,568
59	EARLIER	FILING DATE:	1997-04-11
60	EARLIER	APPLICATION NUMBER:	60/043,314
61	EARLIER	FILING DATE:	1997-04-11
62	EARLIER	APPLICATION NUMBER:	60/043,569
63	EARLIER	FILING DATE:	1997-04-11
64	EARLIER	APPLICATION NUMBER:	60/043,311
65	EARLIER	FILING DATE:	1997-04-11
66	EARLIER	APPLICATION NUMBER:	60/043,671
67	EARLIER	FILING DATE:	1997-04-11
68	EARLIER	APPLICATION NUMBER:	60/043,674
69	EARLIER	FILING DATE:	1997-04-11
70	EARLIER	APPLICATION NUMBER:	60/043,669
71	EARLIER	FILING DATE:	1997-04-11
72	EARLIER	APPLICATION NUMBER:	60/043,312
73	EARLIER	FILING DATE:	1997-04-11

1	EARLIER APPLICATION NUMBER: 60/043,313
2	EARLIER FILING DATE: 1997-04-11
3	EARLIER APPLICATION NUMBER: 60/043,672
4	EARLIER FILING DATE: 1997-04-11
5	EARLIER APPLICATION NUMBER: 60/043,315
6	EARLIER FILING DATE: 1997-04-11
7	EARLIER APPLICATION NUMBER: 60/048,974
8	EARLIER FILING DATE: 1997-06-06
9	EARLIER APPLICATION NUMBER: 60/056,886
10	EARLIER FILING DATE: 1997-08-22
11	EARLIER APPLICATION NUMBER: 60/056,877
12	EARLIER FILING DATE: 1997-08-22
13	EARLIER APPLICATION NUMBER: 60/056,889
14	EARLIER FILING DATE: 1997-08-22
15	EARLIER APPLICATION NUMBER: 60/056,893
16	EARLIER FILING DATE: 1997-08-22
17	EARLIER APPLICATION NUMBER: 60/056,630
18	EARLIER FILING DATE: 1997-08-22
19	EARLIER APPLICATION NUMBER: 60/056,878
20	EARLIER FILING DATE: 1997-08-22
21	EARLIER APPLICATION NUMBER: 60/056,662
22	EARLIER FILING DATE: 1997-08-22
23	EARLIER APPLICATION NUMBER: 60/056,872
24	EARLIER FILING DATE: 1997-08-22
25	EARLIER APPLICATION NUMBER: 60/056,882
26	EARLIER FILING DATE: 1997-08-22
27	EARLIER APPLICATION NUMBER: 60/056,637
28	EARLIER FILING DATE: 1997-08-22
29	EARLIER APPLICATION NUMBER: 60/056,903
30	EARLIER FILING DATE: 1997-08-22
31	EARLIER APPLICATION NUMBER: 60/056,888
32	EARLIER FILING DATE: 1997-08-22
33	EARLIER APPLICATION NUMBER: 60/056,879
34	EARLIER FILING DATE: 1997-08-22
35	EARLIER APPLICATION NUMBER: 60/056,880
36	EARLIER FILING DATE: 1997-08-22
37	EARLIER APPLICATION NUMBER: 60/056,894
38	EARLIER FILING DATE: 1997-08-22
39	EARLIER APPLICATION NUMBER: 60/056,911
40	EARLIER FILING DATE: 1997-08-22
41	EARLIER APPLICATION NUMBER: 60/056,636
42	EARLIER FILING DATE: 1997-08-22
43	EARLIER APPLICATION NUMBER: 60/056,874
44	EARLIER FILING DATE: 1997-08-22
45	EARLIER APPLICATION NUMBER: 60/056,910
46	EARLIER FILING DATE: 1997-08-22
47	EARLIER APPLICATION NUMBER: 60/056,864
48	EARLIER FILING DATE: 1997-08-22
49	EARLIER APPLICATION NUMBER: 60/057,761
50	EARLIER FILING DATE: 1997-08-22
51	EARLIER APPLICATION NUMBER: 60/047,595
52	EARLIER FILING DATE: 1997-05-23
53	EARLIER APPLICATION NUMBER: 60/047,585
54	EARLIER FILING DATE: 1997-05-23
55	EARLIER APPLICATION NUMBER: 60/047,586
56	EARLIER FILING DATE: 1997-05-23
57	EARLIER APPLICATION NUMBER: 60/047,590
58	EARLIER FILING DATE: 1997-05-23
59	EARLIER APPLICATION NUMBER: 60/047,594
60	EARLIER FILING DATE: 1997-05-23
61	EARLIER APPLICATION NUMBER: 60/047,589
62	EARLIER FILING DATE: 1997-05-23
63	EARLIER APPLICATION NUMBER: 60/047,593
64	EARLIER FILING DATE: 1997-05-23

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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match          71.7%; Score 17.2; DB 3; Length 1776;
Best Local Similarity 79.2%; Pred. No. 66;
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGTTTCG 24
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Db 878 CAAGTCGAATTGGAAGRACTGCG 901

RESULT 23
US-09-149-476-226
; Sequence 226, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
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; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
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; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
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; EARLIER FILING DATE: 1997-03-07
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
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; EARLIER APPLICATION NUMBER: 60/047,632
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; EARLIER FILING DATE: 1997-04-11
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; EARLIER APPLICATION NUMBER: 60/043,311
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,894
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; EARLIER APPLICATION NUMBER: 60/056,911
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; EARLIER APPLICATION NUMBER: 60/056,845
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; EARLIER APPLICATION NUMBER: 60/047,590
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
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; EARLIER APPLICATION NUMBER: 60/047,614
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; EARLIER APPLICATION NUMBER: 60/043,578
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; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11

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; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
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; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-08-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match          71.7%; Score 17.2; DB 3; Length 1791;
Best Local Similarity 79.2%; Pred. No. 66;
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy      1 CAAGTCGAACGGAAGGCTTTTCG 24
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Db      973 CAAGTCGAATTGAAAGACTCTCG 996

RESULT 24
US-07-915-922-1
; Sequence 1, Application US/07915922
; Patent No. 5422242
; GENERAL INFORMATION:
; APPLICANT: Young, Karen K.Y.
; TITLE OF INVENTION: Mycobacterium Primers and Probes
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/07915,922
; APPLICATION NUMBER: 19920717
; FILING DATE: 19920717
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sias, Stacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 8616
; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 522-1285
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-915-322-1
Query Match 70.8%; Score 17; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGG 17
Db 7 CAAGTCGAACGGAAGG 23

RESULT 25
US-09-039-866-5
; Sequence 5, Application US/09039866
; Patent No. 6001611
; GENERAL INFORMATION:
; APPLICANT: Will, Stephen G.
; TITLE OF INVENTION: MODIFIED NUCLEIC ACID AMPLIFICATION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; STREET: 1080 U.S. Highway 202
; CITY: Branchburg
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 08876
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/039,866
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 1023P
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-039-866-5
Query Match 70.8%; Score 17; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGG 17
Db 7 CAAGTCGAACGGAAGG 23

RESULT 26
US-09-949-016-13974/c
; Sequence 13974, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 13974
; LENGTH: 106418
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc feature
; LOCATION: (1)-(106418)
; OTHER INFORMATION: n = A, T, C or G
US-09-949-016-13974
Query Match 69.2%; Score 16.6; DB 3; Length 106418;
Best Local Similarity 82.6%; Pred. No. 3.1e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCTTTTCG 24
Db 10377 AAGTCCTACGGAAGGCTTTTG 10355

RESULT 27
US-09-949-016-16621/c
; Sequence 16621, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 16621
; LENGTH: 108341
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16621
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Best Local Similarity 82.6%; Pred. No. 3.1e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTTTC 23
Db 94196 CAAGTCGAAGGAAGGCATTTC 94174

RESULT 28
US-09-949-016-13781/c
; Sequence 13781, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
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; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13781
; LENGTH: 228851
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(228851)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13781

Query Match 69.2%; Score 16.6; DB 3; Length 228851;
Best Local Similarity 82.6%; Pred. No. 3.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCTTTTCG 24
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Db 132603 AAGTCCTACGGAAGGCTTTTG 132581

RESULT 29
US-08-485-602-61
; Sequence 61, Application US/08485602
; Patent No. 5712095
; GENERAL INFORMATION:
; APPLICANT: Britschgi, Theresa B.
; APPLICANT: Cangalosi, Gerard A.
; TITLE OF INVENTION: Rapid and Sensitive Detection of
; TITLE OF INVENTION: Antibiotic-Resistant Mycobacteria Using Oligonucleotide
; TITLE OF INVENTION: Probes Specific for Ribosomal RNA Precursors
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,602
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,068
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 11652-79-1
; TELEPHONE: (415) 543-9600
; TELECOMMUNICATION INFORMATION:
; INFORMATION FOR SEQ ID NO: 61:
; TYPE: nucleic acid
; LENGTH: 25 base pairs
; STRANDEDNESS: unknown
```

```
; TOPOLOGY: unknown
; MOLECULE TYPE: rRNA
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium habana
US-08-485-602-61

Query Match 68.3%; Score 16.4; DB 2; Length 25;
Best Local Similarity 78.9%; Pred. No. 68;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CGAACGGAAGGCTTTTCG 24
||||| ||||| ||||| |||||
Db 1 CGAACGGAAGNCCCUUCG 19

RESULT 30
US-08-757-180-60
; Sequence 60, Application US/08757180
; Patent No. 5726021
; GENERAL INFORMATION:
; APPLICANT: Britschgi, Theresa B.
; APPLICANT: Cangalosi, Gerard A.
; TITLE OF INVENTION: RAPID LYSIS METHODS FOR RELEASING INTACT
; TITLE OF INVENTION: RIBOSOMAL RNA PRECURSORS FROM MYCOBACTERIUM
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,180
; FILING DATE: 27-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,068
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hsi, Petrina S.
; REGISTRATION NUMBER: 38,496
; REFERENCE/DOCKET NUMBER: BD3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: rRNA
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium simiae
US-08-757-180-60

Query Match 68.3%; Score 16.4; DB 2; Length 25;
Best Local Similarity 78.9%; Pred. No. 68;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CGAACGGAAGGCTTTTCG 24
||||| ||||| ||||| |||||
Db 1 CGAACGGAAGNCCCUUCG 19

RESULT 31
US-08-745-638-61
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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 69524
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016--69524

Query Match
Best Local Similarity 67.5%; Score 16.2; DB 3; Length 601;
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 AAGTCGAACGGAAGGCGCTTTG 24
      ||||| |:||||| |||||
Db 293 AAGTCCTAYGGAAGGCGCTTTG 315

RESULT 33
US-09-949-016-76807
; Sequence 76807, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 76807
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-76807

Query Match
Best Local Similarity 67.5%; Score 16.2; DB 3; Length 601;
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 AAGTCGAACGGAAGGCGCTTTG 24
      ||||| ||||| ||||| |||||
Db 285 AAGTCCTACGGAAGGCGCTTTG 307

RESULT 34
US-09-533-559-7113
; Sequence 7113, Application US/095333559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjørke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 5849.200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7113

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Query Match      67.5%; Score 16.2; DB 3; Length 1499;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2  AAGTCGAACGGAAAGCCTTT 22
          |||||
Db      512 AAGTCGAACGGAATGCTGT 492

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RESULT 38
US-09-608-285A-53/c
; Sequence 53, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-608-285A-53

Query Match      67.5%; Score 16.2; DB 3; Length 1588;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGGCCTTT 22
        |||||
Db      659 AAGTCGAACGGAATGCTCTGT 639

RESULT 39
US-09-557-800C-53/c
; Sequence 53, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
```

```
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-557-800C-53

Query Match      67.5%; Score 16.2; DB 3; Length 1588;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGGCCTTT 22
        |||||
Db      659 AAGTCGAACGGAATGCTCTGT 639

RESULT 40
US-09-608-285A-49/c
; Sequence 49, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 2294
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-608-285A-49

Query Match      67.5%; Score 16.2; DB 3; Length 2294;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGGCCTTT 22
        |||||
Db      191 AAGTCGAACGGAATGCTCTGT 171
```

```
RESULT 41
US-09-557-800C-49/c
; Sequence 49, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 49
; LENGTH: 2294
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-557-800C-49

Query Match      67.5%; Score 16.2; DB 3; Length 2294;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGGCCTTT 22
      |||||
Db      191 AAGTCGAACGGAATGCTCTGT 171

RESULT 42
US-09-608-285A-46/c
; Sequence 46, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
```

```
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 46
; LENGTH: 2371
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-608-285A-46

Query Match      67.5%; Score 16.2; DB 3; Length 2371;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGGCCTTT 22
      |||||
Db      268 AAGTCGAACGGAATGCTCTGT 248

RESULT 43
US-09-557-800C-46/c
; Sequence 46, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 46
; LENGTH: 2371
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-557-800C-46

Query Match      67.5%; Score 16.2; DB 3; Length 2371;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGGCCTTT 22
      |||||
Db      268 AAGTCGAACGGAATGCTCTGT 248

RESULT 44
US-09-608-285A-51/c
; Sequence 51, Application US/09608285A
```

```
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 2497
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-608-285A-51

Query Match      67.5%; Score 16.2; DB 3; Length 2497;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGGCCTTT 22
      |||||
Db      394 AAGTCGAACGGAATGCTCTGT 374

RESULT 45
US-09-557-800C-51/c
; Sequence 51, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
```

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; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 2497
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-557-800C-51

Query Match      67.5%; Score 16.2; DB 3; Length 2497;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGGCCTTT 22
      |||||
Db      394 AAGTCGAACGGAATGCTCTGT 374

RESULT 46
US-09-608-285A-48/c
; Sequence 48, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 2693
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-608-285A-48

Query Match      67.5%; Score 16.2; DB 3; Length 2693;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGGCCTTT 22
      |||||
Db      590 AAGTCGAACGGAATGCTCTGT 570

RESULT 47
US-09-557-800C-48/c
; Sequence 48, Application US/09557800C
```

; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 2693
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-557-800C-48

Query Match 67.5%; Score 16.2; DB 3; Length 2693;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCTTT 22
|||||
Db 590 AAGTCGAACGGAATGCTCTGT 570

RESULT 48
US-09-608-285A-26/c
; Sequence 26, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-608-285A-52

Query Match 67.5%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCTTT 22
|||||
Db 659 AAGTCGAACGGAATGCTCTGT 639

; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (148)..(1599)
US-09-608-285A-26

Query Match 67.5%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCTTT 22
|||||
Db 659 AAGTCGAACGGAATGCTCTGT 639

RESULT 49
US-09-608-285A-52/c
; Sequence 52, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-608-285A-52

Query Match 67.5%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCTTT 22
|||||
Db 659 AAGTCGAACGGAATGCTCTGT 639

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RESULT 50
US-09-240-639-1/c
; Sequence 1, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240.639
; CURRENT FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1599)
US-09-240-639-1
Query Match          67.5%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGGCTTT 22
      |||||
Db      659 AAGTCGAACGGAATGCTGT 639

RESULT 51
US-09-370-265-26/c
; Sequence 26, Application US/09370265
; Patent No. 6447771
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 2811/35908
; CURRENT APPLICATION NUMBER: US/09/370.265
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: PCT/US99/16180
; EARLIER FILING DATE: 1999-07-16
; EARLIER APPLICATION NUMBER: 09/350.836
; EARLIER FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: 09/273.447
; EARLIER FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: 09/244.444
; EARLIER FILING DATE: 1999-02-04
; EARLIER APPLICATION NUMBER: 09/118.205
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (148)..(1599)
US-09-370-265-26
Query Match          67.5%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGGCTTT 22
      |||||
Db      659 AAGTCGAACGGAATGCTGT 639

RESULT 52
US-09-557-800C-26/c
; Sequence 26, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (148)..(1599)
US-09-557-800C-26
Query Match          67.5%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGGCTTT 22
      |||||
Db      659 AAGTCGAACGGAATGCTGT 639

RESULT 53
US-09-557-800C-52/c
; Sequence 52, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
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; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-557-800C-52

Query Match 67.5%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCTTT 22
|||||
Db 659 AAGTCGAACGGAATGCTCTGT 639

RESULT 54
US-09-370-625A-26/c
; Sequence 26, Application US/09370625A
; Patent No. 6600032
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/09/370,625A
; CURRENT FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (148)..(1599)
US-09-370-625A-26

Query Match 67.5%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCTTT 22
|||||
Db 659 AAGTCGAACGGAATGCTCTGT 639

RESULT 55
US-09-510A-1/c
; Sequence 1, Application US/09908510A
; Patent No. 6759214
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND ACIDS
; FILE REFERENCE: 28110/36120E
; CURRENT APPLICATION NUMBER: US/09/908,510A

; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1599)
; OTHER INFORMATION:
US-09-908-510A-1

Query Match 67.5%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCTTT 22
|||||
Db 659 AAGTCGAACGGAATGCTCTGT 639

RESULT 56
US-09-905-744B-1/c
; Sequence 1, Application US/09905744B
; Patent No. 6780410
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND ACIDS
; FILE REFERENCE: 28110/36120A
; CURRENT APPLICATION NUMBER: US/09/905,744B
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1599)
; OTHER INFORMATION:
US-09-905-744B-1

Query Match 67.5%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCTTT 22
|||||
Db 659 AAGTCGAACGGAATGCTCTGT 639

RESULT 57
US-10-107-660-1/c
; Sequence 1, Application US/10107660
; Patent No. 6780977
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND NUCLEIC ACIDS
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/10/107,660
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US/09/240,639
; PRIOR FILING DATE: 1998-01-29

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; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1599)
US-10-107-660-1

Query Match          67.5%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 AAGTCGAACGAAAGGCCTTT 22
    |||||
Db  659 AAGTCGAACGGAATGCTCTGT 639

RESULT 58
US-10-107-576-1/c
; Sequence 1, Application US/10107576
; Patent No. 6783959
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; FILE REFERENCE: 28110/36120H
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US/10/107,576
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1599)
; OTHER INFORMATION:
US-10-107-576-1

Query Match          67.5%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 AAGTCGAACGAAAGGCCTTT 22
    |||||
Db  659 AAGTCGAACGGAATGCTCTGT 639

RESULT 59
US-09-905-732B-1/c
; Sequence 1, Application US/09905732B
; Patent No. 6787328
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; FILE REFERENCE: 28110/36120B
; CURRENT APPLICATION NUMBER: US/09/905,732B
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
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; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1599)
; OTHER INFORMATION:
US-09-905-732B-1

Query Match          67.5%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 AAGTCGAACGAAAGGCCTTT 22
    |||||
Db  659 AAGTCGAACGGAATGCTCTGT 639

RESULT 60
US-09-905-743B-1/c
; Sequence 1, Application US/09905743B
; Patent No. 6828423
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; FILE REFERENCE: 28110/36120C
; CURRENT APPLICATION NUMBER: US/09/905,743B
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1599)
; OTHER INFORMATION:
US-09-905-743B-1

Query Match          67.5%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 AAGTCGAACGAAAGGCCTTT 22
    |||||
Db  659 AAGTCGAACGGAATGCTCTGT 639

RESULT 61
US-09-905-589-1/c
; Sequence 1, Application US/09905589
; Patent No. 6884872
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/905,589
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US/09/240,639
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
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; LOCATION: (232)..(1599)
US-09-905-589-1
  Query Match      67.5%; Score 16.2; DB 3; Length 2762;
  Best Local Similarity 85.7%; Pred. No. 2.3e+02;
  Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCTTT 22
   |||||
Db 659 AAGTCGAACGGAATGCTGT 639

RESULT 62
US-10-108-171A-1/c
; Sequence 1, Application US/10108171A
; Patent No. 6899875
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Friesch, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; FILE REFERENCE: 28110/36120F
; CURRENT APPLICATION NUMBER: US/10/108,171A
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1599)
; OTHER INFORMATION:
US-10-108-171A-1
  Query Match      67.5%; Score 16.2; DB 3; Length 2762;
  Best Local Similarity 85.7%; Pred. No. 2.3e+02;
  Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCTTT 22
   |||||
Db 659 AAGTCGAACGGAATGCTGT 639

RESULT 63
US-09-608-285A-50/c
; Sequence 50, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
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; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 2805
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-608-285A-50
  Query Match      67.5%; Score 16.2; DB 3; Length 2805;
  Best Local Similarity 85.7%; Pred. No. 2.3e+02;
  Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCTTT 22
   |||||
Db 659 AAGTCGAACGGAATGCTGT 639

RESULT 64
US-09-557-800C-50/c
; Sequence 50, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 2805
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-557-800C-50
  Query Match      67.5%; Score 16.2; DB 3; Length 2805;
  Best Local Similarity 85.7%; Pred. No. 2.3e+02;
  Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCTTT 22
   |||||
Db 659 AAGTCGAACGGAATGCTGT 639

RESULT 65
US-09-608-285A-54/c
; Sequence 54, Application US/09608285A
```


; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 2882
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-608-285A-54

Query Match 67.5%; Score 16.2; DB 3; Length 2882;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCGCTTT 22
|||||
Db 659 AAGTCGAACGGAATGCTCTGT 639

RESULT 66
US-09-557-800C-54/c
; Sequence 54, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444

; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 2882
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-557-800C-54

Query Match 67.5%; Score 16.2; DB 3; Length 2882;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCGCTTT 22
|||||
Db 659 AAGTCGAACGGAATGCTCTGT 639

RESULT 67
US-09-738-274-28
; Sequence 28, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02 UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-28

Query Match 66.7%; Score 16; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTCGAACGGAAGGCC 19
|||||
Db 1 GTCGAACGGAAGGCC 16

RESULT 68
US-09-974-300-6612/c
; Sequence 6612, Application US/09974300
; Patent No. 7018794
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27

```
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6612
; LENGTH: 161
; TYPE: DNA
; ORGANISM: Bacillus clausii
US-09-974-300-6612

Query Match          66.7%; Score 16; DB 5; Length 161;
Best Local Similarity 79.2%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGAAAGGCCTTTTCG 24
   ||| ||| ||| ||| ||| ||| ||| |||
Db 81 CAAGGCAACGCGCAATGCTTTTCG 58
   ||| ||| ||| ||| ||| ||| ||| |||

RESULT 69
US-09-252-991A-2715/c
; Sequence 2715, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 2715
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2715

Query Match          66.7%; Score 16; DB 3; Length 417;
Best Local Similarity 79.2%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGAAAGGCCTTTTCG 24
   ||| ||| ||| ||| ||| ||| ||| |||
Db 180 CAAGTGAAGGAGGAGGCCTTTCG 157
   ||| ||| ||| ||| ||| ||| ||| |||

RESULT 70
US-09-252-991A-6201
; Sequence 6201, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6201
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6201

Query Match          66.7%; Score 16; DB 3; Length 552;
Best Local Similarity 79.2%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6612
; LENGTH: 161
; TYPE: DNA
; ORGANISM: Bacillus clausii
US-09-974-300-6612

Query Match          66.7%; Score 16; DB 5; Length 161;
Best Local Similarity 79.2%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGAAAGGCCTTTTCG 24
   ||| ||| ||| ||| ||| ||| ||| |||
Db 81 CAAGGCAACGCGCAATGCTTTTCG 58
   ||| ||| ||| ||| ||| ||| ||| |||

RESULT 69
US-09-252-991A-2715/c
; Sequence 2715, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 2715
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2715

Query Match          66.7%; Score 16; DB 3; Length 417;
Best Local Similarity 79.2%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGAAAGGCCTTTTCG 24
   ||| ||| ||| ||| ||| ||| ||| |||
Db 180 CAAGTGAAGGAGGAGGCCTTTCG 157
   ||| ||| ||| ||| ||| ||| ||| |||

RESULT 70
US-09-252-991A-6201
; Sequence 6201, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6201
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6201

Query Match          66.7%; Score 16; DB 3; Length 552;
Best Local Similarity 79.2%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6612
; LENGTH: 161
; TYPE: DNA
; ORGANISM: Bacillus clausii
US-09-974-300-6612

Query Match          66.7%; Score 16; DB 5; Length 161;
Best Local Similarity 79.2%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGAAAGGCCTTTTCG 24
   ||| ||| ||| ||| ||| ||| ||| |||
Db 81 CAAGGCAACGCGCAATGCTTTTCG 58
   ||| ||| ||| ||| ||| ||| ||| |||

RESULT 69
US-09-252-991A-2715/c
; Sequence 2715, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79652
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-79652

Query Match          66.7%; Score 16; DB 3; Length 601;
Best Local Similarity 79.2%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGAAAGGCCTTTTCG 24
   ||| ||| ||| ||| ||| ||| ||| |||
Db 328 CAAAACGACGCGAAATGCTTTTCG 351
   ||| ||| ||| ||| ||| ||| ||| |||

RESULT 72
US-09-949-016-201683/c
; Sequence 201683, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201683
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-201683

Query Match          66.7%; Score 16; DB 3; Length 601;
Best Local Similarity 79.2%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGAAAGGCCTTTTCG 24
   ||| ||| ||| ||| ||| ||| ||| |||
Db 228 CAAGTTGAATGGAATTCCTTTTCG 205
   ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 73
US-09-311-170-1
; Sequence 1, Application US/09311170
; Patent No. 6121034
; GENERAL INFORMATION:
; APPLICANT: Laroche et al., Andre L.
; TITLE OF INVENTION: Xylanase cxy1
; FILE REFERENCE: xylanase cxy1
; CURRENT APPLICATION NUMBER: US/09/311.170
; CURRENT FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Coniothyrium minitans
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(1179)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (88)..(180)
; OTHER INFORMATION: Cellulose-binding domain
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (181)..(273)
; OTHER INFORMATION: hinge region
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (274)..(1179)
; OTHER INFORMATION: catalytic domain
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (25)..(75)
; OTHER INFORMATION: putative signal peptide
US-09-311-170-1

Query Match 66.7%; Score 16; DB 3; Length 1269;
Best Local Similarity 79.2%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCGCTTTCG 24
DB 477 CAGCTCGAACGGAAGGCTGCTCG 500

RESULT 74
US-09-252-991A-887
; Sequence 887, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 887
; LENGTH: 1698
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-887

Query Match 66.7%; Score 16; DB 3; Length 1698;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGTCGAACGGAAGG 17
DB 361 AAGTCGAACGGAAGG 376

RESULT 75
US-09-799-451-258
; Sequence 258, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunding
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 258
; LENGTH: 2103
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1184)..(1303)
US-09-799-451-258

Query Match 66.7%; Score 16; DB 3; Length 2103;
Best Local Similarity 79.2%; Pred. No. 2.8e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCGCTTTCG 24
DB 993 CAAGTCGATTTGAAGAGACTGTCG 1016

RESULT 76
US-09-252-991A-6717
; Sequence 6717, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6717
; LENGTH: 2106
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa

Qy 1 CAAGTCGAACGGAAAGGCCTTTCG 24
||| ||| ||| ||| ||| ||| ||| |||
Db 492 CAAGTCGAACGGAGAGGCCTTTCG 515

Query Match 65.8%; Score 15.8; DB 3; Length 375;
Best Local Similarity 89.5%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CGACGGAAGCCTTCG 24
|||||

Db 332 CGACGGAAGCCTTCG 350
|||||

RESULT 85
US-08-008-216-7
; Sequence 7, Application US/08008216
; Patent No. 5366887
; GENERAL INFORMATION:
; APPLICANT: Slightom, Jerry L.
; APPLICANT: Tepfer, David A.
; TITLE OF INVENTION: Ri T-DNA Promoters
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY, CARY, AMES & FRYE
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/008,216
; FILING DATE: 25-JAN-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhorst, Marnie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: P1020US1
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 573 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORGANISM: Agrobacterium rhizogenes
; STRAIN: Strain A4
; IMMEDIATE SOURCE:
; LIBRARY: Convolvulus arvensis plant cells
; CLONE: Clone 7
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (1..573)
; OTHER INFORMATION: /label= ORF7
; OTHER INFORMATION: /note= "Sequence ORF7 corresponds to bases 5071
; OTHER INFORMATION: through 5643 of Seq. ID No. 5366887 19. It is read 5' to
; OTHER INFORMATION: 3' from the complementary strand."
US-08-008-216-7

Query Match 65.8%; Score 15.8; DB 2; Length 573;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GTCGAACGGAAGCCTTT 22
|||||

Db 507 GTCGAACGACAAGGCCTTT 525
RESULT 86
US-08-459-569-7
; Sequence 7, Application US/08459569
; Patent No. 5543501
; GENERAL INFORMATION:
; APPLICANT: Slightom, Jerry L.
; APPLICANT: Tepfer, David A.
; TITLE OF INVENTION: Ri T-DNA Promoters
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY, CARY, AMES & FRYE
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,569
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,216
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhorst, Marnie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: P1020US1
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 573 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORGANISM: Agrobacterium rhizogenes
; STRAIN: Strain A4
; IMMEDIATE SOURCE:
; LIBRARY: Convolvulus arvensis plant cells
; CLONE: Clone 7
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (1..573)
; OTHER INFORMATION: /label= ORF7
; OTHER INFORMATION: /note= "Sequence ORF7 corresponds to bases 5071
; Patent No. 5543501
; OTHER INFORMATION: through 5643 of Seq. ID No. 5543501 19. It is read 5' to
; OTHER INFORMATION: 3' from the complementary strand."
US-08-459-569-7

Query Match 65.8%; Score 15.8; DB 2; Length 573;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GTCGAACGGAAGCCTTT 22
|||||

Db 507 GTCGAACGACAAGGCCTTT 525
|||||

RESULT 87

```
US-08-458-831-7
; Sequence 7, Application US/08458831
; Patent No. 5824866
; GENERAL INFORMATION:
; APPLICANT: Slightom, Jerry L.
; APPLICANT: Tepfer, David A.
; TITLE OF INVENTION: R1 T-DNA Promoters
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY, CARY, AMES & FRYE
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,831
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,216
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhorst, Marnie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: P1020US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 573 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Agrobacterium rhizogenes
; STRAIN: Strain A4
; IMMEDIATE SOURCE:
; LIBRARY: Convolvulus arvensis plant cells
; CLONE: Clone 7
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (1..573)
; OTHER INFORMATION: /label= ORF7
; OTHER INFORMATION: /note= "Sequence ORF7 corresponds to bases 5071
; Patent No. 5824866
; OTHER INFORMATION: through 5643 of Seq. ID No. 5824866 19. It is read 5' to
; OTHER INFORMATION: 3' from the complementary strand."
US-08-458-831-7

Query Match 65.8%; Score 15.8; DB 2; Length 573;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GTCGAACGGAAGGCCTTT 22
Db 507 GTCGAACGACAAAGGCCTTT 525

RESULT 88
US-09-949-016-82725
; Sequence 82725, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 82725
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-82725

Query Match 65.8%; Score 15.8; DB 3; Length 601;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGTCGAACGGAAGGCCTT 21
Db 204 AGTCAACGGAAGGCATT 222

RESULT 90
US-09-949-016-82727
; Sequence 82727, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 82726
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-82726

Query Match 65.8%; Score 15.8; DB 3; Length 601;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGTCGAACGGAAGGCCTT 21
Db 204 AGTCAACGGAAGGCATT 222

RESULT 89
US-09-949-016-82726
; Sequence 82726, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 82726
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-82726

Query Match 65.8%; Score 15.8; DB 3; Length 601;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGTCGAACGGAAGGCCTT 21
Db 437 AGTCAACGGAAGGCATT 455
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; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82727
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-82727

Query Match 65.8%; Score 15.8; DB 3; Length 601;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 AGTCGAACGGAAGGCCTTT 21
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Db 45 AGTCAACGGAAGGCATT 63

RESULT 91

US-08-008-216-6
; Sequence 6, Application US/08008216
; Patent No. 5366887

; GENERAL INFORMATION:
; APPLICANT: Slightom, Jerry L.
; APPLICANT: Tepfer, David A.
; TITLE OF INVENTION: Ri T-DNA Promoters
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY, CARY, AMES & FRYE
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-4297

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/008,216
; FILING DATE: 25-JAN-1993

; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; NAME: Barnhorst, Marnie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: P1020US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1074 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Agrobacterium rhizogenes
; STRAIN: Strain A4
; IMMEDIATE SOURCE:
; LIBRARY: Convolvulus arvensis plant cells
; CLONE: Clone 7
; FEATURE:

; NAME/KEY: misc_feature
; LOCATION: 1..1074
; OTHER INFORMATION: /label= ORF6
; OTHER INFORMATION: /note= "Sequence ORF6 corresponds to bases 5143
; OTHER INFORMATION: through 6216 of Seq. ID No. 5366887 19."
US-08-008-216-6

Query Match 65.8%; Score 15.8; DB 2; Length 1074;
Best Local Similarity 89.5%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4 GTCGAACGGAAGGCCTTT 22
|||||
Db 435 GTCGAACGGAAGGCCTTT 453

RESULT 92

US-08-459-569-6
; Sequence 6, Application US/08459569
; Patent No. 5543501

; GENERAL INFORMATION:
; APPLICANT: Slightom, Jerry L.
; APPLICANT: Tepfer, David A.
; TITLE OF INVENTION: Ri T-DNA Promoters
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY, CARY, AMES & FRYE
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-4297

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,569
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,216
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985

; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhorst, Marnie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: P1020US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1074 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Agrobacterium rhizogenes
; STRAIN: Strain A4
; IMMEDIATE SOURCE:
; LIBRARY: Convolvulus arvensis plant cells
; CLONE: Clone 7
; FEATURE:

; NAME/KEY: misc_feature
; LOCATION: 1..1074
; OTHER INFORMATION: /label= ORF6
; OTHER INFORMATION: /note= "Sequence ORF6 corresponds to bases 5143
; Patent No. 5543501
; OTHER INFORMATION: through 6216 of Seq. ID No. 5543501 19."

US-08-459-569-6

Query Match 65.8%; Score 15.8; DB 2; Length 1074;
Best Local Similarity 89.5%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GTCGAACGGAAGGCCTTT 22
Db 435 GTCGAACGACAGGCCTTT 453

RESULT 93

US-08-458-831-6
; Sequence 6, Application US/08458831
; Patent No. 5824866
; GENERAL INFORMATION:
; APPLICANT: Slightom, Jerry L.
; APPLICANT: Tepfer, David A.
; TITLE OF INVENTION: Ri T-DNA Promoters
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY, CARY, AMES & FRYE
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent'n Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/458,831
; APPLICATION NUMBER: US/08/458,831
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,216
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhorst, Marnie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: P1020US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1074 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Agrobacterium rhizogenes
; STRAIN: Strain A4
; IMMEDIATE SOURCE:
; LIBRARY: Convolvulus arvensis plant cells
; CLONE: Clone 7
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..1074
; OTHER INFORMATION: /label= ORF6
; OTHER INFORMATION: /note= "Sequence ORF6 corresponds to bases 5143
; Patent No. 5824866
; OTHER INFORMATION: through 6216 of Seq. ID No. 5824866 19."
US-08-458-831-6

Query Match 65.8%; Score 15.8; DB 2; Length 1074;
Best Local Similarity 89.5%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GTCGAACGGAAGGCCTTT 22
Db 435 GTCGAACGACAGGCCTTT 453

RESULT 94

US-09-583-110-1172
; Sequence 1172, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 1172
; LENGTH: 1551
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-1172

Query Match 65.8%; Score 15.8; DB 3; Length 1551;
Best Local Similarity 89.5%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCT 20
Db 299 AAGCCGAACGGAAGGCCT 317

RESULT 95

US-09-107-433-1056
; Sequence 1056, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 1056:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1566 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8) LOCATION 1...1566
; SEQUENCE DESCRIPTION: SEQ ID NO: 1056:
US-09-107-433-1056

Query Match 65.8%; Score 15.8; DB 3; Length 1566;
Best Local Similarity 89.5%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCT 20
Db 314 AAGCGAACTGAAGGCCT 332

RESULT 96
US-09-270-767-163
; Sequence 163, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 163
; LENGTH: 4029
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-163

Query Match 65.8%; Score 15.8; DB 3; Length 4029;
Best Local Similarity 89.5%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGTCGAACGGAAGGCCTT 21
Db 1400 AGCGAACGGAAGGCCAT 1418

RESULT 97
US-09-270-767-15445
; Sequence 15445, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15445
; LENGTH: 4029
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-15445

Query Match 65.8%; Score 15.8; DB 3; Length 4029;
Best Local Similarity 89.5%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGTCGAACGGAAGGCCTT 21
Db 1400 AGCGAACGGAAGGCCAT 1418

RESULT 98
US-08-961-527-19
; Sequence 19, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4820 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-19

Query Match 65.8%; Score 15.8; DB 3; Length 4820;
Best Local Similarity 89.5%; Pred. No. 4.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCT 20
Db 2907 AAGCGAACTGAAGGCCT 2925

RESULT 99
US-08-008-216-19
; Sequence 19, Application US/08008216
; Patent No. 5366887
; GENERAL INFORMATION:
; APPLICANT: Slightom, Jerry L.
; APPLICANT: Tepfer, David A.
; TITLE OF INVENTION: R1 T-DNA Promoters
```

NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: GRAY, CARY, AMES & FRYE
STREET: 401 B Street, Suite 1700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-4297
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/008,216
FILING DATE: 25-JAN-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/725,368
FILING DATE: 22-APR-1985
ATTORNEY/AGENT INFORMATION:
NAME: Barnhorst, Marnie W.
REGISTRATION NUMBER: 36,740
REFERENCE/DOCKET NUMBER: P1020US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 699-2700
TELEFAX: (619) 236-1048
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 21126 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Agrobacterium rhizogenes
STRAIN: STRAIN A4
IMMEDIATE SOURCE:
LIBRARY: CONVULVULUS ARVENSIS PLANT CELLS
CLONE: CLONE 7
FEATURE:
NAME/KEY: misc feature
LOCATION: complement (937..2262)
OTHER INFORMATION: /label= ORF1SUBSEQUENCE
FEATURE:
NAME/KEY: misc feature
LOCATION: complement (2649..3458)
OTHER INFORMATION: /label= ORF2SUBSEQUENCE
FEATURE:
NAME/KEY: misc feature
LOCATION: 3726..4799
OTHER INFORMATION: /label= ORF3SUBSEQUENCE
FEATURE:
NAME/KEY: misc feature
LOCATION: complement (4041..4400)
OTHER INFORMATION: /label= ORF4SUBSEQUENCE
FEATURE:
NAME/KEY: misc feature
LOCATION: complement (4607..4918)
OTHER INFORMATION: /label= ORF5SUBSEQUENCE
FEATURE:
NAME/KEY: misc feature
LOCATION: 5143..6216
OTHER INFORMATION: /label= ORF6SUBSEQUENCE
FEATURE:
NAME/KEY: misc feature
LOCATION: complement (5071..5643)
OTHER INFORMATION: /label= ORF7SUBSEQUENCE
FEATURE:
NAME/KEY: misc feature
LOCATION: 6609..8888
OTHER INFORMATION: /label= ORF8SUBSEQUENCE

FEATURE:
NAME/KEY: misc feature
LOCATION: complement (6576..6830)
OTHER INFORMATION: /label= ORF9SUBSEQUENCE
FEATURE:
NAME/KEY: misc feature
LOCATION: 9748..10044
OTHER INFORMATION: /label= ORF10SUBSEQUENCE
FEATURE:
NAME/KEY: misc feature
LOCATION: complement (10509..11282)
OTHER INFORMATION: /label= ORF11SUBSEQUENCE
FEATURE:
NAME/KEY: misc feature
LOCATION: 12466..13002
OTHER INFORMATION: /label= ORF12SUBSEQUENCE
FEATURE:
NAME/KEY: misc feature
LOCATION: 13723..14319
OTHER INFORMATION: /label= ORF13SUBSEQUENCE
FEATURE:
NAME/KEY: misc feature
LOCATION: 15659..16210
OTHER INFORMATION: /label= ORF14SUBSEQUENCE
FEATURE:
NAME/KEY: misc feature
LOCATION: complement (16517..17545)
OTHER INFORMATION: /label= ORF15SUBSEQUENCE
FEATURE:
NAME/KEY: misc feature
LOCATION: complement (17737..18189)
OTHER INFORMATION: /label= ORF16SUBSEQUENCE
FEATURE:
NAME/KEY: misc feature
LOCATION: complement (18177..18743)
OTHER INFORMATION: /label= ORF17SUBSEQUENCE
FEATURE:
NAME/KEY: misc feature
LOCATION: complement (19031..19390)
OTHER INFORMATION: /label= ORF18SUBSEQUENCE
US-08-008-216-19
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US-08-459-569-19
Sequence 19, Application US/08459569
Patent No. 5543501
GENERAL INFORMATION:
APPLICANT: Slightom, Jerry L.
TITLE OF INVENTION: R1 T-DNA Promoters
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: GRAY, CARY, AMES & FRYE
STREET: 401 B Street, Suite 1700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-4297
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/459,569
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,216
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhorst, Marlie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: P1020US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 19:
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
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Best Local Similarity 89.5%; Pred. No. 5,7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 5577 GTCGACGACAAAGGCCCTTT 5595
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 OM nucleic - nucleic search, using sw model
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 (without alignments)
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 Perfect score: 24
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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US-09-738-274-21
; Sequence 21, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
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US-09-738-274-21

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; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
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; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
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; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
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; ORGANISM: Mycobacterium fortuitum
US-10-697-802A-6

Query Match 93.3%; Score 22.4; DB 10; Length 1449;
Best Local Similarity 95.8%; Pred. No. 1.4;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAGGCGCTTTTCG 24
Db 21 CAAAGTCGAACGGAAGGCGCTTTTCG 44

RESULT 6
US-10-697-802A-13
; Sequence 13, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 13
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Mycobacterium mucogenicum
US-10-697-802A-13

Query Match 93.3%; Score 22.4; DB 10; Length 1455;
Best Local Similarity 95.8%; Pred. No. 1.4;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAGGCGCTTTTCG 24
Db 31 CAAAGTCGAACGGAAGGCGCTTTTCG 54

RESULT 7
US-10-697-802A-5
; Sequence 5, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 5
; LENGTH: 1482
; TYPE: DNA
; ORGANISM: Mycobacterium farcinogenes
US-10-697-802A-5

```
Query Match      93.3%; Score 22.4; DB 10; Length 1482;
Best Local Similarity 95.8%; Pred. No. 1.4;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
   |||||
Db 29 CAAGTCGAACGGAAGGCGCTTTCG 52

RESULT 8
US-09-738-274-23
; Sequence 23, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-23

Query Match      87.5%; Score 21; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTCGAACGGAAGGCGCTTTCG 24
   |||||
Db 1 GTCGAACGGAAGGCGCTTTCG 21

RESULT 9
US-10-665-708-23
; Sequence 23, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-10-665-708-23

Query Match      87.5%; Score 21; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTCGAACGGAAGGCGCTTTCG 24
   |||||
Db 1 GTCGAACGGAAGGCGCTTTCG 21

RESULT 10
US-10-522-454-1
; Sequence 1, Application US/10522454
; Publication No. US20050244938A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Russell T.
; APPLICANT: Hamann, Mark T.
; APPLICANT: Peraud, Olivier
; APPLICANT: Kabanah, Noer
; TITLE OF INVENTION: MANZAMINE-PRODUCING ACTINOMYCETES
; FILE REFERENCE: 4115-180
; CURRENT APPLICATION NUMBER: US/10/522,454
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: PCT/USO3/24238
; PRIOR FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 1403
; TYPE: DNA
; ORGANISM: Actinomycetes sp.
US-10-522-454-1

Query Match      86.7%; Score 20.8; DB 10; Length 1403;
Best Local Similarity 91.7%; Pred. No. 8.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
   |||||
Db 26 CAAGTCGAACGGAAGGCGCTTTCG 49

RESULT 11
US-11-035-296-1
; Sequence 1, Application US/11035296
; Publication No. US20050203005A1
; GENERAL INFORMATION:
; APPLICANT: VICURON PHARMACEUTICALS INC.
; APPLICANT: LAZZARINI, Ameriga
; APPLICANT: GASTALDO, Luciano
; APPLICANT: CANDIANI, Gianpaolo
; APPLICANT: CICILIATO, Ismaela
; APPLICANT: LOSI, Daniele
; APPLICANT: MARINELLI, Flavia
; APPLICANT: SELVA, Enrico
; APPLICANT: PARENTI, Franco
; TITLE OF INVENTION: ANTIBIOTIC 107891, ITS FACTORS A1 AND A2, PHARMACEUTICALLY
; ACCEPTABLE SALTS AND COMPOSITIONS, AND USE THEREOF
; FILE REFERENCE: 892,280-195
; CURRENT APPLICATION NUMBER: US/11/035,296
; CURRENT FILING DATE: 2005-01-12
; PRIOR APPLICATION NUMBER: US 10/521,336
; PRIOR FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: PCT/EP2004/007658
; PRIOR FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: EP 03016306.7
; PRIOR FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
```

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; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Microbispora sp. ATCC PTA-5024
US-11-035-296-1

Query Match      86.7%; Score 20.8; DB 13; Length 1443;
Best Local Similarity 91.7%; Pred. No. 8.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCCTTTCG 24
   ||||| ||||| ||||| ||||| |||||
Db 31 CAAGTCGAGCGGAAAGGCCCTTCG 54

RESULT 12
US-11-045-628-1
; Sequence 1, Application US/11045628
; Publication No. US20050233952A1
; GENERAL INFORMATION:
; APPLICANT: VICURON PHARMACEUTICALS INC.
; APPLICANT: LAZZARINI, Ameriga
; APPLICANT: GASTALDO, Luciano
; APPLICANT: CANDIANI, Gianpaolo
; APPLICANT: CICILIATO, Imaela
; APPLICANT: LOSI, Daniele
; APPLICANT: MARINELLI, Flavia
; APPLICANT: SELVA, Enrico
; APPLICANT: PARENTI, Franco
; TITLE OF INVENTION: ANTIBIOTIC 107891, ITS FACTORS A1 AND A2, PHARMACEUTICALLY
; TITLE OF INVENTION: ACCEPTABLE SALTS AND COMPOSITIONS, AND USE THEREOF
; FILE REFERENCE: 892,280-500
; CURRENT APPLICATION NUMBER: US/11/045,628
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: US 11/035,296
; PRIOR FILING DATE: 2005-01-12
; PRIOR APPLICATION NUMBER: US 10/521,336
; PRIOR FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: PCT/EP2004/007658
; PRIOR FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: EP 03016306.7
; PRIOR FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Microbispora sp. ATCC PTA-5024
US-11-045-628-1

Query Match      86.7%; Score 20.8; DB 13; Length 1443;
Best Local Similarity 91.7%; Pred. No. 8.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCCTTTCG 24
   ||||| ||||| ||||| ||||| |||||
Db 31 CAAGTCGAGCGGAAAGGCCCTTCG 54

RESULT 13
US-10-697-802A-7
; Sequence 7, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 7
; LENGTH: 1461
; TYPE: DNA
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; ORGANISM: Mycobacterium gordonae
US-10-697-802A-7

Query Match      86.7%; Score 20.8; DB 10; Length 1461;
Best Local Similarity 91.7%; Pred. No. 8.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCCTTTCG 24
   ||||| ||||| ||||| ||||| |||||
Db 21 CAAGTCGACGGTAAGGCCCTTCG 44

RESULT 14
US-11-228-416-5
; Sequence 5, Application US/11228416
; Publication No. US20060008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1480
; TYPE: DNA
; ORGANISM: Salinospira sp. CNH898 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1423)..(1423)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
US-11-228-416-5

Query Match      86.7%; Score 20.8; DB 16; Length 1480;
Best Local Similarity 91.7%; Pred. No. 8.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCCTTTCG 24
   ||||| ||||| ||||| ||||| |||||
Db 51 CAAGTCGAGCGGAAAGGCCCTTCG 74

RESULT 15
US-11-228-416-6
; Sequence 6, Application US/11228416
; Publication No. US20060008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
```

```

; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1480
; TYPE: DNA
; ORGANISM: Salinospora sp. CNH440 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1423)..(1423)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
; US-11-228-416-6

Query Match      86.7%; Score 20.8; DB 16; Length 1480;
Best Local Similarity 91.7%; Pred. No. 8.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CAAGTCGACGGAAGGCCCTTTCG 24
    ||||| ||||| ||||| ||||| |||||
Db 51 CAAGTCGAGCGGAAGGCCCTTTCG 74

RESULT 16
US-11-228-416-8
; Sequence 8, Application US/11228416
; Publication No. US2006008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 1480
; TYPE: DNA
; ORGANISM: Salinospora sp. CNH725 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1423)..(1423)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
; US-11-228-416-9

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; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1423)..(1423)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
; US-11-228-416-8

Query Match      86.7%; Score 20.8; DB 16; Length 1480;
Best Local Similarity 91.7%; Pred. No. 8.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CAAGTCGACGGAAGGCCCTTTCG 24
    ||||| ||||| ||||| ||||| |||||
Db 51 CAAGTCGAGCGGAAGGCCCTTTCG 74

RESULT 17
US-11-228-416-9
; Sequence 9, Application US/11228416
; Publication No. US2006008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1480
; TYPE: DNA
; ORGANISM: Salinospora sp. CNH964 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1423)..(1423)
; OTHER INFORMATION: n is signature nucleotide g position 1456 of 16S rDNA
; US-11-228-416-9

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```
Query Match      86.7%; Score 20.8; DB 16; Length 1480;
Best Local Similarity 91.7%; Pred. No. 8.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
    ||||| ||||| ||||| ||||| |||||
Db 51 CAAGTCGAGCGGAAGGCGCTTTCG 74

RESULT 18
US-11-228-416-3
; Sequence 3, Application US/11228416
; Publication No. US20060008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; PRIOR FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1481
; TYPE: DNA
; ORGANISM: Salinospora sp. CNH643 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (352)..(352)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1424)..(1424)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
US-11-228-416-3

Query Match      86.7%; Score 20.8; DB 16; Length 1481;
Best Local Similarity 91.7%; Pred. No. 8.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
    ||||| ||||| ||||| ||||| |||||
Db 51 CAAGTCGAGCGGAAGGCGCTTTCG 74

RESULT 19
US-11-228-416-4
; Sequence 4, Application US/11228416
; Publication No. US20060008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
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FILE REFERENCE: UCSD1630-1
CURRENT APPLICATION NUMBER: US/11/228,416
CURRENT FILING DATE: 2005-09-15
PRIOR APPLICATION NUMBER: US/09/991,518B
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: US 60/249,356
PRIOR FILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 1482
TYPE: DNA
ORGANISM: Salinospora sp. CNH646 16S ribosomal RNA gene, partial sequence
FEATURE:
NAME/KEY: misc feature
LOCATION: (198)..(198)
OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
FEATURE:
NAME/KEY: misc feature
LOCATION: (351)..(351)
OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
FEATURE:
NAME/KEY: misc feature
LOCATION: (442)..(442)
OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
FEATURE:
NAME/KEY: misc feature
LOCATION: (443)..(443)
OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
FEATURE:
NAME/KEY: misc feature
LOCATION: (1425)..(1425)
OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
US-11-228-416-4

Query Match      86.7%; Score 20.8; DB 16; Length 1482;
Best Local Similarity 91.7%; Pred. No. 8.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
    ||||| ||||| ||||| ||||| |||||
Db 51 CAAGTCGAGCGGAAGGCGCTTTCG 74

RESULT 20
US-11-228-416-7
; Sequence 7, Application US/11228416
; Publication No. US20060008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1483
; TYPE: DNA
; ORGANISM: Salinospora sp. CNH536 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
```

; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (444)..(444)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1426)..(1426)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
US-11-228-416-7

Query Match 86.7%; Score 20.8; DB 16; Length 1483;
Best Local Similarity 91.7%; Pred. No. 8.1; Mismatches 2; Indels 0; Gaps 0;
Matches 22; Conservative 0;

Qy 1 CAAGTCGAACGGAAGGCCTTTTCG 24
Db 51 CAAGTCGAACGGAAGGCCTTCG 74

RESULT 21

US-09-738-972-7
; Sequence 7, Application US/09738972
; Patent No. US20020012918A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: primer
US-09-738-972-7

Query Match 85.0%; Score 20.4; DB 3; Length 32;
Best Local Similarity 95.5%; Pred. No. 11; Mismatches 1; Indels 0; Gaps 0;
Matches 21; Conservative 0;

Qy 1 CAAGTCGAACGGAAGGCCTTTT 22
Db 2 CAAGTCGAACGGAAGGCCTCT 23

RESULT 22

US-09-738-972-14/c
; Sequence 14, Application US/09738972
; Patent No. US20020012918A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR FILING DATE: 1999-12-15

; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: probe
US-09-738-972-14

Query Match 85.0%; Score 20.4; DB 3; Length 32;
Best Local Similarity 95.5%; Pred. No. 11; Mismatches 1; Indels 0; Gaps 0;
Matches 21; Conservative 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22
Db 31 CAAGTCGAACGGAAGGCCTCT 10

RESULT 23

US-10-862-026-7
; Sequence 7, Application US/10862026
; Publication No. US20040224348A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/10/862,026
; CURRENT FILING DATE: 2004-06-04
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: primer
US-10-862-026-7

Query Match 85.0%; Score 20.4; DB 9; Length 32;
Best Local Similarity 95.5%; Pred. No. 11; Mismatches 1; Indels 0; Gaps 0;
Matches 21; Conservative 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22
Db 2 CAAGTCGAACGGAAGGCCTCT 23

RESULT 24

US-10-862-026-14/c
; Sequence 14, Application US/10862026
; Publication No. US20040224348A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/10/862,026
; CURRENT FILING DATE: 2004-06-04
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 32
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: probe
US-10-862-026-14

Query Match 85.0%; Score 20.4; DB 9; Length 32;
Best Local Similarity 95.5%; Pred. No. 11;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22
|||||
Db 31 CAAGTCGAACGGAAGGCCTCT 10
|||||

RESULT 25

US-10-478-633A-23
; Sequence 23, Application US/10478633A
; Publication No. US2005059000A1
; GENERAL INFORMATION:

; APPLICANT: TAKARA BIO INC.
; TITLE OF INVENTION: A stabilization method and a preservation method for a reagent for

; FILE REFERENCE: 663232
; CURRENT APPLICATION NUMBER: US/10/478.633A
; CURRENT FILING DATE: 2003-11-25

; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2001-177737
; PRIOR FILING DATE: 2001-06-12

; PRIOR APPLICATION NUMBER: JP 2001-249689
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 173

; SEQ ID NO 23
; LENGTH: 560
; TYPE: DNA

; ORGANISM: Mycobacterium avium
US-10-478-633A-23

Query Match 85.0%; Score 20.4; DB 10; Length 560;
Best Local Similarity 95.5%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22
|||||
Db 31 CAAGTCGAACGGAAGGCCTCT 52
|||||

RESULT 26

US-10-697-802A-12
; Sequence 12, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:

; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.

; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697.802A

; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145

; SEQ ID NO 12
; LENGTH: 1421
; TYPE: DNA

; ORGANISM: Mycobacterium lentiflavum
US-10-697-802A-12

Query Match 85.0%; Score 20.4; DB 10; Length 1421;
Best Local Similarity 95.5%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22
|||||
Db 21 CAAGTCGAACGGAAGGCCTCT 42
|||||

RESULT 27

US-10-697-802A-2

; Sequence 2, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:

; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.

; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697.802A

; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145

; SEQ ID NO 2
; LENGTH: 1454
; TYPE: DNA

; ORGANISM: Mycobacterium avium
US-10-697-802A-2

Query Match 85.0%; Score 20.4; DB 10; Length 1454;
Best Local Similarity 95.5%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22
|||||
Db 31 CAAGTCGAACGGAAGGCCTCT 52
|||||

RESULT 28

US-10-029-397A-32

; Sequence 32, Application US/10029397A
; Publication No. US20030175709A1
; GENERAL INFORMATION:

; APPLICANT: MURPHY, GEORGE L.
; APPLICANT: WHITLEY, J. PENN

; TITLE OF INVENTION: METHOD AND SYSTEM FOR DEPLETING rRNA POPULATIONS
; FILE REFERENCE: AMBI:076US
; CURRENT APPLICATION NUMBER: US/10/029.397A

; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 32
; LENGTH: 1465

; TYPE: DNA
; ORGANISM: Mycobacterium avium

; FEATURE:
; NAME/KEY: modified_base

; LOCATION: (298)..(881)
; OTHER INFORMATION: N = A, C, G or T/U

US-10-029-397A-32

Query Match 85.0%; Score 20.4; DB 7; Length 1465;
Best Local Similarity 95.5%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22
|||||
Db 21 CAAGTCGAACGGAAGGCCTCT 42
|||||

RESULT 29

US-10-831-286A-1517

; Sequence 1517, Application US/10831286A
; Publication No. US20060046246A1
; GENERAL INFORMATION:

; APPLICANT: ZENG, QIANDONG
; APPLICANT: CHATELLIER, SONIA

; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA

; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES

; FILE REFERENCE: 032796-174.001
; CURRENT APPLICATION NUMBER: US/10/831.286A

; CURRENT FILING DATE: 2004-04-26

; PRIOR APPLICATION NUMBER: 60/464,955
; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1517
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Corynebacterium diphtheriae
US-10-831-286A-1517

Query Match 83.3%; Score 20; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCT 20
|||||
Db 1 CAAGTCGAACGGAAGGCCT 20
|||||

RESULT 30

US-10-831-286A-8212
; Sequence 8212, Application US/10831286A
; Publication No. US20060046246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, QIANDONG
; APPLICANT: CHATELIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001
; CURRENT APPLICATION NUMBER: US/10/831.286A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/464,955
; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8212
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Corynebacterium kutscheri
US-10-831-286A-8212

Query Match 80.8%; Score 19.4; DB 11; Length 30;
Best Local Similarity 95.2%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
|||||
Db 1 CAAGTCGAACGGAAGGCCTT 21
|||||

RESULT 31

US-10-438-774-15
; Sequence 15, Application US/10438774
; Publication No. US20040010504A1
; GENERAL INFORMATION:
; APPLICANT: Hinrichs, Steven
; APPLICANT: Mohammed, Amr
; APPLICANT: Ali, Hesham
; APPLICANT: Kuyper, Dan
; TITLE OF INVENTION: Custom Sequence Databases and Methods of
; FILE REFERENCE: UNMC.63174-US
; CURRENT APPLICATION NUMBER: US/10/438,774
; CURRENT FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: 60/381,015
; PRIOR FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 454
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-438-774-15

Query Match 80.8%; Score 19.4; DB 7; Length 454;
Best Local Similarity 95.2%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GTCGAACGGAAGGCCTTTCG 24
|||||
Db 1 GTCGAACGGAAGGCCTTTCG 21
|||||

RESULT 32

US-10-085-871C-1
; Sequence 1, Application US/10085871C
; Publication No. US20030199047A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Fang-Yu
; APPLICANT: Lee, Ming-Liang
; APPLICANT: Anderson, Hong C.
; APPLICANT: Chiu, Chung-Ching
; TITLE OF INVENTION: New Strains of Saccharothrix, Process for Producing Pravastatin U
; FILE REFERENCE: 004135.P005
; CURRENT APPLICATION NUMBER: US/10/085,871C
; CURRENT FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1437
; TYPE: DNA
; ORGANISM: Saccharothrix 44442
US-10-085-871C-1

Query Match 80.0%; Score 19.2; DB 7; Length 1437;
Best Local Similarity 87.5%; Pred. No. 49;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAACTCGAAGCGTAAGGCCTTCG 24
|||||
Db 31 CAACTCGAAGCGTAAGGCCTTCG 54
|||||

RESULT 33

US-10-727-643-1
; Sequence 1, Application US/10727643
; Publication No. US20050064566A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Fang-Yu
; APPLICANT: Anderson, Hong C.
; APPLICANT: Chiu, Chung-Ching
; TITLE OF INVENTION: New Strains of Saccharothrix, Process for Producing Pravastatin U
; FILE REFERENCE: 004135.P005
; CURRENT APPLICATION NUMBER: US/10/727,643
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: US/10/085,871
; PRIOR FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1437
; TYPE: DNA
; ORGANISM: Saccharothrix 44442
US-10-727-643-1

Query Match 80.0%; Score 19.2; DB 10; Length 1437;
Best Local Similarity 87.5%; Pred. No. 49;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCGCTTTTCG 24
|||||
Db 31 CAAGTCGAGCGGTAAAGGCCCTTCG 54

RESULT 34
US-10-230-026-6
; Sequence 6, Application US/10230026
; Publication No. US20030124695A1
; GENERAL INFORMATION:
; APPLICANT: MICHAEL G. BRAMUCCI
; APPLICANT: PATRICIA C. BRZOSTOWICZ
; APPLICANT: KRISTY N. KOSTICHKA
; APPLICANT: VASANTHA NAGARAJAN
; APPLICANT: PIERRE E. ROUVIERE
; APPLICANT: STUART M. THOMAS
; TITLE OF INVENTION: GENES ENCODING BABYER-VILLIGER MONOOXYGENASES
; FILE REFERENCE: CL1789 US NA
; CURRENT APPLICATION NUMBER: US/10/230,026
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 60/315,546
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 1439
; TYPE: DNA
; ORGANISM: Rhodococcus erythropolis AN12
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1417)..(1417)
; OTHER INFORMATION: N = G or A or T or C
US-10-230-026-6

Query Match 80.0%; Score 19.2; DB 7; Length 1439;
Best Local Similarity 87.5%; Pred. No. 49;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCGCTTTTCG 24
|||
Db 32 CAATTCGAGCGGTAAAGGCCCTTCG 55

RESULT 35
US-10-486-307-6
; Sequence 6, Application US/10486307
; Publication No. US20040267001A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours, Inc.
; TITLE OF INVENTION: GENES ENCODING BABYER-VILLIGER MONOOXYGENASES
; FILE REFERENCE: CL1789 PCT
; CURRENT APPLICATION NUMBER: US/10/486,307
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: 60/315,546
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 1439
; TYPE: DNA
; ORGANISM: Rhodococcus erythropolis AN12
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1417)..(1417)
; OTHER INFORMATION: N = G or A or T or C
US-10-486-307-6

Query Match 80.0%; Score 19.2; DB 9; Length 1439;
Best Local Similarity 87.5%; Pred. No. 49;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCGCTTTTCG 24
|||
Db 32 CAATTCGAGCGGTAAAGGCCCTTCG 55

Db 32 CAATTCGAGCGGTAAAGGCCCTTCG 55

RESULT 36
US-10-085-871C-2
; Sequence 2, Application US/10085871C
; Publication No. US20030199047A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Fang-Yu
; APPLICANT: Lee, Ming-Liang
; APPLICANT: Anderson, Hong C.
; APPLICANT: Chiu, Schung-Ching
; TITLE OF INVENTION: New Strains of Saccharothrix, Process for Producing Pravastatin U
; FILE REFERENCE: 004135.P005
; CURRENT APPLICATION NUMBER: US/10/085,871C
; CURRENT FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1471
; TYPE: DNA
; ORGANISM: Saccharothrix 45494
US-10-085-871C-2

Query Match 80.0%; Score 19.2; DB 7; Length 1471;
Best Local Similarity 87.5%; Pred. No. 49;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCGCTTTTCG 24
|||||
Db 31 CAAGTCGAGCGGTAAAGGCCCTTCG 54

RESULT 37
US-10-727-643-2
; Sequence 2, Application US/10727643
; Publication No. US20050064566A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Fang-Yu
; APPLICANT: Lee, Ming-Liang
; APPLICANT: Anderson, Hong C.
; APPLICANT: Chiu, Schung-Ching
; TITLE OF INVENTION: New Strains of Saccharothrix, Process for Producing Pravastatin U
; FILE REFERENCE: 004135.P005
; CURRENT APPLICATION NUMBER: US/10/727,643
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: US/10/085,871
; PRIOR FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1471
; TYPE: DNA
; ORGANISM: Saccharothrix 45494
US-10-727-643-2

Query Match 80.0%; Score 19.2; DB 10; Length 1471;
Best Local Similarity 87.5%; Pred. No. 49;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCGCTTTTCG 24
|||||
Db 31 CAAGTCGAGCGGTAAAGGCCCTTCG 54

RESULT 38
US-10-756-683-1
; Sequence 1, Application US/10756683
; Publication No. US20040180960A1
; GENERAL INFORMATION:
; APPLICANT: Korea Chungang Educational Foundation

; APPLICANT: Hwang, Byong Kook
; APPLICANT: Lee, Jung Yeop
; TITLE OF INVENTION: Thiobactin and Antifungal Composition for Controlling Plant
; TITLE OF INVENTION: Diseases Using the Same
; FILE REFERENCE: 4228-102
; CURRENT APPLICATION NUMBER: US/10/756,683
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: KP 10-2003-0015628
; PRIOR FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: KP 10-2003-0015629
; PRIOR FILING DATE: 2003-03-13
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1488
; TYPE: DNA
; ORGANISM: Lechevalieria aerocolonigenes
US-10-756-683-1

Query Match 80.0%; Score 19.2; DB 9; Length 1488;
Best Local Similarity 87.5%; Pred. No. 49;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAAGTCGACGGAAGGCTTTCG 24
Db 43 CAAGTCGAGCGTAAGGCCCTTCG 66

RESULT 39

US-10-875-161-2
; Sequence 2, Application US/10875161
; Publication No. US20050009151A1
; GENERAL INFORMATION:
; APPLICANT: Chase, Matthew
; APPLICANT: Clayton, Robert
; APPLICANT: Landis, Bryan
; APPLICANT: Banerjee, Amit
; TITLE OF INVENTION: Methods for the Stereoselective Synthesis and Enantiomeric
; TITLE OF INVENTION: Enrichment of Beta-Amino Acids
; FILE REFERENCE: S0-3262-2-PR-US
; CURRENT APPLICATION NUMBER: US/10/875,161
; CURRENT FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 1514
; TYPE: DNA
; ORGANISM: Rhodococcus opacus
; FEATURE:
; NAME/KEY: rRNA
; LOCATION: (1)..(1514)
; OTHER INFORMATION: 16s rRNA gene (rDNA) from Rhodococcus opacus
; FEATURE:
; NAME/KEY: misc difference
; LOCATION: (1)..(1514)
; OTHER INFORMATION: Alignment 0.17% different from 16s rRNA gene (rDNA) of
; OTHER INFORMATION: Rhodococcus opacus
US-10-875-161-2

Query Match 80.0%; Score 19.2; DB 9; Length 1514;
Best Local Similarity 87.5%; Pred. No. 49;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAAGTCGACGGAAGGCTTTCG 24
Db 54 CAAGTCGAGCGTAAGGCCCTTCG 77

RESULT 40

US-09-738-274-27
; Sequence 27, Application US/09738274
; Publication No. US20030165924A1
; GENERAL INFORMATION:

; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-27

Query Match 79.2%; Score 19; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCC 19
Db 1 CAAGTCGAACGGAAGGCC 19

RESULT 41

US-10-665-708-27
; Sequence 27, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-10-665-708-27

Query Match 79.2%; Score 19; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCC 19
Db 1 CAAGTCGAACGGAAGGCC 19

RESULT 42

US-10-830-943-11

```
; Sequence 11, Application US/10830943
; Publication No. US20050009053A1
; GENERAL INFORMATION:
; APPLICANT: Boecker, Sebastian
; APPLICANT: van den Boom, Dirk
; TITLE OF INVENTION: FRAGMENTATION-BASED METHODS AND SYSTEMS
; TITLE OF INVENTION: FOR DE NOVO SEQUENCING
; FILE REFERENCE: 17082-079001
; CURRENT APPLICATION NUMBER: US/10/830,943
; CURRENT FILING DATE: 2004-04-22
; PRIOR FILING DATE: 2004-04-22
; PRIOR FILING DATE: 2003-04-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: amplicon sequence
US-10-830-943-11

Query Match          79.2%; Score 19; DB 9; Length 80;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCC 19
   |||||
Db 51 CAAGTCGAACGGAAGGCC 69

RESULT 43
US-10-478-633A-24
; Sequence 24, Application US/10478633A
; Publication No. US20050059000A1
; GENERAL INFORMATION:
; APPLICANT: TAKARA BIO INC.
; TITLE OF INVENTION: A stabilization method and a preservation method for a reagent for
; TITLE OF INVENTION: acid amplification or detection reaction
; FILE REFERENCE: 683232
; CURRENT APPLICATION NUMBER: US/10/478,633A
; CURRENT FILING DATE: 2003-11-25
; PRIOR FILING DATE: 2001-177737
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2001-249689
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 24
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Mycobacterium intracellulare
US-10-478-633A-24

Query Match          79.2%; Score 19; DB 10; Length 560;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCC 19
   |||||
Db 43 CAAGTCGAACGGAAGGCC 61

RESULT 44
US-10-697-802A-11
; Sequence 11, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
```

```
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 11
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Mycobacterium kubicae
US-10-697-802A-11

Query Match          79.2%; Score 19; DB 10; Length 1321;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCC 19
   |||||
Db 15 CAAGTCGAACGGAAGGCC 33

RESULT 45
US-10-697-802A-14
; Sequence 14, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 14
; LENGTH: 1415
; TYPE: DNA
; ORGANISM: Mycobacterium paraffinicum
US-10-697-802A-14

Query Match          79.2%; Score 19; DB 10; Length 1415;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCC 19
   |||||
Db 16 CAAGTCGAACGGAAGGCC 34

RESULT 46
US-10-062-777-1
; Sequence 1, Application US/10062777
; Publication No. US20020119514A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: A PROCESS FOR PRODUCING A BRAN PICKLES FLAVORING SOLUTION
; FILE REFERENCE: 11142W0
; CURRENT APPLICATION NUMBER: US/10/062,777
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/463,618
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Corynebacterium sp.NK-1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (166)
; OTHER INFORMATION: n is "a" or "g" or "c" or "t".
US-10-062-777-1

Query Match          79.2%; Score 19; DB 6; Length 1460;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCC 19
   |||||
```

```
Db          39 CAAGTCGAACGGAAGGCC 57

RESULT 47
US-10-419-095-1
; Sequence 1, Application US/10419095
; Publication No. US20030162244A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: A PROCESS FOR PRODUCING A BRAN PICKLES FLAVORING SOLUTION
; FILE REFERENCE: 11142WO
; CURRENT APPLICATION NUMBER: US/10/419,095
; CURRENT FILING DATE: 2003-04-21
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US/09/463,618
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: H10-166226
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Corynebacterium sp.NK-1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (166)
; OTHER INFORMATION: n is "a" or "g" or "c" or "t".
US-10-419-095-1

Query Match          79.2%; Score 19; DB 7; Length 1460;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 CAAGTCGAACGGAAGGCC 19
            |||||
Db          39 CAAGTCGAACGGAAGGCC 57

RESULT 48
US-10-697-802A-16
; Sequence 16, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 16
; LENGTH: 1462
; TYPE: DNA
; ORGANISM: Mycobacterium szulgai
US-10-697-802A-16

Query Match          79.2%; Score 19; DB 10; Length 1462;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 CAAGTCGAACGGAAGGCC 19
            |||||
Db          21 CAAGTCGAACGGAAGGCC 39

RESULT 49
US-10-697-802A-15
; Sequence 15, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
```

```
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 15
; LENGTH: 1484
; TYPE: DNA
; ORGANISM: Mycobacterium simiae
US-10-697-802A-15

Query Match          79.2%; Score 19; DB 10; Length 1484;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 CAAGTCGAACGGAAGGCC 19
            |||||
Db          21 CAAGTCGAACGGAAGGCC 39

RESULT 50
US-10-697-802A-8
; Sequence 8, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 8
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Mycobacterium heckeshornense
US-10-697-802A-8

Query Match          79.2%; Score 19; DB 10; Length 1527;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 CAAGTCGAACGGAAGGCC 19
            |||||
Db          45 CAAGTCGAACGGAAGGCC 63

RESULT 51
US-09-738-274-14
; Sequence 14, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02 UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 60/172,190
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-14
```

Query Match 78.3%; Score 18.8; DB 3; Length 32;
Best Local Similarity 90.9%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22
Db 2 CAAGTCGAACGGAAGGCTCT 23

RESULT 52

US-10-665-708-14
; Sequence 14, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAI, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: Gp107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR FILING DATE: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-665-708-14

Query Match 78.3%; Score 18.8; DB 10; Length 32;
Best Local Similarity 90.9%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22
Db 2 CAAGTCGAACGGAAGGCTCT 23

RESULT 53

US-10-697-802A-17
; Sequence 17, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 17
; LENGTH: 1416
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-697-802A-17

Query Match 78.3%; Score 18.8; DB 10; Length 1416;
Best Local Similarity 90.9%; Pred. No. 76;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22

Db 21 CAAGTCGAACGGAAGGCTCT 42

RESULT 54

US-10-697-802A-3
; Sequence 3, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 3
; LENGTH: 1421
; TYPE: DNA
; ORGANISM: Mycobacterium bovis
US-10-697-802A-3

Query Match 78.3%; Score 18.8; DB 10; Length 1421;
Best Local Similarity 90.9%; Pred. No. 76;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22
Db 21 CAAGTCGAACGGAAGGCTCT 42

RESULT 55

US-10-697-802A-10
; Sequence 10, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 10
; LENGTH: 1463
; TYPE: DNA
; ORGANISM: Mycobacterium kansasii
US-10-697-802A-10

Query Match 78.3%; Score 18.8; DB 10; Length 1463;
Best Local Similarity 90.9%; Pred. No. 76;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22
Db 20 CAAGTCGAACGGAAGGCTCT 41

RESULT 56

US-09-726-774-7
; Sequence 7, Application US/09726774
; Patent No. US20020082226A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/09/726,774
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7

```
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-726-774-7

Query Match      78.3%; Score 18.8; DB 3; Length 1464;
Best Local Similarity 90.9%; Pred. No. 76;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCCTTT 22
    |||||
Db 21 CAACTCGAACGGAAGGTCCT 42
    |||||

RESULT 57
US-10-719-633-7
; Sequence 7, Application US/10719633
; Publication No. US20040137485A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/10/719,633
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/09/726,774
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-719-633-7

Query Match      78.3%; Score 18.8; DB 8; Length 1464;
Best Local Similarity 90.9%; Pred. No. 76;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCCTTT 22
    |||||
Db 21 CAACTCGAACGGAAGGTCCT 42
    |||||

RESULT 58
US-10-220-212A-34
; Sequence 34, Application US/10220212A
; Publication No. US20040110129A1
; GENERAL INFORMATION:
; APPLICANT: Secretary of the United States of America as represented by the
; APPLICANT: Health
; APPLICANT: Beckman Coulter, Inc.
; TITLE OF INVENTION: Multiplex Hybridization System for the Identification of Pathogen
; FILE REFERENCE: 4239-58135
; CURRENT APPLICATION NUMBER: US/10/220,212A
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/186,840
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-220-212A-34

Query Match      78.3%; Score 18.8; DB 8; Length 1524;
Best Local Similarity 90.9%; Pred. No. 76;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 CAACTCGAACGGAAGGCCTTT 22
    |||||
Db 51 CAACTCGAACGGAAGGTCCT 72
    |||||

RESULT 59
US-10-029-397A-33
; Sequence 33, Application US/10029397A
; Publication No. US20030175709A1
; GENERAL INFORMATION:
; APPLICANT: MURPHY, GEORGE L.
; APPLICANT: WHITLEY, J. PENN
; TITLE OF INVENTION: METHOD AND SYSTEM FOR DEPLETING rRNA POPULATIONS
; FILE REFERENCE: AMBI:076US
; CURRENT APPLICATION NUMBER: US/10/029,397A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-029-397A-33

Query Match      78.3%; Score 18.8; DB 7; Length 1536;
Best Local Similarity 90.9%; Pred. No. 76;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 CAACTCGAACGGAAGGCCTTT 22
    |||||
Db 60 CAACTCGAACGGAAGGTCCT 81
    |||||

RESULT 60
US-10-029-397A-34
; Sequence 34, Application US/10029397A
; Publication No. US20030175709A1
; GENERAL INFORMATION:
; APPLICANT: MURPHY, GEORGE L.
; APPLICANT: WHITLEY, J. PENN
; TITLE OF INVENTION: METHOD AND SYSTEM FOR DEPLETING rRNA POPULATIONS
; FILE REFERENCE: AMBI:076US
; CURRENT APPLICATION NUMBER: US/10/029,397A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-029-397A-34

Query Match      78.3%; Score 18.8; DB 7; Length 1536;
Best Local Similarity 90.9%; Pred. No. 76;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 CAACTCGAACGGAAGGCCTTT 22
    |||||
Db 60 CAACTCGAACGGAAGGTCCT 81
    |||||

RESULT 61
US-09-925-065A-906221/c
; Sequence 906221, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
```

```
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 906221
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-925-065A-906221

Query Match      75.8%; Score 18.2; DB 4; Length 600;
Best Local Similarity 87.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTTC 23
    ||||| ||| ||||| |||||
Db 298 CAAGTGGACCTGAAGGCCTTTC 276

RESULT 62
US-09-925-065A-906221/c
; Sequence 906221, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 906221
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-925-065A-906221

Query Match      75.8%; Score 18.2; DB 5; Length 600;
Best Local Similarity 87.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTTC 23
    ||||| ||| ||||| |||||
Db 298 CAAGTGGACCTGAAGGCCTTTC 276

RESULT 63
US-09-738-274-24
; Sequence 24, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-10-665-708-24

Query Match      75.0%; Score 18; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GAACGGAAGGCCTTTCG 24
    ||||| ||||| ||||| |||||
Db 1 GAACGGAAGGCCTTTCG 18

RESULT 64
US-10-665-708-24
; Sequence 24, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-10-665-708-24

Query Match      75.0%; Score 18; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GAACGGAAGGCCTTTCG 24
    ||||| ||||| ||||| |||||
Db 1 GAACGGAAGGCCTTTCG 18

RESULT 65
US-10-425-114-30427
; Sequence 30427, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
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; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 30427
; LENGTH: 1366
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73019F09_FLI
US-10-425-114-30427

Query Match          74.2%; Score 17.8; DB 8; Length 1366;
Best Local Similarity 90.5%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
    ||||| ||||| ||||| |||||
Db 896 CAAGTGAACGAAAGGCCTT 916

RESULT 66
US-09-917-800A-1684
; Sequence 1684, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1684
; LENGTH: 4540
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_021266
US-09-917-800A-1684

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Query Match 74.2%; Score 17.8; DB 3; Length 4540;

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Best Local Similarity 90.5%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
    ||||| ||||| ||||| |||||
Db 105 CAAGTCGAACGAAAGGCCTT 125

RESULT 67
US-11-136-527-299
; Sequence 299, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays for Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 299
; LENGTH: 4770
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-299

Query Match          74.2%; Score 17.8; DB 16; Length 4770;
Best Local Similarity 90.5%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
    ||||| ||||| ||||| |||||
Db 105 CAAGTCGAACGAAAGGCCTT 125

RESULT 68
US-10-087-192-1004
; Sequence 1004, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1004
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-087-192-1004

Query Match          73.3%; Score 17.6; DB 6; Length 960;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTTCG 24
    ||||| ||||| ||||| |||||
Db 811 CAAGTCGAGCAGAAAGTCCTTACG 834

RESULT 69
US-10-956-157-9594

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; Sequence 9594, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9594
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-956-157-9594

Query Match      73.3%; Score 17.6; DB 10; Length 1400;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTTCG 24
    ||||| ||||| ||||| |||||
Db 554 CAAGTCGAATTGAAAGGACTGTGCG 577

RESULT 70
US-10-956-157-4359
; Sequence 4359, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4359
; LENGTH: 1786
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-956-157-4359

Query Match      73.3%; Score 17.6; DB 10; Length 1786;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTTCG 24
    ||||| ||||| ||||| |||||
Db 940 CAAGTCGAATTGAAAGGACTGTGCG 963

RESULT 71
US-10-087-192-1003
; Sequence 1003, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
```

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; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 1003
; LENGTH: 43800
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-087-192-1003

Query Match      73.3%; Score 17.6; DB 6; Length 43800;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTTCG 24
    ||||| ||||| ||||| |||||
Db 33651 CAAGTCGAGCAGAAAGTCCTTACG 33674

RESULT 72
US-10-697-802A-9
; Sequence 9, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 9
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Mycobacterium intracellulare
; US-10-697-802A-9

Query Match      72.5%; Score 17.4; DB 10; Length 1452;
Best Local Similarity 94.7%; Pred. No. 3.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCC 19
    ||||| ||||| ||||| |||||
Db 11 CAAGTCGAACGGAAGGCC 29

RESULT 73
US-10-767-701-31297
; Sequence 31297, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 31297
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 18066455
; US-10-767-701-31297

Query Match      71.7%; Score 17.2; DB 8; Length 622;
Best Local Similarity 86.4%; Pred. No. 4.4e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AGTCGACGGAAGGCGCTTTTCG 24
    ||||| ||||| ||||| |||||
Db 31 AGTCGGAAGGAATGGCGCTTTTCG 52
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RESULT 74
US-09-925-065A-481777
; Sequence 481777, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 481777
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-481777

Query Match          71.7%; Score 17.2; DB 4; Length 654;
Best Local Similarity 86.4%; Pred. No. 4.4e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGGCCTTTC 23
Db      403 AAGTGAACGGAACGGCCTTTC 424

RESULT 75
US-09-925-065A-481777
; Sequence 481777, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 481777
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-481777

Query Match          71.7%; Score 17.2; DB 5; Length 654;
Best Local Similarity 86.4%; Pred. No. 4.4e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGGCCTTTC 23
Db      403 AAGTGAACGGAACGGCCTTTC 424

RESULT 76
US-09-809-391-59
; Sequence 59, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 1776
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (713)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (862)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1752)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1773)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-809-391-59

Query Match          71.7%; Score 17.2; DB 3; Length 1776;
Best Local Similarity 79.2%; Pred. No. 4.6e+02;
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CAAGTCGAACGGAAGGCCTTTCG 24
Db      878 CAAGTCGAATTGAAAGRACGTCTCG 901

RESULT 77
US-09-882-171-59
; Sequence 59, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
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1	PRIOR FILING DATE: 1997-08-22	
2	PRIOR APPLICATION NUMBER: 60/056,877	
3	PRIOR FILING DATE: 1997-08-22	
4	PRIOR APPLICATION NUMBER: 60/056,889	
5	PRIOR FILING DATE: 1997-08-22	
6	PRIOR APPLICATION NUMBER: 60/056,893	
7	PRIOR FILING DATE: 1997-08-22	
8	PRIOR APPLICATION NUMBER: 60/056,630	
9	PRIOR FILING DATE: 1997-08-22	
10	PRIOR APPLICATION NUMBER: 60/056,878	
11	PRIOR FILING DATE: 1997-08-22	
12	PRIOR APPLICATION NUMBER: 60/056,662	
13	PRIOR FILING DATE: 1997-08-22	
14	PRIOR APPLICATION NUMBER: 60/056,872	
15	PRIOR FILING DATE: 1997-08-22	
16	PRIOR APPLICATION NUMBER: 60/056,882	
17	PRIOR FILING DATE: 1997-08-22	
18	PRIOR APPLICATION NUMBER: 60/056,637	
19	PRIOR FILING DATE: 1997-08-22	
20	PRIOR APPLICATION NUMBER: 60/056,903	
21	PRIOR FILING DATE: 1997-08-22	
22	PRIOR APPLICATION NUMBER: 60/056,888	
23	PRIOR FILING DATE: 1997-08-22	
24	PRIOR APPLICATION NUMBER: 60/056,879	
25	PRIOR FILING DATE: 1997-08-22	
26	PRIOR APPLICATION NUMBER: 60/056,880	
27	PRIOR FILING DATE: 1997-08-22	
28	PRIOR APPLICATION NUMBER: 60/056,894	
29	PRIOR FILING DATE: 1997-08-22	
30	PRIOR APPLICATION NUMBER: 60/056,911	
31	PRIOR FILING DATE: 1997-08-22	
32	PRIOR APPLICATION NUMBER: 60/056,636	
33	PRIOR FILING DATE: 1997-08-22	
34	PRIOR APPLICATION NUMBER: 60/056,874	
35	PRIOR FILING DATE: 1997-08-22	
36	PRIOR APPLICATION NUMBER: 60/056,910	
37	PRIOR FILING DATE: 1997-08-22	
38	PRIOR APPLICATION NUMBER: 60/056,864	
39	PRIOR FILING DATE: 1997-08-22	
40	PRIOR APPLICATION NUMBER: 60/056,631	
41	PRIOR FILING DATE: 1997-08-22	
42	PRIOR APPLICATION NUMBER: 60/056,845	
43	PRIOR FILING DATE: 1997-08-22	
44	PRIOR APPLICATION NUMBER: 60/056,892	
45	PRIOR FILING DATE: 1997-08-22	
46	PRIOR APPLICATION NUMBER: 60/057,761	
47	PRIOR FILING DATE: 1997-08-22	
48	PRIOR APPLICATION NUMBER: 60/047,595	
49	PRIOR FILING DATE: 1997-05-23	
50	PRIOR APPLICATION NUMBER: 60/047,599	
51	PRIOR FILING DATE: 1997-05-23	
52	PRIOR APPLICATION NUMBER: 60/047,588	
53	PRIOR FILING DATE: 1997-05-23	
54	PRIOR APPLICATION NUMBER: 60/047,585	
55	PRIOR FILING DATE: 1997-05-23	
56	PRIOR APPLICATION NUMBER: 60/047,586	
57	PRIOR FILING DATE: 1997-05-23	
58	PRIOR APPLICATION NUMBER: 60/047,590	
59	PRIOR FILING DATE: 1997-05-23	
60	PRIOR APPLICATION NUMBER: 60/047,594	
61	PRIOR FILING DATE: 1997-05-23	
62	PRIOR APPLICATION NUMBER: 60/047,589	
63	PRIOR FILING DATE: 1997-05-23	
64	PRIOR APPLICATION NUMBER: 60/047,593	
65	PRIOR FILING DATE: 1997-05-23	
66	PRIOR APPLICATION NUMBER: 60/047,614	
67	PRIOR FILING DATE: 1997-05-23	
68	PRIOR APPLICATION NUMBER: 60/043,578	
69	PRIOR FILING DATE: 1997-04-11	
70	PRIOR APPLICATION NUMBER: 60/043,576	
71	PRIOR FILING DATE: 1997-04-11	
72	PRIOR APPLICATION NUMBER: 60/047,501	
73	PRIOR FILING DATE: 1997-05-23	

; PRIOR APPLICATION NUMBER: 60/043,670
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/056,632
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,876
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,881
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,909
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,875
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,862
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,887
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05

Query Match 71.7%; Score 17.2; DB 3; Length 1776;
Best Local Similarity 79.2%; Pred. No. 4.6e+02;
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTTTCG 24
Db 878 CAAGTCGAATTGAAGRACTGTCTG 901
|||||

RESULT 78
US-10-164-861-59
; Sequence 59, Application US/10164861
; Publication No. US20030225248A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/10/164,861
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 1776
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (713)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (862)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1752)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1773)

; OTHER INFORMATION: n equals a,t,g, or c
US-10-164-861-59

Query Match 71.7%; Score 17.2; DB 7; Length 1776;
Best Local Similarity 79.2%; Pred. No. 4.6e+02;
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTTTCG 24
Db 878 CAAGTCGAATTGAAGRACTGTCTG 901
|||||

RESULT 79
US-11-144-947-59
; Sequence 59, Application US/11144947
; Publication No. US20060084082A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2C2
; CURRENT APPLICATION NUMBER: US/11/144,947
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: 09/882,171
; PRIOR FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/190,068
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 10/164,861
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 1776
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (713)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (862)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1752)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1773)
; OTHER INFORMATION: n equals a,t,g, or c
US-11-144-947-59

Query Match 71.7%; Score 17.2; DB 16; Length 1776;
Best Local Similarity 79.2%; Pred. No. 4.6e+02;
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTTTCG 24
|||||


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; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,882
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,637
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,903
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,888
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,879
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,880
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,894
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,911
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,636
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,874
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,910
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,864
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,631
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,845
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,892
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,761
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/047,595
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,599
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,588
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,585
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,586
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,590
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,594
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,589
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,593
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,614
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,578
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,576
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/047,501
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,670
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/056,632
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,876
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,881
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,909
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,875
; PRIOR FILING DATE: 1997-08-22
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; PRIOR APPLICATION NUMBER: 60/056,862
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,887
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05

Query Match 71.7%; Score 17.2; DB 3; Length 1791;
Best Local Similarity 79.2%; Pred. No. 4.6e+02;
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTTTCG 24
|||||
Db 973 CAAGTCGAATTGAAAGRACTGCTCG 996

RESULT 82
US-10-164-861-226
; Sequence 226, Application US/10164861
; Publication No. US20030225248A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/10/164,861
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 226
; LENGTH: 1791
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-164-861-226

Query Match 71.7%; Score 17.2; DB 7; Length 1791;
Best Local Similarity 79.2%; Pred. No. 4.6e+02;
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTTTCG 24
|||||
Db 973 CAAGTCGAATTGAAAGRACTGCTCG 996

RESULT 83
US-11-144-947-226
; Sequence 226, Application US/11144947
; Publication No. US20060084082A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2C2
; CURRENT APPLICATION NUMBER: US/11/144,947
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: 09/882,171
; PRIOR FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/190,068
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 10/164,861
; PRIOR FILING DATE: 2002-06-10
```

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; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 226
; LENGTH: 1791
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-947-226

Query Match          71.7%; Score 17.2; DB 16; Length 1791;
Best Local Similarity 79.2%; Pred. No. 4.6e+02;
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGAAAGGCCTTTCG 24
Db 973 CAAGTCGAATTGAAAGRACTGTCG 996

RESULT 84
US-09-925-065A-553599
; Sequence 553599, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 553599
; LENGTH: 2258
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-553599

Query Match          71.7%; Score 17.2; DB 4; Length 2258;
Best Local Similarity 86.4%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGAAAGGCCTTT 22
Db 1256 CAAGTCGAACGAAAGGCCTGT 1277

RESULT 85
US-09-925-065A-553599
; Sequence 553599, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 553599
; LENGTH: 2258
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-553599

Query Match          71.7%; Score 17.2; DB 4; Length 2258;
Best Local Similarity 86.4%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGAAAGGCCTTT 22
Db 1256 CAAGTCGAACGAAAGGCCTGT 1277

RESULT 86
US-10-369-493-35634/c
; Sequence 35634, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 35634
; LENGTH: 2919
; TYPE: DNA
; ORGANISM: Mesorhizobium loti
US-10-369-493-35634

Query Match          71.7%; Score 17.2; DB 7; Length 2919;
Best Local Similarity 86.4%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGAAAGGCCTTT 22
Db 2385 CACGGCGAACGCAAGGCCTTT 2364

RESULT 87
US-10-425-115-40860/c
; Sequence 40860, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
```

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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 553599
; LENGTH: 2258
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-553599

Query Match          71.7%; Score 17.2; DB 5; Length 2258;
Best Local Similarity 86.4%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGAAAGGCCTTT 22
Db 1256 CAAGTCGAACGAAAGGCCTGT 1277

RESULT 86
US-10-369-493-35634/c
; Sequence 35634, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 35634
; LENGTH: 2919
; TYPE: DNA
; ORGANISM: Mesorhizobium loti
US-10-369-493-35634

Query Match          71.7%; Score 17.2; DB 7; Length 2919;
Best Local Similarity 86.4%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGAAAGGCCTTT 22
Db 2385 CACGGCGAACGCAAGGCCTTT 2364

RESULT 87
US-10-425-115-40860/c
; Sequence 40860, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
```

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; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 40860
; LENGTH: 3096
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_137265C.1
US-10-425-115-40860

Query Match          71.7%; Score 17.2; DB 9; Length 3096;
Best Local Similarity 86.4%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 AAGTCGAACGGAAGGCGCTTTC 23
    ||||| || ||||| |||||
Db  3089 AAGTCCAAGGAATGCGCTTTC 3068

RESULT 88
US-10-831-286A-12801
; Sequence 12801, Application US/10831286A
; Publication No. US20060046246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, QIANDONG
; APPLICANT: CHATELLIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001
; CURRENT APPLICATION NUMBER: US/10/831,286A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/464,955
; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12801
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Corynebacterium ulcerans
US-10-831-286A-12801

Query Match          70.8%; Score 17; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  3 AGTCGAACGGAAGGCC 19
    ||||| ||||| |||||
Db  4 AGTCGAACGGAAGGCC 20

RESULT 89
US-10-831-286A-23905
; Sequence 23905, Application US/10831286A
; Publication No. US20060046246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, QIANDONG
; APPLICANT: CHATELLIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001
; CURRENT APPLICATION NUMBER: US/10/831,286A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/464,955
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; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23905
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Corynebacterium ulcerans
US-10-831-286A-23905

Query Match          70.8%; Score 17; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  3 AGTCGAACGGAAGGCC 19
    ||||| ||||| |||||
Db  3 AGTCGAACGGAAGGCC 19

RESULT 90
US-10-956-157-105928
; Sequence 105928, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 105928
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-105928

Query Match          69.2%; Score 16.6; DB 10; Length 25;
Best Local Similarity 82.6%; Pred. No. 7.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  2 AAGTCGAACGGAAGGCGCTTTCG 24
    ||||| ||||| ||||| |||||
Db  1 AAGTCGAATCGAAAGGACTGTGCG 23

RESULT 91
US-10-956-157-105929
; Sequence 105929, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 105929
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-105929

Query Match          69.2%; Score 16.6; DB 10; Length 25;
Best Local Similarity 82.6%; Pred. No. 7.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  1 CAAGTCGAACGGAAGGCGCTTTC 23
    ||||| ||||| ||||| |||||
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Db      3 CAAGTCGAATTGAAAGGACTGTC 25

RESULT 92
; Sequence 738727, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 738727
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-738727

Query Match      69.2%; Score 16.6; DB 4; Length 552;
Best Local Similarity 82.6%; Pred. No. 8.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CAAGTCGAACGGAAGGCCTTTC 23
      ||||| ||| ||||| ||||| |||||
Db      487 CAAGCGGAATGGAAGGCATTTTC 465

RESULT 93
; Sequence 738727, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 738727
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-738727

Query Match      69.2%; Score 16.6; DB 4; Length 552;
Best Local Similarity 82.6%; Pred. No. 8.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 5; Gaps 0;

Qy      1 CAAGTCGAACGGAAGGCCTTTC 23
      ||||| ||| ||||| ||||| |||||
Db      487 CAAGCGGAATGGAAGGCATTTTC 465

RESULT 94
; Sequence 646509, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 646509
; LENGTH: 572
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-646509

Query Match      69.2%; Score 16.6; DB 4; Length 572;
Best Local Similarity 82.6%; Pred. No. 8.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CAAGTCGAACGGAAGGCCTTTC 23
      ||||| ||| ||||| ||||| |||||
Db      125 CAAGGCGCAAGAAAGGCCTTTC 103

RESULT 95
; Sequence 646509, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 646509
; LENGTH: 572
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-646509

Query Match      69.2%; Score 16.6; DB 5; Length 552;
Best Local Similarity 82.6%; Pred. No. 8.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Query Match      69.2%; Score 16.6; DB 5; Length 572;
Best Local Similarity 82.6%; Pred. No. 8.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CAAGTCGAACGGAAGGCGCTTTC 23
Db      125 CAAGGCCAAGAAAGGCGCTTTC 103

RESULT 96
US-10-972-079-55955/c
; Sequence 55955, Application US/10972079
; Publication No. US20050153317A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEER
; FILE REFERENCE: MM1110-2
; CURRENT APPLICATION NUMBER: US/10/972,079
; CURRENT FILING DATE: 2004-10-22
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 96631
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 55955
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Chicken 19866894310123_1
US-10-972-079-55955

Query Match      69.2%; Score 16.6; DB 10; Length 600;
Best Local Similarity 82.6%; Pred. No. 8.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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RESULT 97
US-10-972-079-55956/c
; Sequence 55956, Application US/10972079
; Publication No. US20050153317A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEER
; FILE REFERENCE: MM1110-2
; CURRENT APPLICATION NUMBER: US/10/972,079
; CURRENT FILING DATE: 2004-10-22
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 96631
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 55956
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Chicken 19866894310123_2
US-10-972-079-55956

Query Match      69.2%; Score 16.6; DB 10; Length 600;
Best Local Similarity 82.6%; Pred. No. 8.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Db      113 CAAGGGGACGGAAGGACTTTC 91
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RESULT 98
US-10-301-480-553054/c
; Sequence 553054, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 553054
; LENGTH: 999
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-553054
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Best Local Similarity 82.6%; Pred. No. 8.8e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Db      920 CAAGTCGAACAGAAAGGCGCTTCC 898
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RESULT 99
US-10-301-480-1166463/c
; Sequence 1166463, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1166463
; LENGTH: 999
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1166463
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Query Match      69.2%; Score 16.6; DB 12; Length 999;
Best Local Similarity 82.6%; Pred. No. 8.8e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Qy      1 CAAGTCGAACGGAAGGCGCTTTC 23
Db      920 CAAGTCGAACAGAAAGGCGCTTCC 898
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RESULT 100
US-10-282-122A-11374
; Sequence 11374, Application US/1028122A
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; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11374
; LENGTH: 1392
; TYPE: DNA
; ORGANISM: Burkholderia cepacia
; US-10-282-122A-11374

Query Match      69.2%; Score 16.6; DB 8; Length 1392;
Best Local Similarity 82.6%; Pred. No. 8.9e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db      869 AAGTCGAACGGAATCGCATTCG 891

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Job time : 974.747 secs
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 03:57:04 ; Search time 14.8916 Seconds
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Title: US-10-665-708-22

Perfect score: 24

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Searched: 224314 seqs, 35277956 residues

Total number of hits satisfying chosen parameters: 448628

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	16	66.7	2397	7	US-11-217-529-254 Sequence 254, App
4	15.2	63.3	1260	7	US-11-217-529-5375 Sequence 5375, App
5	15.2	63.3	11611	6	US-10-541-993-4 Sequence 4, Appli
6	15	62.5	1157	6	US-10-196-749-391 Sequence 391, App
7	15	62.5	1157	7	US-11-101-316-145 Sequence 145, App
8	15	62.5	2952	7	US-11-217-529-4946 Sequence 4946, App
9	14.8	61.7	497	6	US-10-488-619-2156 Sequence 2075, App
10	14.8	61.7	599	6	US-10-488-619-2156 Sequence 2156, App
11	14.8	61.7	784	6	US-10-488-619-2155 Sequence 2155, App
12	14.6	60.8	25	7	US-11-217-529-110320 Sequence 110320, A
13	14.6	60.8	471	7	US-11-217-529-77805 Sequence 77805, A
14	14.6	60.8	1350	7	US-11-217-529-730 Sequence 730, App
15	14.6	60.8	2541	7	US-11-217-529-514 Sequence 514, App
16	14.6	60.8	2883	7	US-11-217-529-82268 Sequence 82268, A
17	14.4	60.0	225	7	US-11-217-529-56270 Sequence 56270, A
18	14.4	60.0	750	7	US-11-217-529-4661 Sequence 4661, App
19	14.4	60.0	1600	7	US-11-324-517-36 Sequence 36, Appl
20	14.4	60.0	1872	7	US-11-217-529-3010 Sequence 3010, App
21	14.4	60.0	2013	7	US-11-217-529-75610 Sequence 75610, A
22	14.4	60.0	2376	7	US-11-217-529-3183 Sequence 3183, App
23	14.4	60.0	2454	7	US-11-217-529-6038 Sequence 6038, App
24	14.4	60.0	3663	7	US-11-217-529-1369 Sequence 1369, App
25	14.4	60.0	4365	7	US-11-217-529-4529 Sequence 4529, App

26	14.2	59.2	480	7	US-11-217-529-75552 Sequence 75552, A
27	14.2	59.2	858	7	US-11-217-529-1257 Sequence 1257, App
28	14.2	59.2	858	7	US-11-217-529-77141 Sequence 77141, A
29	14	58.3	25	7	US-11-217-529-60921 Sequence 60921, A
30	14	58.3	25	7	US-11-217-529-117575 Sequence 117575, A
31	14	58.3	25	7	US-11-217-529-152173 Sequence 152173, A
32	14	58.3	150	7	US-11-139-257-9 Sequence 9, Appli
33	14	58.3	210	7	US-11-139-257-12 Sequence 12, Appl
34	14	58.3	213	7	US-11-139-257-12 Sequence 12, Appl
35	14	58.3	363	7	US-11-217-529-81538 Sequence 81538, A
36	14	58.3	381	7	US-11-217-529-79564 Sequence 79564, A
37	14	58.3	438	7	US-11-217-529-78815 Sequence 78815, A
38	14	58.3	579	7	US-11-217-529-2487 Sequence 2487, App
39	14	58.3	666	7	US-11-217-529-81387 Sequence 81387, A
40	14	58.3	837	7	US-11-217-529-4416 Sequence 4416, App
41	14	58.3	1080	6	US-10-975-697-7 Sequence 7, Appli
42	14	58.3	1080	6	US-10-975-697-9 Sequence 9, Appli
43	14	58.3	1080	6	US-10-975-697-11 Sequence 11, Appl
44	14	58.3	1194	7	US-11-217-529-78457 Sequence 78457, A
45	14	58.3	1245	6	US-10-196-749-223 Sequence 223, App
46	14	58.3	1452	1	US-09-949-925-62 Sequence 62, Appl
47	14	58.3	1887	7	US-11-217-529-1925 Sequence 1925, App
48	14	58.3	1950	7	US-11-217-529-77876 Sequence 77876, A
49	14	58.3	2511	7	US-11-217-529-522 Sequence 522, App
50	14	58.3	2700	7	US-11-217-529-75493 Sequence 75493, A
51	14	58.3	2706	7	US-11-217-529-3368 Sequence 3368, App
52	14	58.3	2787	7	US-11-217-529-76324 Sequence 76324, A
53	14	58.3	3093	7	US-11-217-529-3215 Sequence 3215, App
54	14	58.3	4806	7	US-11-217-529-82660 Sequence 82660, A
55	14	58.3	6805	6	US-10-520-210-29 Sequence 29, Appl
56	14	58.3	7330	6	US-10-520-210-31 Sequence 31, Appl
57	14	58.3	7701	6	US-10-520-210-25 Sequence 25, Appl
58	14	58.3	7926	6	US-10-520-210-24 Sequence 24, Appl
59	14	58.3	151830	6	US-10-519-335-37 Sequence 37, Appl
60	14	58.3	394191	6	US-10-506-549-3 Sequence 3, Appli
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62	13.8	57.5	1380	7	US-11-217-529-79704 Sequence 79704, A
63	13.8	57.5	1931	1	US-09-949-925-78 Sequence 78, Appl
64	13.8	57.5	1932	1	US-09-949-925-11 Sequence 12, Appl
65	13.6	56.7	25	7	US-11-217-529-98883 Sequence 98883, A
66	13.6	56.7	25	7	US-11-217-529-130040 Sequence 130040, A
67	13.6	56.7	25	7	US-11-217-529-188129 Sequence 2026, App
68	13.6	56.7	523	6	US-10-488-619-2026 Sequence 4440, App
69	13.6	56.7	903	7	US-11-217-529-4440 Sequence 107, App
70	13.6	56.7	927	6	US-10-473-173-107 Sequence 174359, A
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72	13.6	56.7	1224	7	US-11-217-529-3863 Sequence 3863, App
73	13.6	56.7	1242	7	US-11-217-529-78935 Sequence 78935, A
74	13.6	56.7	1479	7	US-11-217-529-76764 Sequence 76764, A
75	13.6	56.7	1667	6	US-10-505-928-419 Sequence 419, App
76	13.6	56.7	1797	7	US-11-217-529-82107 Sequence 82107, A
77	13.6	56.7	2040	7	US-11-217-529-5081 Sequence 5081, App
78	13.6	56.7	2436	7	US-11-217-529-82283 Sequence 82283, A
79	13.6	56.7	2595	7	US-11-217-529-76785 Sequence 76785, A
80	13.4	55.8	25	7	US-11-217-529-32547 Sequence 32547, A
81	13.4	55.8	25	7	US-11-217-529-94649 Sequence 94649, A
82	13.4	55.8	393	7	US-11-217-529-166591 Sequence 166591, A
83	13.4	55.8	487	6	US-10-488-619-2473 Sequence 2473, App
84	13.4	55.8	510	6	US-10-488-619-2473 Sequence 2473, App
85	13.4	55.8	562	6	US-10-488-619-2770 Sequence 2770, App
86	13.4	55.8	624	7	US-11-301-554-1914 Sequence 1914, App
87	13.4	55.8	636	7	US-11-301-554-1668 Sequence 1668, App
88	13.4	55.8	696	7	US-11-217-529-79746 Sequence 79746, A
89	13.4	55.8	762	7	US-11-217-529-5130 Sequence 5130, App
90	13.4	55.8	814	6	US-10-525-126-124 Sequence 124, App
91	13.4	55.8	918	7	US-11-217-529-5478 Sequence 5478, App
92	13.4	55.8	990	7	US-11-217-529-191032 Sequence 191032, A
93	13.4	55.8	1107	7	US-11-217-529-1564 Sequence 1564, App
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c 100	13.4	55.8	1716	7	US-11-217-529-2406	Sequence 2406, Ap	c 173	13	54.2	2283	7	US-11-217-529-3378	Sequence 3378, Ap
c 101	13.4	55.8	1869	7	US-11-217-529-78128	Sequence 78128, A	c 174	13	54.2	2397	6	US-10-196-749-29	Sequence 29, Appl
c 102	13.4	55.8	1893	7	US-11-217-529-625	Sequence 625, App	c 175	13	54.2	2487	7	US-11-217-529-77452	Sequence 77452, A
c 103	13.4	55.8	1893	7	US-11-217-529-1992	Sequence 1992, Ap	c 176	13	54.2	2853	7	US-11-217-529-76130	Sequence 76130, A
c 104	13.4	55.8	1983	7	US-11-217-529-82221	Sequence 82221, A	c 177	13	54.2	3309	7	US-11-217-529-1900	Sequence 1900, Ap
c 105	13.4	55.8	2175	7	US-11-217-529-500	Sequence 500, App	c 178	13	54.2	3399	7	US-11-217-529-73	Sequence 73, Appl
c 106	13.4	55.8	2269	6	US-10-505-928-303	Sequence 303, App	c 179	13	54.2	3403	7	US-11-145-2078-74	Sequence 74, Appl
c 107	13.4	55.8	2286	7	US-11-217-529-728	Sequence 728, App	c 180	13	54.2	3450	7	US-11-217-529-977	Sequence 977, App
c 108	13.4	55.8	2435	6	US-10-946-650-35	Sequence 35, Appl	c 181	13	54.2	3669	7	US-11-181-115-36	Sequence 36, Appl
c 109	13.4	55.8	2454	7	US-11-217-529-76817	Sequence 76817, A	c 182	13	54.2	4005	7	US-11-217-529-3980	Sequence 3980, Ap
c 110	13.4	55.8	2535	7	US-11-217-529-1209	Sequence 1209, Ap	c 183	13	54.2	4308	7	US-11-217-529-82409	Sequence 82409, A
c 111	13.4	55.8	2556	7	US-11-217-529-76405	Sequence 76405, A	c 184	13	54.2	4654	6	US-10-505-928-20	Sequence 20, Appl
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c 113	13.4	55.8	3354	7	US-11-217-529-75390	Sequence 75390, A	c 186	13	54.2	6557	6	US-10-511-937-388	Sequence 388, App
c 114	13.4	55.8	3903	7	US-11-217-529-2311	Sequence 2311, Ap	c 187	13	54.2	7131	7	US-11-217-529-77074	Sequence 77074, A
c 115	13.4	55.8	4806	7	US-11-217-529-82660	Sequence 82660, A	c 188	13	54.2	8178	6	US-10-473-173-52	Sequence 52, Appl
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c 117	13.4	55.8	138941	6	US-10-489-730-10	GENERAL INFORMATI	c 190	13	54.2	8687	7	US-11-297-317-16	Sequence 16, Appl
c 118	13.2	55.0	492	7	US-11-217-529-173378	Sequence 173378, Ap	c 191	13	54.2	9362	7	US-11-297-317-18	Sequence 18, Appl
c 119	13.2	55.0	806	6	US-10-488-619-2939	Sequence 2939, Ap	c 192	13	54.2	9400	7	US-11-297-317-17	Sequence 17, Appl
c 120	13.2	55.0	1242	7	US-11-217-529-75628	Sequence 75628, A	c 193	13	54.2	11611	6	US-10-541-993-4	Sequence 4, Appli
c 121	13.2	55.0	1377	7	US-11-217-529-4877	Sequence 4877, Ap	c 194	13	54.2	12918	6	US-10-501-834-4	Sequence 32, Appl
c 122	13.2	55.0	1443	7	US-11-217-529-2620	Sequence 2620, Ap	c 195	13	54.2	37426	6	US-10-473-173-32	Sequence 107378,
c 123	13.2	55.0	1446	7	US-11-264-784-35	Sequence 35, Appl	c 196	13	54.2	37426	6	US-11-217-529-107378	Sequence 115745,
c 124	13.2	55.0	1611	7	US-11-312-529-3860	Sequence 3860, Ap	c 197	13	54.2	37426	6	US-11-217-529-15745	Sequence 152423,
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c 127	13.2	55.0	2545	7	US-11-301-554-1900	Sequence 1900, Ap	c 200	13	54.2	37426	6	US-10-488-619-2110	Sequence 2110, Ap
c 128	13.2	55.0	2850	7	US-11-217-529-79139	Sequence 79139, A	c 201	13	54.2	37426	6	US-10-488-619-1455	Sequence 1455, Ap
c 129	13.2	55.0	3267	7	US-11-217-529-78066	Sequence 78066, A	c 202	13	54.2	37426	6	US-10-488-619-1979	Sequence 1979, Ap
c 130	13.2	55.0	3330	7	US-11-217-529-3415	Sequence 3415, Ap	c 203	13	54.2	37426	6	US-10-488-619-1859	Sequence 1859, Ap
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c 151	13	54.2	1173	7	US-11-217-529-77948	Sequence 77948, A	c 224	13	54.2	37426	6	US-10-196-749-147	Sequence 147, App
c 152	13	54.2	1203	7	US-11-217-529-998	Sequence 998, App	c 225	13	54.2	37426	6	US-11-101-316-31	Sequence 31, Appl
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c 285 12.6 52.5 1413 7 US-11-217-529-5563 Sequence 5563, App
c 286 12.6 52.5 1467 7 US-11-217-529-398 Sequence 398, App
c 287 12.6 52.5 1614 7 US-11-217-529-6108 Sequence 6108, App
c 288 12.6 52.5 1653 6 US-10-505-928-587 Sequence 587, App
c 289 12.6 52.5 1716 7 US-11-226-605-42 Sequence 42, Appl
c 290 12.6 52.5 1716 7 US-11-217-529-78630 Sequence 78630, A
c 291 12.6 52.5 1790 7 US-11-242-505A-1 Sequence 1, Appli
c 292 12.6 52.5 1833 7 US-11-217-529-4667 Sequence 4667, App
c 293 12.6 52.5 1854 7 US-11-217-529-1678 Sequence 1678, App
c 294 12.6 52.5 1947 7 US-11-217-529-4699 Sequence 4699, App
c 295 12.6 52.5 2007 7 US-11-217-529-81504 Sequence 81504, A
c 296 12.6 52.5 2043 7 US-11-217-529-2687 Sequence 2687, App
c 297 12.6 52.5 2180 6 US-10-981-760-1 Sequence 1, Appli
c 298 12.6 52.5 2200 6 US-10-981-760-3 Sequence 3, Appli
c 299 12.6 52.5 2225 6 US-10-505-928-24 Sequence 24, Appl
c 300 12.6 52.5 2341 6 US-10-511-937-349 Sequence 349, App

ALIGNMENTS

RESULT 1
US-11-217-529-80747
; Sequence 80747, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

Query Match 66.7%; Score 16; DB 7; Length 1824;
Best Local Similarity 79.2%; Pred. No. 9.1;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCTTTTCG 24
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Db 265 CAATTCCAACTGAATGGCTTTTCG 288

RESULT 2
US-11-217-529-79690/c
; Sequence 79690, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

Query Match 66.7%; Score 16; DB 7; Length 1824;
Best Local Similarity 79.2%; Pred. No. 9.1;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCTTTTCG 24
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Db 752 CAATTCGACGGAATGACTTACG 729

RESULT 3
US-11-217-529-254
; Sequence 254, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

Query Match 66.7%; Score 16; DB 7; Length 1824;
Best Local Similarity 79.2%; Pred. No. 9.1;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCTTTTCG 24
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Db 752 CAATTCGACGGAATGACTTACG 729
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; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 254
; LENGTH: 2397
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-254

Query Match 66.7%; Score 16; DB 7; Length 2397;
Best Local Similarity 79.2%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTTG 24
Db 397 CACGTCGAGCGGAATGCTATTG 420

RESULT 4
US-11-217-529-5375/c
; Sequence 5375, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5375
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5375

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Best Local Similarity 85.0%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 5
US-10-541-993-4
; Sequence 4, Application US/10541993
; Publication No. US20060099670A1
; GENERAL INFORMATION:
; APPLICANT: Matuschek, Markus
; APPLICANT: Heinkeamp, Thorsten
; APPLICANT: Schmidt, Andre
; APPLICANT: Brakhage, Axel
; TITLE OF INVENTION: Method for the genetic modification of organisms of the genus
; FILE REFERENCE: 13311-00010-US
; CURRENT APPLICATION NUMBER: US/10/541,993
; CURRENT FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: PCT/EP2004/000100
; PRIOR FILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: DE 103 00 649.4
; PRIOR FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: DE 103 41 272.7
; PRIOR FILING DATE: 2003-09-08
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 4
; LENGTH: 11611
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; OTHER INFORMATION: Vector
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (227)..(227)
; OTHER INFORMATION: n is a, c, g, or t
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; NAME/KEY: misc feature
; LOCATION: (318)..(318)
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; OTHER INFORMATION: n is a, c, g, or t
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; NAME/KEY: misc feature
; LOCATION: (10028)..(10028)
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US-10-541-993-4

Query Match 63.3%; Score 15.2; DB 6; Length 11611;
Best Local Similarity 85.0%; Pred. No. 30;
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RESULT 6
US-10-196-749-391
; Sequence 391, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540

; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 391
; LENGTH: 1157
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-749-391

Query Match 62.5%; Score 15; DB 6; Length 1157;
Best Local Similarity 78.3%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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RESULT 7
US-11-101-316-145
; Sequence 145, Application US/11101316
; Publication No. US20060099657A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
; FILE REFERENCE: P3230R1C17C1
; CURRENT APPLICATION NUMBER: US/11/101,316
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: 10/063526
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCR/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCR/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 145
; LENGTH: 1157
; TYPE: DNA
; ORGANISM: Homo Sapien
US-11-101-316-145

Query Match 62.5%; Score 15; DB 7; Length 1157;
Best Local Similarity 78.3%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTC 23
||||| ||||| ||||| ||||| |||||
Db 155 CAAGTGAACGGAAGGCGCCTGC 177

RESULT 8
US-11-217-529-4946/c
; Sequence 4946, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA

; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4946
; LENGTH: 2952
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4946

Query Match 62.5%; Score 15; DB 7; Length 2952;
Best Local Similarity 78.3%; Pred. No. 31;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCGCTTTCG 24
||||| ||||| ||||| ||||| |||||
Db 2664 AATTCGATCTGGAAGGCGCCTTCG 2642

RESULT 9
US-10-488-619-2075
; Sequence 2075, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2075
; LENGTH: 497
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2075

Query Match 61.7%; Score 14.8; DB 6; Length 497;
Best Local Similarity 88.9%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGC 18
||||| ||||| ||||| |||||
Db 69 CCAGTCGCACGGAAGGC 86

RESULT 10
US-10-488-619-2156
; Sequence 2156, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2156
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2156


```
Query Match      61.7%; Score 14.8; DB 6; Length 599;
Best Local Similarity 88.9%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGC 18
Db 537 CCAAGTCGCACGGAAGGC 554

RESULT 11
US-10-488-619-2155/c
; Sequence 2155, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2155
; LENGTH: 784
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2155

Query Match      61.7%; Score 14.8; DB 6; Length 784;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGC 18
Db 397 CCAAGTCGCACGGAAGGC 380

RESULT 12
US-11-217-529-110320
; Sequence 110320, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 110320
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-110320

Query Match      60.8%; Score 14.6; DB 7; Length 25;
Best Local Similarity 81.0%; Pred. No. 25;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GTCGAACGGAAGGCCTTTCG 24
Db 5 GTCCACGGAAGAACCGCGTCG 25

RESULT 13
US-11-217-529-77805
; Sequence 77805, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77805
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77805

Query Match      60.8%; Score 14.6; DB 7; Length 471;
Best Local Similarity 81.0%; Pred. No. 38;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GTCGAACGGAAGGCCTTTCG 24
Db 152 GTCCACGGAAGAACCGCGTCG 172

RESULT 14
US-11-217-529-730
; Sequence 730, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 730
; LENGTH: 1350
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-730

Query Match      60.8%; Score 14.6; DB 7; Length 1350;
Best Local Similarity 81.0%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
Db 1128 CAAGTCCTAACGACAAAGTCCTT 1148

RESULT 15
US-11-217-529-514/c
; Sequence 514, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
```

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; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 514
; LENGTH: 2541
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-514

Query Match          60.8%; Score 14.6; DB 7; Length 2541;
Best Local Similarity 81.0%; Pred. No. 48;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCTTT 22
    ||||| ||||| ||||| ||||| |||||
Db 2480 AAGTCAATGTAATGGCCTTT 2460

RESULT 16
US-11-217-529-82268/c
; Sequence 82268, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82268
; LENGTH: 2883
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82268

Query Match          60.8%; Score 14.6; DB 7; Length 2883;
Best Local Similarity 81.0%; Pred. No. 49;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCTTT 22
    ||||| ||||| ||||| ||||| |||||
Db 2230 AAGTAGAAGGAACGCGCTTT 2210

RESULT 17
US-11-217-529-56270/c
; Sequence 56270, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
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; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 56270
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-56270

Query Match          60.0%; Score 14.4; DB 7; Length 25;
Best Local Similarity 93.8%; Pred. No. 32;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGG 17
    ||||| ||||| ||||| |||||
Db 18 AAGTCGAATGGAAGG 3

RESULT 18
US-11-217-529-4661
; Sequence 4661, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4661
; LENGTH: 750
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4661

Query Match          60.0%; Score 14.4; DB 7; Length 750;
Best Local Similarity 75.0%; Pred. No. 51;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTCG 24
    ||||| ||||| ||||| ||||| |||||
Db 297 CAAGTCGATGAAGGCCGTTAG 320

RESULT 19
US-11-324-517-36
; Sequence 36, Application US/11324517
; Publication No. US20060099221A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, MARY
; APPLICANT: GICQUEL, BRIGITTE
; TITLE OF INVENTION: METHOD OF SCREENING ANTI-MYCObACTERIAL MOLECULES
; FILE REFERENCE: 03495.0182-01
; CURRENT APPLICATION NUMBER: US/11/324,517
; CURRENT FILING DATE: 2006-01-04
; PRIOR APPLICATION NUMBER: US/10/914,165
; PRIOR FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: US/10/383,675
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 09/429,370
; PRIOR FILING DATE: 1999-10-28
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; PRIOR APPLICATION NUMBER: 60/113,375
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/111,813
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 09/181,934
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 1600
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (549)..(1562)
US-11-324-517-36

Query Match          60.0%; Score 14.4; DB 7; Length 1600;
Best Local Similarity 75.0%; Pred. No. 57;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTTCG 24
Db 1476 CAAGTCGACCGGAAGCGCGTACG 1499

RESULT 20
US-11-217-529-3010/c
; Sequence 3010, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3010
; LENGTH: 1872
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3010

Query Match          60.0%; Score 14.4; DB 7; Length 1872;
Best Local Similarity 75.0%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTTCG 24
Db 163 CGATTGCTATGGAATGCTTTTG 140

RESULT 21
US-11-217-529-75610/c
; Sequence 75610, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
```

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; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75610
; LENGTH: 2013
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75610

Query Match          60.0%; Score 14.4; DB 7; Length 2013;
Best Local Similarity 75.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTTCG 24
Db 527 CAATTCATCTGAAAGTCCCTTTTG 504

RESULT 22
US-11-217-529-3183
; Sequence 3183, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3183
; LENGTH: 2376
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3183

Query Match          60.0%; Score 14.4; DB 7; Length 2376;
Best Local Similarity 75.0%; Pred. No. 60;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTTCG 24
Db 1306 CAAGTCGAAGCTAACGGGATTTTCG 1329

RESULT 23
US-11-217-529-6038
; Sequence 6038, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
```

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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6038
; LENGTH: 2454
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (2284)..(2317)
; OTHER INFORMATION: a, c, g, t, unknown, or other
US-11-217-529-6038

Query Match          60.0%; Score 14.4; DB 7; Length 2454;
Best Local Similarity 93.8%; Pred. No. 61;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8 AACGGAAGGCTTTC 23
Db      1022 AATGGAAGGCTTTC 1037

RESULT 24
US-11-217-529-1369/c
; Sequence 1369, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1369
; LENGTH: 3663
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1369

Query Match          60.0%; Score 14.4; DB 7; Length 3663;
Best Local Similarity 75.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      1 CAAGTCGAACGGAAGGCTTTCG 24
Db      348 CAAATCTAACGTAAGGCTTCTG 325

RESULT 25
US-11-217-529-4529/c
; Sequence 4529, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1369
; LENGTH: 3663
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1369
```

```
; SEQ ID NO 4529
; LENGTH: 4365
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4529

Query Match          60.0%; Score 14.4; DB 7; Length 4365;
Best Local Similarity 93.8%; Pred. No. 66;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGG 17
Db      4147 AAGTCGAATCGAAGG 4132

RESULT 26
US-11-217-529-75552
; Sequence 75552, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75552
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75552

Query Match          59.2%; Score 14.2; DB 7; Length 480;
Best Local Similarity 84.2%; Pred. No. 61;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGGCTT 20
Db      212 AAGACGAATCGAGAGGCT 230

RESULT 27
US-11-217-529-1257/c
; Sequence 1257, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1257
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1257
```

```
Query Match          59.2%; Score 14.2; DB 7; Length 858;
Best Local Similarity 84.2%; Pred. NO. 66;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

Qy 5 TCGAACGGAAGGCCTTC 23
Db 187 TCGAAGAGAAAGGCCTTC 169

```

RESULT 28
US-11-217-529-77141/c
; Sequence 77141, Application US/11217529
; Publication No. US2006099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77141
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77141

```

```
Query Match          59.2%; Score 14.2; DB 7; Length 858;
Best Local Similarity 84.2%; Pred. No. 66;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```

RESULT 29
US-11-217-529-60921/c
; Sequence 60921, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIRO
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 60921
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-60921

```

Query Match 58.3%; Score 14; DB 7; Length 25;
Best Local Similarity 77.3%; Pred. No. 51;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

<i>Qy</i>	2	AAGTCGAACGGAAAGGCCTTTC	23
<i>D_b</i>	22	AATTCGATCTGGAAGGCCCTTC	1

```

RESULT 30
US-11-217-529-117575/c
; Sequence 117575, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIRO
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/9332,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 117575
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-117575

```

Query Match	58.3%	Score 14;	DB 7;	Length 25;
Best Local Similarity	77.3%	Pred. No. 51;		
Matches 17;	Conservative	0;	Mismatches	
		5;	Indels	
		0;	Gaps	

RESULT 31
US-11-217-529-152173
; Sequence 152173, Application US/11217529
; Publication No. US2006099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 152173
; LENGTH: 25
; TYPE: DNA
; ORGANISM: *Saccharomyces pastorianus*
US-11-217-529-152173

Query Match	58.3%	Score 14;	DB 7;	Length 25;
Best Local Similarity	77.3%	Pred. No. 51;		
Matches 17;	Conservative	0;	Mismatches	5;
			Indels	0;
			Gaps	0;

```
RESULT 32
US-11-139-257-9
; Sequence 9, Application US/11139257
; Publication No. US2006008849A1
; GENERAL INFORMATION:
; APPLICANT: Happe, Scott
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis of Group B
; FILE OF INVENTION: Streptococcus Infection
; FILE REFERENCE: 25436/2512
; CURRENT APPLICATION NUMBER: US/11/139,257
; PRIOR FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: US 60/575,124
; PRIOR FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 150
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-139-257-9

Query Match      58.3%; Score 14; DB 7; Length 150;
Best Local Similarity 77.3%; Pred. No. 65;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1  CAAGTCGAACGGAAGGCGCTTT 22
Db     10  CATGACAAACGGCAAGGCTTT 31

RESULT 33
US-11-139-257-14
; Sequence 14, Application US/11139257
; Publication No. US2006008849A1
; GENERAL INFORMATION:
; APPLICANT: Happe, Scott
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis of Group B
; FILE OF INVENTION: Streptococcus Infection
; FILE REFERENCE: 25436/2512
; CURRENT APPLICATION NUMBER: US/11/139,257
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: US 60/575,124
; PRIOR FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 210
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Positive internal control
US-11-139-257-14

Query Match      58.3%; Score 14; DB 7; Length 210;
Best Local Similarity 77.3%; Pred. No. 69;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1  CAAGTCGAACGGAAGGCGCTTT 22
Db     40  CATGACAAACGGCAAGGCTTT 61

RESULT 34
US-11-139-257-12
; Sequence 12, Application US/11139257
; Publication No. US2006008849A1
; GENERAL INFORMATION:
; APPLICANT: Happe, Scott
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis of Group B
; FILE OF INVENTION: Streptococcus Infection
; FILE REFERENCE: 25436/2512
; CURRENT APPLICATION NUMBER: US/11/139,257
; CURRENT FILING DATE: 2005-05-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 213
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Control Sequence
US-11-139-257-12

Query Match      58.3%; Score 14; DB 7; Length 213;
Best Local Similarity 77.3%; Pred. No. 69;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1  CAAGTCGAACGGAAGGCGCTTT 22
Db     41  CATGACAAACGGCAAGGCTTT 62

RESULT 35
US-11-217-529-81538
; Sequence 81538, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81538
; LENGTH: 363
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-81538

Query Match      58.3%; Score 14; DB 7; Length 363;
Best Local Similarity 77.3%; Pred. No. 74;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1  CAAGTCGAACGGAAGGCGCTTT 22
Db     90  CAAGTTCTTCGAAAGGCGCTT 111

RESULT 36
US-11-217-529-79564/c
; Sequence 79564, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; NUMBER OF SEQ ID NOS: 197023
```

```
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79564
; LENGTH: 381
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79564

Query Match      58.3%; Score 14; DB 7; Length 381;
Best Local Similarity 77.3%; Pred. No. 74;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCGCTTT 22
Db 108 CAAGTCGATCGGAAGTACTCT 87

RESULT 37
US-11-217-529-78815
; Sequence 78815, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78815
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78815

Query Match      58.3%; Score 14; DB 7; Length 438;
Best Local Similarity 77.3%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AAGTCGAACGGAAGGCGCTTTC 23
Db 1 ATGTCGAAGGAAGGTTTTC 22

RESULT 38
US-11-217-529-2487
; Sequence 2487, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2487
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus

US-11-217-529-2487

Query Match      58.3%; Score 14; DB 7; Length 579;
Best Local Similarity 77.3%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCGCTTT 22
Db 86 CAATTCCACTAAAGGACTTT 107

RESULT 39
US-11-217-529-81387
; Sequence 81387, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81387
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-81387

Query Match      58.3%; Score 14; DB 7; Length 666;
Best Local Similarity 77.3%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AAGTCGAACGGAAGGCGCTTTC 23
Db 374 AAGTGAATGGAAGGCTCTCC 395

RESULT 40
US-11-217-529-4416
; Sequence 4416, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4416
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4416

Query Match      58.3%; Score 14; DB 7; Length 837;
Best Local Similarity 77.3%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 2 AAGTCGAACGGAAGCCCTTTC 23
||||| ||||| ||||| |||||
Db 176 AAGTCAAAAGGAATGTCATTTC 197

RESULT 41
US-10-975-697-7
; Sequence 7, Application US/10975697
; Publication No. US20060094099A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: Inactivated Enzyme Variants And Associated Process and Reagent
; FILE REFERENCE: 5727-76273
; CURRENT APPLICATION NUMBER: US/10/975,697
; CURRENT FILING DATE: 2004-10-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GlucDH variant RC-21
US-10-975-697-7

Query Match 58.3%; Score 14; DB 6; Length 1080;
Best Local Similarity 77.3%; Pred. No. 86;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 AGTCGAACGGAAGCCCTTTCG 24
||||| ||||| ||||| |||||
Db 1014 AGTCGAAGACTGGGCGCTTTCG 1035

RESULT 42
US-10-975-697-9
; Sequence 9, Application US/10975697
; Publication No. US20060094099A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: Inactivated Enzyme Variants And Associated Process and Reagent
; FILE REFERENCE: 5727-76273
; CURRENT APPLICATION NUMBER: US/10/975,697
; CURRENT FILING DATE: 2004-10-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GlucDH variant RC-28
US-10-975-697-9

Query Match 58.3%; Score 14; DB 6; Length 1080;
Best Local Similarity 77.3%; Pred. No. 86;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 AGTCGAACGGAAGCCCTTTCG 24
||||| ||||| ||||| |||||
Db 1014 AGTCGAAGACTGGGCGCTTTCG 1035

RESULT 43
US-10-975-697-11
; Sequence 11, Application US/10975697
; Publication No. US20060094099A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: Inactivated Enzyme Variants And Associated Process and Reagent
```

```
; TITLE OF INVENTION: System
; FILE REFERENCE: 5727-76273
; CURRENT APPLICATION NUMBER: US/10/975,697
; CURRENT FILING DATE: 2004-10-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GlucDH Variant RC-35
US-10-975-697-11

Query Match 58.3%; Score 14; DB 6; Length 1080;
Best Local Similarity 77.3%; Pred. No. 86;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 AGTCGAACGGAAGCCCTTTCG 24
||||| ||||| ||||| |||||
Db 1014 AGTCGAAGACTGGGCGCTTTCG 1035

RESULT 44
US-11-217-529-78457/c
; Sequence 78457, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIRO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78457
; LENGTH: 1194
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78457

Query Match 58.3%; Score 14; DB 7; Length 1194;
Best Local Similarity 77.3%; Pred. No. 87;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGCCCTTTC 22
||||| ||||| ||||| |||||
Db 980 CAGTCGAAGGGTAATGACTTT 959

RESULT 45
US-10-196-749-223/c
; Sequence 223, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
```



```
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 223
; LENGTH: 1245
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-749-223

Query Match      58.3%; Score 14; DB 6; Length 1245;
Best Local Similarity 77.3%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 AAGTCGAACGGAAGGCGCTTTC 23
      ||| ||| ||| ||| ||| ||| |||
Db      807 AAGGCGCCGGAAGGCGGTGC 786

RESULT 46
US-09-949-925-62/c
; Sequence 62, Application US/09949925
; Publication No. US20060099575A9
; GENERAL INFORMATION:
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P203P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus

Query Match      58.3%; Score 14; DB 6; Length 1245;
Best Local Similarity 77.3%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 AAGTCGAACGGAAGGCGCTTTC 23
      ||| ||| ||| ||| ||| ||| |||
Db      807 AAGGCGCCGGAAGGCGGTGC 786

RESULT 47
US-11-217-529-1925/c
; Sequence 1925, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1925
; LENGTH: 1887
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1925

Query Match      58.3%; Score 14; DB 7; Length 1887;
Best Local Similarity 77.3%; Pred. No. 93;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 AAGTCGAACGGAAGGCGCTTTC 23
      ||| ||| ||| ||| ||| ||| |||
Db      971 AAGTCTAACGGTAATACCTTGC 950

RESULT 48
US-11-217-529-77876
; Sequence 77876, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77876
; LENGTH: 1950
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
```

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-949-925-62

Query Match      58.3%; Score 14; DB 1; Length 1452;
Best Local Similarity 77.3%; Pred. No. 90;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 AAGTCGAACGGAAGGCGCTTTC 23
      ||| ||| ||| ||| ||| ||| |||
Db      947 AAGTATAAGGTAAGGCGCTTGC 926

RESULT 47
US-11-217-529-1925/c
; Sequence 1925, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1925
; LENGTH: 1887
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1925

Query Match      58.3%; Score 14; DB 7; Length 1887;
Best Local Similarity 77.3%; Pred. No. 93;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 AAGTCGAACGGAAGGCGCTTTC 23
      ||| ||| ||| ||| ||| ||| |||
Db      971 AAGTCTAACGGTAATACCTTGC 950

RESULT 48
US-11-217-529-77876
; Sequence 77876, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77876
; LENGTH: 1950
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
```



```
RESULT 53
US-11-217-529-3215/c
; Sequence 3215, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3215
; LENGTH: 3093
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3215

Query Match      58.3%; Score 14; DB 7; Length 3093;
Best Local Similarity 77.3%; Pred. No. 1.e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1  CAAGTCGAACGGAAGGCGCTTT 22
Db      1579 CAAGTTGATAGAAAGGCGTTT 1558

RESULT 54
US-11-217-529-82660/c
; Sequence 82660, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82660
; LENGTH: 4806
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82660

Query Match      58.3%; Score 14; DB 7; Length 4806;
Best Local Similarity 77.3%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2  AAGTCGAACGGAAGGCGCTTTC 23
Db      836 AATTCAAACGGAATAGGCTTTC 815

RESULT 55
US-10-520-210-29/c
; Sequence 29, Application US/10520210
; Publication No. US20060099692A1
; GENERAL INFORMATION:
; APPLICANT: YOCUM, R. ROGERS
; APPLICANT: PATTERSON, THOMAS A.
; APPLICANT: PERO, JANICE G.
; APPLICANT: HERMANN, THERON
; TITLE OF INVENTION: MICROORGANISMS AND PROCESSES FOR ENHANCED PRODUCTION OF
; FILE REFERENCE: BGI-154US
; CURRENT APPLICATION NUMBER: US/10/520,210
; CURRENT FILING DATE: 2005-01-03
; PRIOR APPLICATION NUMBER: PCT/US2003/021336
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 6805
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-10-520-210-29

Query Match      58.3%; Score 14; DB 6; Length 7330;
Best Local Similarity 77.3%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      3  AGTCGAACGGAAGGCGCTTTCG 24
Db      1258 AGTCGAAGAGACTGGGCGCTTTCG 1237

RESULT 56
US-10-520-210-31/c
; Sequence 31, Application US/10520210
; Publication No. US20060099692A1
; GENERAL INFORMATION:
; APPLICANT: YOCUM, R. ROGERS
; APPLICANT: PATTERSON, THOMAS A.
; APPLICANT: PERO, JANICE G.
; APPLICANT: HERMANN, THERON
; TITLE OF INVENTION: MICROORGANISMS AND PROCESSES FOR ENHANCED PRODUCTION OF
; FILE REFERENCE: BGI-154US
; CURRENT APPLICATION NUMBER: US/10/520,210
; CURRENT FILING DATE: 2005-01-03
; PRIOR APPLICATION NUMBER: PCT/US2003/021336
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 7330
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-10-520-210-31

Query Match      58.3%; Score 14; DB 6; Length 7330;
Best Local Similarity 77.3%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      3  AGTCGAACGGAAGGCGCTTTCG 24
Db      1258 AGTCGAAGAGACTGGGCGCTTTCG 1237

RESULT 57
US-10-520-210-25/c
; Sequence 25, Application US/10520210
; Publication No. US20060099692A1
; GENERAL INFORMATION:
; APPLICANT: YOCUM, R. ROGERS
; APPLICANT: PATTERSON, THOMAS A.
```

```
; APPLICANT: Pero, Janice G.
; APPLICANT: Hermann, Theron
; TITLE OF INVENTION: MICROORGANISMS AND PROCESSES FOR ENHANCED PRODUCTION OF
; TITLE OF INVENTION: PANTOTHENATE
; FILE REFERENCE: BGI-154US
; CURRENT APPLICATION NUMBER: US/10/520,210
; CURRENT FILING DATE: 2005-01-03
; PRIOR APPLICATION NUMBER: PCT/US2003/021336
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 7701
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:glya overexpression
;
US-10-520-210-25

Query Match      58.3%; Score 14; DB 6; Length 7701;
Best Local Similarity 77.3%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      3 AGTCGAACGGAAGGCCTTCG 24
Db      1263 AGTCGAAGACTGGGCTTCG 1242

RESULT 58
US-10-520-210-24/c
; Sequence 24, Application US/10520210
; Publication No. US20060099692A1
; GENERAL INFORMATION:
; APPLICANT: Yocum, R. Rogers
; APPLICANT: Patterson, Thomas A.
; APPLICANT: Pero, Janice G.
; APPLICANT: Hermann, Theron
; TITLE OF INVENTION: MICROORGANISMS AND PROCESSES FOR ENHANCED PRODUCTION OF
; TITLE OF INVENTION: PANTOTHENATE
; FILE REFERENCE: BGI-154US
; CURRENT APPLICATION NUMBER: US/10/520,210
; CURRENT FILING DATE: 2005-01-03
; PRIOR APPLICATION NUMBER: PCT/US2003/021336
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 7926
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:serA overexpression
;
US-10-520-210-24

Query Match      58.3%; Score 14; DB 6; Length 7926;
Best Local Similarity 77.3%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      3 AGTCGAACGGAAGGCCTTCG 24
Db      1263 AGTCGAAGACTGGGCTTCG 1242

RESULT 59
US-10-519-335-37/c
; Sequence 37, Application US/10519335
; Publication No. US20060099210A1
; GENERAL INFORMATION:
; APPLICANT: Cavarec, Laurent
```

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; APPLICANT: Chumakov, Ilya
; APPLICANT: Destenaves, Benoit
; APPLICANT: Gonthier, Catherine
; APPLICANT: Elias, Isabelle
; TITLE OF INVENTION: NOVEL KCNQ POLYPEPTIDES, MODULATORS THEREOF, AND THEIR USES IN TH
; TITLE OF INVENTION: TREATMENT OF MENTAL DISORDERS
; FILE REFERENCE: G-194US03PCT
; CURRENT APPLICATION NUMBER: US/10/519,335
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 60/391,359
; PRIOR FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 151830
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (60402)..(60402)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (61110)..(61110)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (98207)..(98207)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (98208)..(98208)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (98209)..(98209)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (98210)..(98210)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (98211)..(98211)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (99743)..(99743)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (108055)..(108055)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (109094)..(109094)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (109125)..(109125)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (118900)..(118900)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (119052)..(119052)
; OTHER INFORMATION: n = a or c or g or t
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;
; NAME/KEY: misc feature
; LOCATION: (119053)..(119112)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (119115)..(119121)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (119123)..(119123)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (141674)..(141674)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (142063)..(142063)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (142137)..(142137)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (142967)..(142967)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (143077)..(143077)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (143506)..(143506)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (143587)..(143587)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (143629)..(143629)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (149079)..(149079)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5363)..(5363)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8080)..(8080)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10296)..(10296)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14528)..(14528)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15336)..(15336)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15457)..(15457)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
```

```
;
; NAME/KEY: misc feature
; LOCATION: (16288)..(16288)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16306)..(16307)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16316)..(16316)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16397)..(16397)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (56012)..(56012)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (57662)..(57662)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(54)
; OTHER INFORMATION: exon 1
; FEATURE:
; NAME/KEY: exon
; LOCATION: (55)..(124)
; OTHER INFORMATION: exon 1
; FEATURE:
; NAME/KEY: exon
; LOCATION: (91147)..(91244)
; OTHER INFORMATION: exon 2
; FEATURE:
; NAME/KEY: exon
; LOCATION: (93669)..(93834)
; OTHER INFORMATION: exon 3
; FEATURE:
; NAME/KEY: exon
; LOCATION: (96310)..(96422)
; OTHER INFORMATION: exon 4
; FEATURE:
; NAME/KEY: exon
; LOCATION: (99546)..(99723)
; OTHER INFORMATION: exon 5
; FEATURE:
; NAME/KEY: exon
; LOCATION: (125441)..(125605)
```

Query Match 58.3%; Score 14; DB 6; Length 151830;
Best Local Similarity 77.3%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy 1 CAAGTCGAACGGAAAGGCGCTTT 22
      ||||| ||||| ||||| |||||
Db 127951 CAAGGCGATCAAGGGCGCTTT 127930
```

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RESULT 60
US-10-506-549-3/c
; Sequence 3, Application US/10506549
; Publication No. US20060100417A1
; GENERAL INFORMATION:
; APPLICANT: APPLERA CORPORATION
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001361-US
; CURRENT APPLICATION NUMBER: US/10/506,549
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/361,343
```

; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 394191
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(394191)
; OTHER INFORMATION: n = A,T,C or G
US-10-506-549-3

Query Match 58.3%; Score 14; DB 6; Length 394191;
Best Local Similarity 77.3%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 AGTCGAACGGAAGCGCTTCG 24
Db 388331 AGGCAATGGAAGGCTTTAG 388310

RESULT 61

US-11-529-75992
; Sequence 75992, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75992
; LENGTH: 1236
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-529-75992

Query Match 57.5%; Score 13.8; DB 7; Length 1236;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGG 17
Db 1176 CAAGTCGAAGGGAATG 1192

RESULT 62

US-11-529-79704
; Sequence 79704, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02

; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79704
; LENGTH: 1380
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79704

Query Match 57.5%; Score 13.8; DB 7; Length 1380;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGC 18
Db 1061 AATTCGAACGGAAGGC 1077

RESULT 63

US-09-949-925-78/c
; Sequence 78, Application US/09949925
; Publication No. US20060099575A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2023P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1212)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-949-925-78

Query Match 57.5%; Score 13.8; DB 1; Length 1931;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 TCGAACGGAAGGCGCTT 21
Db 248 TCGAAGGGAAGGCATT 232

RESULT 64

US-09-949-925-12/c
; Sequence 12, Application US/09949925
; Publication No. US20060099575A9
; GENERAL INFORMATION:

; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 67 Human secreted proteins
 ; FILE REFERENCE: P2023P2
 ; CURRENT APPLICATION NUMBER: US/09/949,925
 ; CURRENT FILING DATE: 2001-09-12
 ; PRIOR APPLICATION NUMBER: US 60/232,150
 ; PRIOR FILING DATE: 2000-12-09
 ; PRIOR APPLICATION NUMBER: PCT/US99/01621
 ; PRIOR FILING DATE: 1999-01-27
 ; PRIOR APPLICATION NUMBER: US 60/073,160
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: US 60/073,159
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: US 60/073,165
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: US 60/073,164
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: US 60/073,167
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: US 60/073,162
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: US 60/073,161
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: US 60/073,170
 ; PRIOR FILING DATE: 1998-01-30
 ; NUMBER OF SEQ ID NOS: 298
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 12
 ; LENGTH: 1932
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-949-925-12

Query Match 57.5%; Score 13.8; DB 1; Length 1932;
 Best Local Similarity 88.2%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 TCGAACGGAAGGCCTT 21
 ||||| ||||| ||||| ||||| |||||
 DB 248 TCGAAGGGAAGGCATT 232

RESULT 65
 US-11-217-529-98883
 ; Sequence 98883, Application US/11217529
 ; Publication No. US20060099612A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUNTORY LIMITED
 ; APPLICANT: NAKAO, YOSHIHIRO
 ; APPLICANT: NAKAMURA, NORIHIISA
 ; APPLICANT: KODAMA, YUKIKO
 ; APPLICANT: FUJIMURA, TOMOKO
 ; APPLICANT: ASHIKARI, TOSHIHIKO
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 ; FILE REFERENCE: S-38-285
 ; CURRENT APPLICATION NUMBER: US/11/217,529
 ; CURRENT FILING DATE: 2005-09-02
 ; PRIOR APPLICATION NUMBER: US 10/932,182
 ; PRIOR FILING DATE: 2004-09-02
 ; NUMBER OF SEQ ID NOS: 197023
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 98883
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Saccharomyces pastorianus
 US-11-217-529-98883

Query Match 56.7%; Score 13.6; DB 7; Length 25;
 Best Local Similarity 80.0%; Pred. No. 81;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AAGTCGACGGAAGGCCTT 21
 ||||| ||||| ||||| ||||| |||||

Db 6 AAGTCACACGCAAGGCCTT 25
 RESULT 66
 US-11-217-529-130040/c
 ; Sequence 130040, Application US/11217529
 ; Publication No. US20060099612A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUNTORY LIMITED
 ; APPLICANT: NAKAO, YOSHIHIRO
 ; APPLICANT: NAKAMURA, NORIHIISA
 ; APPLICANT: KODAMA, YUKIKO
 ; APPLICANT: FUJIMURA, TOMOKO
 ; APPLICANT: ASHIKARI, TOSHIHIKO
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 ; FILE REFERENCE: S-38-285
 ; CURRENT APPLICATION NUMBER: US/11/217,529
 ; CURRENT FILING DATE: 2005-09-02
 ; PRIOR APPLICATION NUMBER: US 10/932,182
 ; PRIOR FILING DATE: 2004-09-02
 ; NUMBER OF SEQ ID NOS: 197023
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 130040
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Saccharomyces pastorianus
 US-11-217-529-130040

Query Match 56.7%; Score 13.6; DB 7; Length 25;
 Best Local Similarity 80.0%; Pred. No. 81;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAAGTCGACGGAAGGCCTT 20
 ||||| ||||| ||||| ||||| |||||
 DB 21 CAAGTCGATCGGAAGTGACT 2

RESULT 67
 US-11-217-529-188129
 ; Sequence 188129, Application US/11217529
 ; Publication No. US20060099612A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUNTORY LIMITED
 ; APPLICANT: NAKAO, YOSHIHIRO
 ; APPLICANT: NAKAMURA, NORIHIISA
 ; APPLICANT: KODAMA, YUKIKO
 ; APPLICANT: FUJIMURA, TOMOKO
 ; APPLICANT: ASHIKARI, TOSHIHIKO
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 ; FILE REFERENCE: S-38-285
 ; CURRENT APPLICATION NUMBER: US/11/217,529
 ; CURRENT FILING DATE: 2005-09-02
 ; PRIOR APPLICATION NUMBER: US 10/932,182
 ; PRIOR FILING DATE: 2004-09-02
 ; NUMBER OF SEQ ID NOS: 197023
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 188129
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Saccharomyces pastorianus
 US-11-217-529-188129

Query Match 56.7%; Score 13.6; DB 7; Length 25;
 Best Local Similarity 80.0%; Pred. No. 81;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AAGTCGACGGAAGGCCTT 21
 ||||| ||||| ||||| ||||| |||||
 DB 3 AACTCTACCTGGAAGGCCTT 22

RESULT 68
 US-10-488-619-2026

```
; Sequence 2026, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2026
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2026

Query Match          56.7%; Score 13.6; DB 6; Length 523;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      3 AGTCGAACGGAAGGCCTT 22
Db      257 AATCAAAAGGAAGGACTTT 276

RESULT 69
US-11-217-529-4440
; Sequence 4440, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4440
; LENGTH: 903
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4440

Query Match          56.7%; Score 13.6; DB 7; Length 903;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      5 TCGAACGGAAGGCCTTCG 24
Db      268 TCGAACGGAAGGACTTGG 287

RESULT 70
US-10-473-173-107/c
; Sequence 107, Application US/10473173
; Publication No. US20060088823A1
; GENERAL INFORMATION:
; APPLICANT: VAN ANDEL INSTITUTE
; TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
; TITLE OF INVENTION: Carcinoma: Prognosis and Drug Target Identification
; FILE REFERENCE: 38345-170094
; CURRENT APPLICATION NUMBER: US/10/473,173
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/279,411
; PRIOR FILING DATE: 2001-03-29
```

```
; NUMBER OF SEQ ID NOS: 498
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 107
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-473-173-107

Query Match          56.7%; Score 13.6; DB 6; Length 927;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CAAGTCGAACGGAAGGCCT 20
Db      564 CAGGAAGCAGCGAAGGCCT 545

RESULT 71
US-11-217-529-174359
; Sequence 174359, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174359
; LENGTH: 984
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-174359

Query Match          56.7%; Score 13.6; DB 7; Length 984;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGGCCTT 21
Db      837 AACTCTACCTGAAAGGCCTT 856

RESULT 72
US-11-217-529-3863
; Sequence 3863, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3863
; LENGTH: 1224
; TYPE: DNA
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; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3863

Query Match          56.7%; Score 13.6; DB 7; Length 1224;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GTCGAACGGAAGGCGCTTTC 23
   ||||| ||||| |||||
Db 309 GTCGAAAAGGAAGCGCTTGC 328

RESULT 73
US-11-217-529-78935
; Sequence 78935, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78935
; LENGTH: 1242
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78935

Query Match          56.7%; Score 13.6; DB 7; Length 1242;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 TCGAACGGAAGGCGCTTTCG 24
   ||||| ||||| |||||
Db 63 TCGAACAGTAAGGCTTTTG 82

RESULT 74
US-11-217-529-76764
; Sequence 76764, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76764
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76764

Query Match          56.7%; Score 13.6; DB 7; Length 1479;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3863

Query Match          56.7%; Score 13.6; DB 7; Length 1224;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 AGTCGAACGGAAGGCGCTTT 22
   ||||| ||||| |||||
Db 7 AGTCGAACACTACAGGCGCTTT 26

RESULT 75
US-10-505-928-419
; Sequence 419, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 419
; LENGTH: 1667
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-419

Query Match          56.7%; Score 13.6; DB 6; Length 1667;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAAAGTCGAACGGAAGGCCT 20
   ||||| ||||| |||||
Db 370 CAAAGTCGAGCGCAAGCACT 389

RESULT 76
US-11-217-529-82107
; Sequence 82107, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82107
; LENGTH: 1797
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82107

Query Match          56.7%; Score 13.6; DB 7; Length 1797;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAAAGTCGAACGGAAGGCCT 20
   ||||| ||||| |||||
Db 485 CAAAGCTCAACGGATAGGCCT 504

RESULT 77
US-11-217-529-5081
; Sequence 5081, Application US/11217529
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```
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: ASHIKARI, TOSHIHIKO
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5081
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5081

Query Match          56.7%; Score 13.6; DB 7; Length 2040;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 AGTCGAACGGAAGGCCTT 22
Db 62 AGACGAACCTTAAGGCATT 81

RESULT 78
US-11-217-529-82283/c
; Sequence 82283, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82283
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82283

Query Match          56.7%; Score 13.6; DB 7; Length 2436;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCTT 21
Db 1920 AACTGAAGGGAAGGCCTT 1901

RESULT 79
US-11-217-529-76785
; Sequence 76785, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
```

```
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76785
; LENGTH: 2595
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76785

Query Match          56.7%; Score 13.6; DB 7; Length 2595;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCTT 21
Db 2545 AAGTCACACGGAAGGCCT 2564

RESULT 80
US-11-217-529-32547/c
; Sequence 32547, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32547
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-32547

Query Match          55.8%; Score 13.4; DB 7; Length 25;
Best Local Similarity 73.9%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTTC 23
Db 23 CAAATGGAACGTCAAAGCTTTC 1

RESULT 81
US-11-217-529-94649
; Sequence 94649, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
```

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; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 94649
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-94649

Query Match          55.8%; Score 13.4; DB 7; Length 25;
Best Local Similarity 73.9%; Pred. No. 1.e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAAGCGCTTTC 23
Db 2 CAACGCGACGGAAACTACTTTC 24

RESULT 82
US-11-217-529-166591
; Sequence 166591, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 166591
; LENGTH: 393
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-166591

Query Match          55.8%; Score 13.4; DB 7; Length 393;
Best Local Similarity 73.9%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAAGCGCTTTC 23
Db 253 CAAGTCGTATGGAAGGAAGCTTC 275

RESULT 83
US-10-488-619-2473/c
; Sequence 2473, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2473
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2473
```

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Query Match          55.8%; Score 13.4; DB 6; Length 487;
Best Local Similarity 73.9%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAAGCGCTTTC 23
Db 78 CAAGTCCTAAGGAATGGCTTAC 56

RESULT 84
US-10-488-619-2474
; Sequence 2474, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2474
; LENGTH: 510
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2474

Query Match          55.8%; Score 13.4; DB 6; Length 510;
Best Local Similarity 73.9%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAAGCGCTTTC 23
Db 399 CAAGTCCTAAGGAATGGCTTAC 421

RESULT 85
US-10-488-619-2770/c
; Sequence 2770, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2770
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2770

Query Match          55.8%; Score 13.4; DB 6; Length 562;
Best Local Similarity 73.9%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAAGCGCTTTC 23
Db 206 CAAGTCGGCGGCGAGGCATTC 184

RESULT 86
US-11-301-554-1914
; Sequence 1914, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
```

```
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1914
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-301-554-1914

Query Match          55.8%; Score 13.4; DB 7; Length 624;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAG 16
        |||||
Db      502 AAGTCGAAGGAAG 516

RESULT 87
US-11-301-554-1668
; Sequence 1668, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongcong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
```

```
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1668
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-301-554-1668

Query Match          55.8%; Score 13.4; DB 7; Length 636;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAG 16
        |||||
Db      505 AAGTCGAAGGAAG 519

RESULT 88
US-11-217-529-79746
; Sequence 79746, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79746
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79746

Query Match          55.8%; Score 13.4; DB 7; Length 696;
Best Local Similarity 73.9%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGCCTTCG 24
        || || ||||| ||||| ||
```



```
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1564
; LENGTH: 1107
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1564

Query Match      55.8%; Score 13.4; DB 7; Length 1107;
Best Local Similarity 73.9%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTC 23
   ||||| ||| ||| |||
Db 592 CAAGTCGAGGCGAAGCGCATATC 614

RESULT 94
US-11-217-529-82255/c
; Sequence 82255, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82255
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82255

Query Match      55.8%; Score 13.4; DB 7; Length 1515;
Best Local Similarity 73.9%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCGCTTTCG 24
   ||||| ||||| |||||
Db 1013 AATTCGAATCAAGGCTTTTG 991

RESULT 95
US-11-256-221-1
; Sequence 1, Application US/11256221
; Publication No. US20060094094A1
; GENERAL INFORMATION:
; APPLICANT: Sugio, Tsuyoshi
; APPLICANT: Miura, Akira
; APPLICANT: Parada Valdecantos, Pilar A.
; APPLICANT: Badilla Ohlbaum, Ricardo
; TITLE OF INVENTION: BACTERIA STRAIN WENELEN DSM 16786, USE OF SAID BACTERIA FOR
; TITLE OF INVENTION: LEACHING OF ORES OR CONCENTRATES CONTAINING METALLIC SULFIDE
; TITLE OF INVENTION: MINERAL SPECIES AND LEACHING PROCESSES BASED ON THE USE OF SAID
; TITLE OF INVENTION: BACTERIA OR MIXTURES THAT CONTAIN SAID BACTERIA
; FILE REFERENCE: 15053.15US01
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; CURRENT APPLICATION NUMBER: US/11/256,221
; CURRENT FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: CL 2731-2004
; PRIOR FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 1531
; TYPE: DNA
; ORGANISM: Bacteria
US-11-256-221-1

Query Match      55.8%; Score 13.4; DB 7; Length 1531;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAA 15
   ||||| ||||| |||
Db 54 CAAGTCGAACGGTAA 68

RESULT 96
US-11-301-554-316
; Sequence 316, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 316
; LENGTH: 1633
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-301-554-316
```

Query Match 55.8%; Score 13.4; DB 7; Length 1633;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGAAAG 16
Db 567 AAGTCGAAGGAAAG 581

RESULT 97

US-11-301-554-788
; Sequence 788, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangut, Chaitanya S.
; APPLICANT: McNabb, Andria

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301.554

; PRIORITY FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 788

; LENGTH: 1633

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-301-554-788

Query Match 55.8%; Score 13.4; DB 7; Length 1633;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGAAAG 16
Db 567 AAGTCGAAGGAAAG 581

RESULT 98

US-11-217-529-80937
; Sequence 80937, Application US/11217529

; Publication No. US20060099612A1
; GENERAL INFORMATION: LIMITED
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80937
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-80937

Query Match 55.8%; Score 13.4; DB 7; Length 1647;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGAAA 15
Db 160 CAAGTCGAACGAAA 174

RESULT 99

US-11-217-529-2385
; Sequence 2385, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:

; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO

; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: S-38-285

; CURRENT APPLICATION NUMBER: US/11/217,529

; CURRENT FILING DATE: 2005-09-02

; PRIOR APPLICATION NUMBER: US 10/932,182

; PRIOR FILING DATE: 2004-09-02

; NUMBER OF SEQ ID NOS: 197023

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 2385

; LENGTH: 1710

; TYPE: DNA

; ORGANISM: Saccharomyces pastorianus

US-11-217-529-2385

Query Match 55.8%; Score 13.4; DB 7; Length 1710;
Best Local Similarity 73.9%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGAAAGCCTTCG 24
Db 1112 AAGTCGATGGAAACCCCTTATCG 1134

RESULT 100

US-11-217-529-2406/c
; Sequence 2406, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:

; APPLICANT: SUNTORY LIMITED

; APPLICANT: NAKAO, YOSHIHIRO

; APPLICANT: NAKAMURA, NORIHISA

; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2406
; LENGTH: 1716
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-2406

Query Match 55.8%; Score 13.4; DB 7; Length 1716;
Best Local Similarity 73.9%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTC 23
||| ||||| ||| |||||
Db 1297 CAATGGACGTCGAAGTCTTTC 1275

Search completed: May 19, 2006, 05:38:17
Job time : 16.8916 secs

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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 02:22:49 ; Search time 259.361 Seconds
(without alignments)
591.412 Million cell updates/sec

Title: US-10-665-708-23

Perfect score: 22
Sequence: 1 gtcgaacggaaggcttcg 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 524920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 300 summaries

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- N_Geneseq_8:*
- 1: Geneseq1980s:*
 - 2: Geneseq1990s:*
 - 3: Geneseq2000s:*
 - 4: Geneseq2001as:*
 - 5: Geneseq2001bs:*
 - 6: Geneseq2002as:*
 - 7: Geneseq2002bs:*
 - 8: Geneseq2003as:*
 - 9: Geneseq2003bs:*
 - 10: Geneseq2003cs:*
 - 11: Geneseq2003ds:*
 - 12: Geneseq2004as:*
 - 13: Geneseq2004bs:*
 - 14: Geneseq2005as:*
 - 15: Geneseq2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	22	100.0	22	4	AD11273
2	22	100.0	22	10	ADG88354
3	22	100.0	22	14	AEA08229
4	21	95.5	24	4	AD11272
5	21	95.5	24	10	ADG88353
6	21	95.5	24	14	AEA08228
7	21	95.5	25	4	AD11271
8	21	95.5	25	10	ADG88352
9	21	95.5	25	14	AEA08227
10	20.4	92.7	500	13	AD220587
11	20.4	92.7	1449	14	AEA22405
12	20.4	92.7	1455	14	AEA22412
13	20.4	92.7	1482	14	AEA22404
14	19	86.4	19	4	AD11274
15	19	86.4	19	10	ADG88355
16	19	86.4	19	14	AEA08230
17	18.8	85.5	50	12	ADF94057
18	18.8	85.5	166	2	AAX32481

Abz76674	Microtetr
Aeb72673	Streptos
Aed64356	Rhodococ
Ado80217	Rhodococ
Adw16264	DNA copy
Adj38609	Micromono
Adw16290	DNA copy
Adz35975	Verrucosi
Adx38843	Microbiop
Aea22406	Mycobacte
Aed35651	Pseudonoc
Adr90327	Rhodococ
Adr90325	Rhodococ
Aed11327	Aliphatic
Aed11084	Coralli
Aed48445	M. echino
Aad57239	Human GCD
Adc61232	Baeyer-Vi
Aav24418	Target se
Aav13026	Mycobacte
Aas30718	Mycobacte
Aas30716	Mycobacte
Aad11024	Probe #4
Aad11017	PCR prime
Aax99195	M. avium
Aax99196	M. fortui
Aeb98762	Mycobacte
Adf94050	Microorga
Aeb98762	Mycobacte
Adk66476	Coryneb
Adk66445	Coryneb
Aaq37639	Mycobacte
Aea22401	Mycobacte
Adb61680	16S rRNA
Adr90572	M. avium 1
Adr90572	M. avium 1
Adf56670	YS-44442
Adf56670	YS-44442
Ady86147	Saccharot
Ady86147	Saccharot
Adf56671	YS-45494
Ady86148	Saccharot
Adf47485	Nocardia
Adf47485	Nocardia
Adw12667	Rhodococ
Aeb98771	Mycobacte
Aat45276	Coryneb
Abn86275	G. polyvis
Aas59540	Propionib
Acf64469	Propionib
Abv75558	Saccharop
Aav24413	Target se
Aax13021	Mycobacte
Aax99201	M. smegma
Adg8711	Rice gene
Adw16249	DNA copy
Ad11277	Mycobacte
Aea08233	Mycobacte
Ad11278	Mycobacte
Adg88359	Mycobacte
Aea08234	Mycobacte
Aeb98776	Mycobacte
Adf94053	Microorga
Adu66542	Cut base
Aeb98763	Mycobacte
Abt23572	Stabili
Aea02278	Human col
Aea22410	Mycobacte

c	92	16	72.7	1344	12	AD085868	Ado85868	Gordonia	165	15.6	70.9	3111	11	ACH97300	Ach97300 Klebsiell
	93	16	72.7	1415	13	AEa22413	AEa22413 Mycobacte		c 166	15.6	70.9	3257	4	AAC84585	Aac84585 Wheat mag
	94	16	72.7	1460	3	Az22765	Az22765 Corynebac		c 167	15.6	70.9	12368	4	AAS46271	Aas46271 DNA encod
	95	16	72.7	1462	14	AEa22415	AEa22415 Mycobacte		c 168	15.6	70.9	39949	12	ADF31997	Adf31997 Full leng
	96	16	72.7	1484	14	AEa22414	AEa22414 Mycobacte		c 169	15.6	70.9	43800	11	ACN44516	Acn44516 Mouse gen
	97	16	72.7	1517	12	ADM92517	Adm92517 Gordonia		c 170	15.6	70.9	48200	12	ADF31998	Adf31998 Cosmid 2A
	98	16	72.7	1517	12	AD071823	Ado71823 DNA of RN		c 171	15.6	70.9	86453	14	ADY25730	Ady25730 SULF rela
	99	16	72.7	1527	14	AEa22407	AEa22407 Mycobacte		c 172	15.6	70.9	110000	6	ABQ69245_16	Continuation (17 o
	100	15.8	71.8	32	4	AD11264	Ad11264 Mycobacte		c 173	15.6	70.9	110000	6	ABQ67195_1	Continuation (2 of
	101	15.8	71.8	32	10	ADG88345	Adg88345 Mycobacte		c 174	15.6	70.9	110000	10	ACF65385_3	Continuation (5 of
	102	15.8	71.8	32	14	AEA08220	AEa08220 Mycobacte		c 175	15.6	70.9	110000	10	ACF65385_4	Continuation (5 of
	103	15.8	71.8	50	2	AAX99199	Rax99199 M. kansas		c 176	15.6	70.9	110000	10	ACF67367_33	Continuation (34 o
	104	15.8	71.8	50	2	AAX99194	Rax99194 M. bovis		c 177	15.6	70.9	264965	12	ADN16203	Adn16203 Human sul
	105	15.8	71.8	50	2	AAX99193	Rax99193 M. tuberc		c 178	15.6	70.9	268685	6	ABS56563	Abs56563 Human SUL
	106	15.8	71.8	50	12	ADP94055	Adf94055 Microorga		c 179	15.4	70.0	27	2	AAV24410	Av24410 Target se
	107	15.8	71.8	50	12	ADP94047	Adf94047 Microorga		c 180	15.4	70.0	27	2	AAV13018	Av13018 Mycobacte
	108	15.8	71.8	170	3	AAA31293	Aaa31293 Plant mic		c 181	15.4	70.0	28	4	AAD11025	Aad11025 Probe #5
	109	15.8	71.8	203	2	AAQ94742	Aeq94742 DNA fragm		c 182	15.4	70.0	28	4	AAD11018	Aad11018 PCR prime
	110	15.8	71.8	209	14	AEb98764	Aeb98764 Mycobacte		c 183	15.4	70.0	28	4	AAD11018	Aad11018 PCR prime
	111	15.8	71.8	211	14	AEb98761	Aeb98761 Mycobacte		c 184	15.4	70.0	36	14	ADU69991	Adu69991 LAMP reac
	112	15.8	71.8	305	3	AAA31415	Aaa31415 Plant mic		c 185	15.4	70.0	37	14	ADU69989	Adu69989 LAMP reac
	113	15.8	71.8	349	13	ADV99481	Adv99481 Meningit		c 186	15.4	70.0	39	14	ADU69984	Adu69984 LAMP reac
	114	15.8	71.8	375	11	ACH95596	Ach95596 Klebsiell		c 187	15.4	70.0	39	14	ADU69983	Adu69983 LAMP reac
	115	15.8	71.8	381	5	AAS77874	Ras77874 DNA encod		c 188	15.4	70.0	39	14	ADU69985	Adu69985 LAMP reac
	116	15.8	71.8	576	5	AAS67301	Ras67301 DNA encod		c 189	15.4	70.0	39	14	AEb98765	Aeb98765 Mycobacte
	117	15.8	71.8	1271	2	AAV24293	Av24293 Mycobacte		c 190	15.4	70.0	39	15	AEF95350	Aef95350 Nucleic a
	118	15.8	71.8	1416	14	AEa22416	AEa22416 Mycobacte		c 191	15.4	70.0	41	14	ADU69960	Adu69960 LAMP reac
	119	15.8	71.8	1421	14	AEa22402	AEa22402 Mycobacte		c 192	15.4	70.0	41	14	ADU69958	Adu69958 LAMP reac
	120	15.8	71.8	1463	14	AEa22409	AEa22409 Mycobacte		c 193	15.4	70.0	42	14	ADU69959	Adu69959 LAMP reac
	121	15.8	71.8	1463	3	AAZ35571	Raz35571 Mycobacte		c 194	15.4	70.0	42	14	ADU69957	Adu69957 LAMP reac
	122	15.8	71.8	1469	5	AAS11027	Ras11027 Mycobacte		c 195	15.4	70.0	455	3	AAC55929	Aac55929 Eucalyptu
	123	15.8	71.8	1469	13	ADR90574	Adr90574 M. kansas		c 196	15.4	70.0	455	3	AAC57218	Aac57218 Eucalyptu
	124	15.8	71.8	1524	4	AAS30719	Ras30719 Mycobacte		c 197	15.4	70.0	861	14	ACL67957	ACL67957 M. xanthu
	125	15.8	71.8	1536	10	ADB61681	Adb61681 16S rRNA		c 198	15.4	70.0	1164	13	ADS56576	Ads56576 Bacterial
	126	15.8	71.8	1536	10	ADB61682	Adb61682 16S rRNA		c 199	15.4	70.0	2642	4	ABL23018	Ab123018 Drosophil
	127	15.8	71.8	1537	10	ADF41649	Adf41649 Mycobacte		c 200	15.4	70.0	3581	4	ABL23036	Ab123036 Drosophil
	128	15.8	71.8	1849	14	AEA51361	Aea51361 Mouse gen		c 201	15.4	70.0	5433	4	ABL04331	Ab104331 Drosophil
	129	15.8	71.8	2000	11	ACL36116	ACL36116 Rice stre		c 202	15.4	70.0	7162	4	ABL04330	Ab104330 Drosophil
	130	15.8	71.8	2896	10	ACC47372	Acc47372 Human lat		c 203	15.4	70.0	23677	14	ACL64755	ACL64755 M. xanthu
	131	15.8	71.8	2898	12	ADC47372	Ad135344 Murine se		c 204	15.2	69.1	365	12	ADF20374	Adf20374 Pinus rad
	132	15.8	71.8	2919	13	ADS59960	Ads59960 Bacterial		c 205	15.2	69.1	409	13	AAU09116	Aaf09116 Fusarium
	133	15.8	71.8	3054	10	ACC47371	Acc47371 Rat late		c 206	15.2	69.1	409	13	ADU53157	Adu53157 Fusarium
	134	15.8	71.8	6883	8	AAI36998	Ral36998 Human mus		c 207	15.2	69.1	409	14	ADZ91160	Adz91160 Fusarium
	135	15.8	71.8	6883	8	ABX59986	Abx59986 cDNA enco		c 208	15.2	69.1	413	14	ACL61303	ACL61303 Human col
	136	15.8	71.8	6883	12	ADJ30736	Adj30736 Human mus		c 209	15.2	69.1	414	5	AAE56015	Aaf56015 Novel hum
	137	15.8	71.8	21126	1	AAAN0970	Ana0970 TL-DNA re		c 210	15.2	69.1	416	4	AAI87098	Aai87098 Human pol
	138	15.8	71.8	21126	12	AD055765	Ado55765 Agrobacte		c 211	15.2	69.1	475	6	ABL78115	Ab178115 Human ova
	139	15.8	71.8	36241	10	ADB74385	Adb74385 Mycobacte		c 212	15.2	69.1	499	9	ACH13049	Ach13049 Human adu
	140	15.8	71.8	36470	10	ADB74374	Adb74374 Mycobacte		c 213	15.2	69.1	561	3	AAC98000	Aac98000 Human col
	141	15.8	71.8	110000	4	AAI99682_14	Continuation (15 o		c 214	15.2	69.1	585	4	AAH10759	Aah10759 Human cdn
	142	15.8	71.8	110000	4	AAI99683_14	Continuation (15 o		c 215	15.2	69.1	622	4	AAU00309	Aas00309 S. pneumo
	143	15.6	70.9	227	9	ADB82110	Adb82110 Human cdn		c 216	15.2	69.1	671	13	ADQ79174	Adq79174 Novel can
	144	15.6	70.9	331	6	ABQ89167	Abq89167 Human pro		c 217	15.2	69.1	861	10	ABZ39185	Abz39185 N. gonorr
	145	15.6	70.9	439	4	AAC84579	Acc84579 Corn magn		c 218	15.2	69.1	978	6	ABN74125	Abn74125 Bovine em
	146	15.6	70.9	465	10	ADB57680	Adb57680 Toxicity-		c 219	15.2	69.1	1374	10	ADE64000	Ad64000 Rat gene
	147	15.6	70.9	471	10	ACC61674	Acc61674 Gene sequ		c 220	15.2	69.1	1374	10	ADBE64000	Ad64000 Rat gene
	148	15.6	70.9	471	10	ADK64173	Adk64173 Disease t		c 221	15.2	69.1	1392	2	AAZ11765	Aaz11765 Maize his
	149	15.6	70.9	524	10	ADK57597	Adk57597 Arabidops		c 222	15.2	69.1	1420	3	AAC69580	Aac69580 Human sec
	150	15.6	70.9	624	10	ADC72425	Adc72425 DNA Seq I		c 223	15.2	69.1	1542	10	ADH84376	Adh84376 Enterococ
	151	15.6	70.9	633	3	ACF70237	Accf70237 Phototrab		c 224	15.2	69.1	1733	5	AAH90021	Aah90021 Human bon
	152	15.6	70.9	784	3	AAC49475	Rac49475 Arabidops		c 225	15.2	69.1	1929	11	ACL38184	ACL38184 Rice stre
	153	15.6	70.9	960	11	ACN44517	Acn44517 Mouse mRN		c 226	15.2	69.1	2501	2	AAV58761	Av58761 Human sec
	154	15.6	70.9	1101	13	AD742264	Adt42264 Bacterial		c 227	15.2	69.1	2635	8	ABT18506	Abt18506 Aspergill
	155	15.6	70.9	1111	13	ADX13192	Adx13192 Plant ful		c 228	15.2	69.1	2996	4	AAH18563	Aah18563 Human cdn
	156	15.6	70.9	1418	8	ABZ25595	Abz25595 Rhodococ		c 229	15.2	69.1	2937	8	ACA23290	Acca23290 Prokaryot
	157	15.6	70.9	1662	11	ACH97324	Ach97324 Klebsiell		c 230	15.2	69.1	2964	8	ACA23290	Acca23290 Prokaryot
	158	15.6	70.9	1675	13	ADS56900	Ads56900 Bacterial		c 231	15.2	69.1	3485	2	AAI13220	Aai13220 Enterococ
	159	15.6	70.9	1718	13	AD081352	Ado81352 Plant ful		c 232	15.2	69.1	3485	6	ABS99015	Abs99015 Enterococ
	160	15.6	70.9	2427	13	ADX60109	Adx60109 Plant ful		c 233	15.2	69.1	3628	10	ADG15051	Adg15051 Human SEC
	161	15.6	70.9	2444	3	AAC56059	Adc56059 Eucalyptu		c 234	15.2	69.1	3846	10	AD121796	Ad121796 Novel hum
	162	15.6	70.9	2460	14	ADW16476	Adw16476 Eucalyptu		c 235	15.2	69.1	3908	4	AAI11067	Aai11067 Human sec
	163	15.6	70.9	2982	6	ABZ14720	Abz14720 Arabidops		c 236	15.2	69.1	3918	5	AHH99908	Aah99908 Human bon
	164	15.6	70.9	2982	10	ADF75190	Adf75190 Thale cre		c 237	15.2	69.1	4001	10	ADF42453	Adf42453 Human PP7

C 238	15.2	69.1	4635	8	ABT17912
C 239	15.2	69.1	4964	8	ABT19726
C 240	15.2	69.1	20320	5	ABA21464
C 241	15.2	69.1	42104	11	ACN44606
C 242	15.2	69.1	89128	6	ABL61995
C 243	15.2	69.1	105305	11	ACN44760
C 244	15.2	69.1	110000	3	AAF22303_4
C 245	15.2	69.1	ABQ69245_02	6	ABQ69245_02
C 246	15.2	69.1	ABQ67197_01	6	ABQ67197_01
C 247	15.2	69.1	110000	6	ABQ67197_02
C 248	15.2	69.1	110000	6	ABQ67197_02
C 249	15.2	69.1	110000	6	ABA03041_02
C 250	15.2	69.1	110000	11	ADM27081_05
C 251	15.2	69.1	136489	14	ADZ12560
C 252	15.2	69.1	170489	13	ABD33314
C 253	15.2	69.1	170506	14	ADZ13520
C 254	15.2	68.2	50	2	AAX99197
C 255	15.2	68.2	592	12	ACH79967
C 256	15.2	68.2	1429	11	ADI131363
C 257	15.2	68.2	1429	13	ADS83430
C 258	15.2	68.2	1453	4	AAX99589
C 259	15.2	68.2	2010	6	ABN59917
C 260	15.2	68.2	2015	5	AAF88159
C 261	15.2	68.2	2098	4	AAS03044
C 262	15.2	68.2	2169	4	AAK94562
C 263	15.2	68.2	2169	12	ADL31436
C 264	15.2	68.2	2173	5	ABA82974
C 265	15.2	68.2	2240	10	ADB76868
C 266	15.2	68.2	3003	4	ABL07155
C 267	15.2	68.2	3293	8	ABX71285
C 268	15.2	68.2	5165	15	AEE83945
C 269	15.2	68.2	8544	4	ABL07154
C 270	14.8	67.3	40	2	AAT70787
C 271	14.8	67.3	87	2	AAX85278
C 272	14.8	67.3	107	10	ACA55810
C 273	14.8	67.3	107	12	ADI55606
C 274	14.8	67.3	321	4	AAI01072
C 275	14.8	67.3	321	4	ABL96538
C 276	14.8	67.3	321	6	ABL76168
C 277	14.8	67.3	341	4	AAS36010
C 278	14.8	67.3	341	4	AAS36011
C 279	14.8	67.3	341	10	ADE46704
C 280	14.8	67.3	341	10	ADE46705
C 281	14.8	67.3	341	13	ADJ08123
C 282	14.8	67.3	341	13	ADJ08122
C 283	14.8	67.3	352	4	AAS35269
C 284	14.8	67.3	352	10	ADE45348
C 285	14.8	67.3	352	13	ADJ06766
C 286	14.8	67.3	362	3	AAC02744
C 287	14.8	67.3	530	8	ABZ53176
C 288	14.8	67.3	543	11	ABD06974
C 289	14.8	67.3	559	6	ABQ28796
C 290	14.8	67.3	559	6	ABQ28797
C 291	14.8	67.3	587	8	ABZ53802
C 292	14.8	67.3	591	4	AAI43438
C 293	14.8	67.3	600	11	ABD07046
C 294	14.8	67.3	637	3	AAFI4590
C 295	14.8	67.3	637	13	ADU58631
C 296	14.8	67.3	637	14	ADZ96634
C 297	14.8	67.3	649	4	AAH69025
C 298	14.8	67.3	795	9	ADA32234
C 299	14.8	67.3	849	13	ADA49436
C 300	14.8	67.3	902	2	AAQ81202

ALIGNMENTS

RESULT 1
AADI1273
ID AADI1273 standard; DNA; 22 BP.
XX
AC AADI1273;

XX	Abt17912 Aspergill	24-SEP-2001 (first entry)	XX
DT	Abt19726 Aspergill		DT
XX	AbA21464 Human ner		XX
DE	Acn44606 Human gen	Mycobacterium 16S rRNA amplifying primer #17.	DE
XX	AbL61995 Colon ade		XX
KW	Acn44760 Mouse gen		KW
KW	Continuation (5 of	Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;	KW
XX	Continuation (3 of	Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.	XX
OS	Continuation (2 of		OS
XX	Continuation (3 of		XX
PN	Continuation (3 of		PN
XX	Adz12560 Human can	WO200144510-A2.	XX
PD	Abd33314 Human can	21-JUN-2001.	PD
XX	Adz13520 Human can		XX
PF	Aax99197 M. sorofu	17-DEC-1999; 99WO-US030346.	PF
XX	Ach79967 Human gen		XX
PR	Adi31363 Human CDN	17-DEC-1999; 99WO-US030346.	PR
XX	Ads83430 Human lym		XX
PA	Aah99589 Human pro	(GENP-) GEN-PROBE INC.	PA
XX	Abn59917 Novel hum	(INMR) BIOMERIEUX SA.	XX
PI	Aaf88159 Human thy		PI
XX	Aas03044 Human dia		XX
XX	Aak94562 Human ful		XX
DR	Adl31436 Full leng	Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;	DR
XX	AbA82974 Human tra	WPI; 2001-398170/42.	XX
PT	AbB76868 A. gossyp	Detecting Mycobacterium species, involves in vitro amplification of 16S	PT
PT	AbL07155 Drosophil	rRNA or DNA encoding RNA in nucleic acid amplification mixture using	PT
PT	Aas25944 Human CDN	specific primers, and detecting the amplified nucleic acid.	PT
XX	Abx73285 Human nov		XX
PS	Aee83945 Human CDN	Claim 1; Page 36; 44pp; English.	PS
XX	AbL07154 Drosophil		XX
CC	Aat70787 Stenotic	The invention relates to a method of detecting Mycobacterium species,	CC
CC	Aax85278 Motif I f	that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA	CC
CC	ACA55810 Mouse sig	encoding 16S rRNA in an in vitro nucleic acid amplification mixture	CC
CC	Adi55606 Human pol	comprising a polymerase, and at least two primers, and then detecting the	CC
CC	Adl01072 Human rep	amplified nucleic acid. The method is relatively simple and useful for	CC
CC	AbL96538 Human tes	detecting the presence of various Mycobacterium species in a biological	CC
CC	AbL76168 Corn tass	sample, and thus important for diagnosis of infections resulting from	CC
CC	Aas36010 Human car	them. The method is especially important for screening opportunistic	CC
CC	Aas36011 Human car	infections caused by M. tuberculosis or a Mycobacterium other than	CC
CC	Ade46704 Human car	tuberculosis (MOTT). The present sequence is a PCR primer used for	CC
CC	Ade46705 Human car	amplifying Mycobacterium 16S rRNA	CC
XX	Adj08123 Human car		XX
XX	Adj08122 Human car	Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;	XX
XX	Aas35269 Human car	Query Match 100.0%; Score 22; DB 4; Length 22;	XX
XX	Ade45348 Human car	Best Local Similarity 100.0%; Pred. No. 0.33;	XX
XX	Adj06766 Human car	Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX
XX	Aac02744 Human sec		XX
XX	Abz53176 Aspergill		XX
XX	Abd06974 Pseudomon	Qy 1 GTCGACGGAAGGCGCTTCGG 22	XX
XX	Abq28796 Oligonuc		XX
XX	Abq28797 Oligonuc	1 GTCGACGGAAGGCGCTTCGG 22	XX
XX	Abz53802 Aspergill		XX
XX	Adi43438 Probe #12		XX
XX	Abd07046 Pseudomon	RESULT 2	XX
XX	Adi4590 Aspergill	ADG88354	XX
XX	Adus8631 Aspergill	ID ADG88354 standard; DNA; 22 BP.	XX
XX	Adz96634 Aspergill		XX
XX	Aah69025 Human cer	AC ADG88354;	XX
XX	Ada32234 DNA encod	XX	XX
XX	Ads49436 Bacterial	DT 11-MAR-2004 (first entry)	XX
XX	Aaq81202 Cloned al	Mycobacterium amplifying PCR primer #23.	XX
XX			XX
XX		In vitro amplification; PCR; primer; ss.	XX
XX			XX
XX		Mycobacterium celatum.	XX
XX			XX
XX		US2003165824-A1.	XX
XX		PN	XX
PD		04-SEP-2003.	PD
PF		15-DEC-2000; 2000US-00738274.	PF

```

XX 17-DEC-1999; 99US-0172190P.
XX (BREN/) BRENTANO S T.
XX (JUCK/) JUCKER M T.
XX (DELG/) DELGADO F D.
XX (CLEU/) CLEUZIAT P.
XX (RODR/) RODRIGUE M.
XX
XX PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2003-898044/82.
XX
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX in a biological sample comprises performing in vitro nucleic acid
XX amplification and detection of amplified products.
XX
XX Claim 1; SEQ ID NO 23; 20pp; English.
XX
XX The present invention relates to a method of detecting Mycobacterium
XX species present in a biological sample comprises performing an in vitro
XX amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
XX detecting the amplified Mycobacterium nucleic acid. The present sequence
XX is Mycobacterium amplifying PCR primer.
XX
XX Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 22; DB 10; Length 22;
XX Best Local Similarity 100.0%; Pred. No. 0.33;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GTCGAACGGAAAGGCTTTCGG 22
XX ||||||||||||||||||
XX DB 1 GTCGAACGGAAAGGCTTTCGG 22
XX ||||||||||||||||||
XX
XX RESULT 4
XX ID AAD11272 standard; DNA; 24 BP.
XX AC AAD11272;
XX XX
XX DT 24-SEP-2001 (first entry)
XX XX
XX DE Mycobacterium 16S rRNA amplifying primer #16.
XX XX
XX KW Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
XX KW Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
XX XX
XX OS Mycobacterium sp.
XX XX
XX PN WO200144510-A2.
XX XX
XX PD 21-JUN-2001.
XX XX
XX PF 17-DEC-1999; 99WO-US030346.
XX XX
XX PR 17-DEC-1999; 99WO-US030346.
XX XX
XX PA (GENP-) GEN-PROBE INC.
XX PA (INMR ) BIOMERIEUX SA.
XX XX
XX PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2001-398170/42.
XX DR
XX XX
XX PT Detecting Mycobacterium species, involves in vitro amplification of 16S
XX rRNA or DNA encoding RNA in nucleic acid amplification mixture using
XX specific primers, and detecting the amplified nucleic acid.
XX
XX Claim 1; Page 36; 44pp; English.
XX
XX The invention relates to a method of detecting Mycobacterium species,
XX that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
XX encoding 16S rRNA in an in vitro nucleic acid amplification mixture
XX comprising a polymerase, and at least two primers, and then detecting the
XX amplified nucleic acid. The method is relatively simple and useful for
XX detecting the presence of various Mycobacterium species in a biological
XX sample, and thus important for diagnosis of infections resulting from
XX them. The method is especially important for screening opportunistic
XX infections caused by M. tuberculosis or a Mycobacterium other than
XX tuberculosis (MOTT). The present sequence is a PCR primer used for
XX amplifying Mycobacterium 16S rRNA
XX
XX SQ Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 95.5%; Score 21; DB 4; Length 24;

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Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTCGAACGGAAGGCTTTTCG 21
Db 4 GTCGAACGGAAGGCTTTTCG 24

RESULT 5
ADG88353
ID ADG88353 standard; DNA; 24 BP.
XX
AC ADG88353;
XX
DT 11-MAR-2004 (first entry)
DE Mycobacterium amplifying PCR primer #22.
XX
KW In vitro amplification; PCR; primer; ss.
XX
OS Mycobacterium celatum.
XX
PN US2003165824-A1.
XX
PD 04-SEP-2003.
XX
PF 15-DEC-2000; 2000US-00738274.
XX
PR 17-DEC-1999; 99US-0172190P.
XX
PA (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAT P.
PA (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
DR WPI; 2003-898044/82.
XX
PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample comprises performing in vitro nucleic acid
PT amplification and detection of amplified products.
XX
PS Claim 1; SEQ ID NO 22; 20pp; English.
XX
CC The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample comprises performing an in vitro
CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
CC detecting the amplified Mycobacterium nucleic acid. The present sequence
CC is Mycobacterium amplifying PCR primer.
XX
SQ Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 95.5%; Score 21; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTCGAACGGAAGGCTTTTCG 21
Db 4 GTCGAACGGAAGGCTTTTCG 24

RESULT 6
AEA08228
ID AEA08228 standard; DNA; 24 BP.
XX
AC AEA08228;
XX
DT 14-JUL-2005 (first entry)
DE Mycobacterium celatum 16S rRNA amplifying non-T7 primer, SEQ ID NO: 22.
XX
XX

Microorganism detection; DNA amplification; 16S ribosomal RNA; 16S rRNA;
PCR; primer; ss.
Mycobacterium celatum.
US2005100915-A1.
12-MAY-2005.
18-SEP-2003; 2003US-00665708.
17-DEC-1999; 99US-0172190P.
15-DEC-2000; 2000US-00738274.
(BREN/) BRENTANO S T.
(JUCK/) JUCKER M T.
(DELG/) DELGADO F D.
(CLEU/) CLEUZIAT P.
(RODR/) RODRIGUE M.
Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
WPI; 2005-345392/35.
Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
in a biological sample, comprises using in vitro nucleic acid
amplification and detection of amplified products.
Claim 8; SEQ ID NO 22; 21pp; English.
The present invention relates to a method of detecting Mycobacterium
species present in a biological sample. The method involves using in
vitro nucleic acid amplification and detection of amplified products. The
invention is useful for diagnostic detection of pathogenic bacteria such
as Mycobacterium species. The present sequence is the Mycobacterium
celatum (ATCC 51130 and ATCC 51131) 16S ribosomal RNA (16SrRNA)
amplifying non-T7 PCR primer.
Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 95.5%; Score 21; DB 14; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTCGAACGGAAGGCTTTTCG 21
Db 4 GTCGAACGGAAGGCTTTTCG 24

RESULT 7
AAD11271
ID AAD11271 standard; DNA; 25 BP.
XX
AC AAD11271;
XX
DT 24-SEP-2001 (first entry)
DE Mycobacterium 16S rRNA amplifying primer #15.
XX
KW Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
KW Mycobacterium other than tuberculosis; MOT7; PCR primer; ss.
XX
OS Mycobacterium sp.
XX
PN WO200144510-A2.
XX
PD 21-JUN-2001.
XX
PF 17-DEC-1999; 99WO-US030346.
XX
PR 17-DEC-1999; 99WO-US030346.
XX
PA (GENP-) GEN-PROBE INC.

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PA (INMR ) BIOMERIEUX SA.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
XX WPI; 2001-398170/42.
XX
XX Detecting Mycobacterium species, involves in vitro amplification of 16S
PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using
PT specific primers, and detecting the amplified nucleic acid.
XX
PS Claim 1; Page 36; 44pp; English.
XX
XX The invention relates to a method of detecting Mycobacterium species,
CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture
CC comprising a polymerase, and at least two primers, and then detecting the
CC amplified nucleic acid. The method is relatively simple and useful for
CC detecting the presence of various Mycobacterium species in a biological
CC sample, and thus important for diagnosis of infections resulting from
CC them. The method is especially important for screening opportunistic
CC infections caused by M. tuberculosis or a Mycobacterium other than
CC tuberculosis (MOTT). The present sequence is a PCR primer used for
CC amplifying Mycobacterium 16S rRNA
XX
XX Sequence 25 BP; 7 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
SQ
Query Match 95.5%; Score 21; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTTTCG 21
DB 5 GTCGAACGGAAGGCCTTTTCG 25

RESULT 8
ADG88352
ID ADG88352 standard; DNA; 25 BP.
XX
XX
AC ADG88352;
XX
XX 11-MAR-2004 (first entry)
XX
XX Mycobacterium amplifying PCR primer #21.
XX
XX In vitro amplification; PCR; primer; ss.
XX
XX Mycobacterium celatum.
XX
XX US2003165824-A1.
XX
XX 04-SEP-2003.
XX
XX 15-DEC-2000; 2000US-00738274.
XX
XX 17-DEC-1999; 99US-0172190P.
XX
XX (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAT P.
PA (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
XX WPI; 2003-898044/82.
XX
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample comprises performing in vitro nucleic acid
PT amplification and detection of amplified products.
XX
PS Claim 1; SEQ ID NO 21; 20pp; English.
XX
CC The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample comprises performing an in vitro
CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
CC detecting the amplified Mycobacterium nucleic acid. The present sequence
CC is Mycobacterium amplifying PCR primer.
XX
SQ Sequence 25 BP; 7 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 95.5%; Score 21; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTTTCG 21
DB 5 GTCGAACGGAAGGCCTTTTCG 25

RESULT 9
AEA08227
ID AEA08227 standard; DNA; 25 BP.
XX
XX AEA08227;
XX
XX 14-JUL-2005 (first entry)
XX
XX Mycobacterium celatum 16SrRNA amplifying non-T7 primer, SEQ ID NO: 21.
XX
XX Microorganism detection; DNA amplification; 16s ribosomal RNA; 16s rRNA;
XX PCR; primer; ss.
XX
XX Mycobacterium celatum.
XX
XX US2005100915-A1.
XX
XX 12-MAY-2005.
XX
XX 18-SEP-2003; 2003US-00665708.
XX
XX 17-DEC-1999; 99US-0172190P.
XX
XX 15-DEC-2000; 2000US-00738274.
XX
XX (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAT P.
PA (RODR/) RODRIGUE M.
XX
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
XX WPI; 2005-345392/35.
XX
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample, comprises using in vitro nucleic acid
PT amplification and detection of amplified products.
XX
XX Claim 8; SEQ ID NO 21; 21pp; English.
XX
XX The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample. The method involves using in
CC vitro nucleic acid amplification and detection of amplified products. The
CC invention is useful for diagnostic detection of pathogenic bacteria such
CC as Mycobacterium species. The present sequence is the Mycobacterium
CC celatum (ATCC 51130 and ATCC 51131) 16S ribosomal RNA (16S-rRNA)
CC amplifying non-T7 PCR primer.
XX
XX Sequence 25 BP; 7 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 95.5%; Score 21; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTTTCG 21

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Db      5  GTCGAACGGAAGGCTTTTCG 25

RESULT 10
ID      ADZ20587
XX      ADZ20587 standard; DNA; 500 BP.
XX      ADZ20587;
XX      16-JUN-2005 (first entry)
XX      Formaldehyde decomposition related Mycobacterium sp. DNA.
XX      decomposition; formaldehyde; ds.
XX      Mycobacterium sp.
XX      JP2003284548-A.
XX      07-OCT-2003.
XX      27-MAR-2002; 2002JP-00089307.
XX      27-MAR-2002; 2002JP-00089307.
XX      (KIMO-) KUMOMOTO KEN PREFECTURE.
XX      (MITS-) MITSUWA CORP YG.
XX      (MITS-) MITSUWA BIPO KK.
XX      WPI; 2004-172963/17.
XX      Decomposing formaldehyde by Mycobacterium and/or growth medium of the
XX      cells.
XX      Example 1; SEQ ID NO 1; 20pp; Japanese.
XX      The invention relates to a novel method for decomposing formaldehyde by
XX      using microbial cells that belong to Mycobacterium sp. or Fusarium
XX      oxysporum, and/or the growth medium of the microbial cells. The invention
XX      further comprises: microbial cells which belong to Mycobacterium sp.
XX      having the ability to decompose formaldehyde; a formaldehyde
XX      decomposition agent comprising Mycobacterium sp. and/or the growth medium
XX      of the microbial cells; and a formaldehyde decomposition agent comprising
XX      F. oxysporum and/or its growth medium. The method is useful for
XX      decomposing formaldehyde in sea water by Mycobacterium sp. or F.
XX      oxysporum that is deposited under FERM P-S18690 or FERM P-18483,
XX      respectively. This polynucleotide sequence represents the Mycobacterium
XX      sp. DNA of the invention.
XX      Sequence 500 BP; 108 A; 119 C; 178 G; 95 T; 0 U; 0 Other;
XX      Query Match          92.7%; Score 20.4; DB 13; Length 500;
XX      Best Local Similarity 95.5%; Pred. No. 3;
XX      Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GTCGAACGGAAGGCTTTTCG 22
Db      57  GTCGAACGGAAGGCTTTTCG 78

RESULT 11
ID      AEA22405
XX      AEA22405 standard; DNA; 1449 BP.
XX      AEA22405;
XX      25-AUG-2005 (first entry)
XX      Mycobacterium fortuitum 16S rRNA sequence SEQ ID NO:6.
XX      microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
XX      Mycobacterium fortuitum.

XX      5  GTCGAACGGAAGGCTTTTCG 25
XX      US2005130168-A1.
XX      16-JUN-2005.
XX      31-OCT-2003; 2003US-00697802.
XX      31-OCT-2003; 2003US-00697802.
XX      (HANX/) HAN X.
XX      (PHAM/) PHAM A S.
XX      Han X, Pham AS;
XX      WPI; 2005-424597/43.
XX      Determining a bacterium species comprises providing oligonucleotide
XX      primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
XX      Disclosure; SEQ ID NO 6; 74pp; English.
XX      The invention relates to a method (M1) for determining a bacterium
XX      species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
XX      extracting a genomic nucleotide from the bacterium to provide a
XX      nucleotide template; (c) annealing a region of a nucleotide template to a
XX      specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
XX      complimentary fashion, the primer set designed to provide a product
XX      having a predetermined size dictated by a complementary primer set; (d)
XX      amplifying the region of the nucleotide template to produce the product;
XX      and (e) determining a species of a bacterium in a nucleotide sequence of
XX      the product. Also described is an alternative method (M2) for determining
XX      a bacterium species comprising: (a) providing a specimen or a sample
XX      having a template; (b) providing a pair of primers selected from: (i) a
XX      first forward primer having consecutive bases of an AFB-f comprising any
XX      of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
XX      or variations and a first reverse primer having consecutive bases of an
XX      AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
XX      or their fragments or variations, (ii) a second forward primer having
XX      consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
XX      bp (AEA22489-AEA22516) or their fragments or variations and a second
XX      reverse primer having consecutive bases of an UB-r comprising any of the
XX      28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
XX      variations, or (iii) a first forward primer having consecutive bases of
XX      an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
XX      second reverse primer having consecutive bases of an UB-r of AEA22517-
XX      AEA22544 or their fragments or variations; (c) the specimen; and (d)
XX      comparing the product from the specimen with a nucleotide sequence from a
XX      database to determine the bacterium species present in the specimen. The
XX      methods are useful for determining a bacterium species. The present
XX      sequence represents a Mycobacterium fortuitum 16S rRNA nucleotide
XX      sequence, which is used in the exemplification of the present invention.
XX      Sequence 1449 BP; 322 A; 342 C; 495 G; 290 T; 0 U; 0 Other;
XX      Query Match          92.7%; Score 20.4; DB 14; Length 1449;
XX      Best Local Similarity 95.5%; Pred. No. 3.4;
XX      Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GTCGAACGGAAGGCTTTTCG 22
Db      24  GTCGAACGGAAGGCTTTTCG 45

RESULT 12
ID      AEA22412
XX      AEA22412 standard; DNA; 1455 BP.
XX      AEA22412;
XX      25-AUG-2005 (first entry)
XX      Mycobacterium mucogenicum 16S rRNA sequence SEQ ID NO:13.

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KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
XX Mycobacterium mucogenicum.
OS
XX US2005130168-A1.
XX
XX 16-JUN-2005.
XX
XX 31-OCT-2003; 2003US-00697802.
XX
XX 31-OCT-2003; 2003US-00697802.
XX
XX (HANK/) HAN X.
XX (PHAM/) PHAM A S.
XX
XX Han X, Pham AS;
XX
XX WPI; 2005-424597/43.
XX
XX Determining a bacterium species comprises providing oligonucleotide
XX primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
XX
XX Disclosure; SEQ ID NO 13; 74pp; English.
XX
XX The invention relates to a method (M1) for determining a bacterium
XX species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
XX extracting a genomic nucleotide from the bacterium to provide a
XX nucleotide template; (c) annealing a region of a nucleotide template to a
XX specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
XX complimentary fashion, the primer set designed to provide a product
XX having a predetermined size dictated by a complimentary primer set; (d)
XX amplifying the region of the nucleotide template to produce the product;
XX and (e) determining a species of a bacterium in a nucleotide sequence of
XX the product. Also described is an alternative method (M2) for determining
XX a bacterium species comprising: (a) providing a specimen or a sample
XX having a template; (b) providing a pair of primers selected from: (i) a
XX first forward primer having consecutive bases of an AFB-f comprising any
XX of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
XX or variations, and a first reverse primer having consecutive bases of an
XX AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
XX or their fragments or variations, (ii) a second forward primer having
XX reverse primer having consecutive bases of an UB-r comprising any of the
XX 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
XX variations, or (iii) a first forward primer having consecutive bases of
XX an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
XX second reverse primer having consecutive bases of an UB-r of AEA22517-
XX AEA22544 or their fragments or variations; (c) the specimen; and (d)
XX comparing the product from the specimen with a nucleotide sequence from a
XX database to determine the bacterium species present in the specimen. The
XX methods are useful for determining a bacterium species. The present
XX sequence represents a Mycobacterium mucogenicum 16S rRNA nucleotide
XX sequence, which is used in the exemplification of the present invention.
XX
XX Sequence 1455 BP; 321 A; 347 C; 500 G; 287 T; 0 U; 0 Other;
XX
XX Query Match 92.7%; Score 20.4; DB 14; Length 1455;
XX Best Local Similarity 95.5%; Pred. No. 3.4;
XX Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 GTCGACGGGAAGGCGCTTCGG 22
XX |||||
XX Db 34 GTCGACGGGAAGGCGCTTCGG 55
XX |||||
XX
XX RESULT 13
XX AEA22404
XX ID AEA22404 standard; DNA; 1482 BP.
XX
XX AC AEA22404;
XX
XX DT 25-AUG-2005 (first entry)
XX
XX Mycobacterium farcinogenes 16S rRNA sequence SEQ ID NO.5.
XX
XX microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
XX
XX Mycobacterium farcinogenes.
XX
XX US2005130168-A1.
XX
XX 16-JUN-2005.
XX
XX 31-OCT-2003; 2003US-00697802.
XX
XX 31-OCT-2003; 2003US-00697802.
XX
XX (HANK/) HAN X.
XX (PHAM/) PHAM A S.
XX
XX Han X, Pham AS;
XX
XX WPI; 2005-424597/43.
XX
XX Determining a bacterium species comprises providing oligonucleotide
XX primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
XX
XX Disclosure; SEQ ID NO 5; 74pp; English.
XX
XX The invention relates to a method (M1) for determining a bacterium
XX species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
XX extracting a genomic nucleotide from the bacterium to provide a
XX nucleotide template; (c) annealing a region of a nucleotide template to a
XX specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
XX complimentary fashion, the primer set designed to provide a product
XX having a predetermined size dictated by a complimentary primer set; (d)
XX amplifying the region of the nucleotide template to produce the product;
XX and (e) determining a species of a bacterium in a nucleotide sequence of
XX the product. Also described is an alternative method (M2) for determining
XX a bacterium species comprising: (a) providing a specimen or a sample
XX having a template; (b) providing a pair of primers selected from: (i) a
XX first forward primer having consecutive bases of an AFB-f comprising any
XX of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
XX or variations, and a first reverse primer having consecutive bases of an
XX AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
XX or their fragments or variations, (ii) a second forward primer having
XX reverse primer having consecutive bases of an UB-r comprising any of the
XX 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
XX variations, or (iii) a first forward primer having consecutive bases of
XX an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
XX second reverse primer having consecutive bases of an UB-r of AEA22517-
XX AEA22544 or their fragments or variations; (c) the specimen; and (d)
XX comparing the product from the specimen with a nucleotide sequence from a
XX database to determine the bacterium species present in the specimen. The
XX methods are useful for determining a bacterium species. The present
XX sequence represents a Mycobacterium farcinogenes 16S rRNA nucleotide
XX sequence, which is used in the exemplification of the present invention.
XX
XX Sequence 1482 BP; 327 A; 353 C; 507 G; 295 T; 0 U; 0 Other;
XX
XX Query Match 92.7%; Score 20.4; DB 14; Length 1482;
XX Best Local Similarity 95.5%; Pred. No. 3.4;
XX Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 GTCGACGGGAAGGCGCTTCGG 22
XX |||||
XX Db 32 GTCGACGGGAAGGCGCTTCGG 53
XX |||||
XX
XX RESULT 14
XX AAD11274
XX ID AAD11274 standard; DNA; 19 BP.
XX
XX

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AC AAD11274;
XX
XX 24-SEP-2001 (first entry)
XX
XX Mycobacterium 16S rRNA amplifying primer #18.
XX
XX Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
KW Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
XX
XX Mycobacterium sp.
XX
XX WO200144510-A2.
XX
XX 21-JUN-2001.
XX
XX 17-DEC-1999; 99WO-US030346.
XX
XX 17-DEC-1999; 99WO-US030346.
XX
XX (GENP-) GEN-PROBE INC.
XX (INMR ) BIOMERIEUX SA.
XX
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2001-398170/42.
XX
XX Detecting Mycobacterium species, involves in vitro amplification of 16S
XX rRNA or DNA encoding RNA in nucleic acid amplification mixture using
XX specific primers, and detecting the amplified nucleic acid.
XX
XX Claim 1; Page 36; 44pp; English.
XX
XX The invention relates to a method of detecting Mycobacterium species,
XX that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
XX encoding 16S rRNA in an in vitro nucleic acid amplification mixture
XX comprising a polymerase, and at least two primers, and then detecting the
XX amplified nucleic acid. The method is relatively simple and useful for
XX detecting the presence of various Mycobacterium species in a biological
XX sample, and thus important for diagnosis of infections resulting from
XX them. The method is especially important for screening opportunistic
XX infections caused by M. tuberculosis or a Mycobacterium other than
XX tuberculosis (MOTT). The present sequence is a PCR primer used for
XX amplifying Mycobacterium 16S rRNA
XX
XX Sequence 19 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 86.4%; Score 19; DB 4; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 11;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 4 GAACGGAAGGCGCTTTCGG 22
XX Db 1 GAACGGAAGGCGCTTTCGG 19
XX
XX RESULT 15
XX ADG88355
XX ID ADG88355 standard; DNA; 19 BP.
XX
XX AC ADG88355;
XX
XX 11-MAR-2004 (first entry)
XX
XX Mycobacterium amplifying PCR primer #24.
XX
XX In vitro amplification; PCR; primer; ss.
XX
XX Mycobacterium xenopi.
XX
XX US2003165824-A1.
XX
XX 04-SEP-2003.
XX

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PF 15-DEC-2000; 2000US-00738274.
XX
XX 17-DEC-1999; 99US-0172190P.
XX
XX (BREN/) BRENTANO S T.
XX (JUCK/) JUCKER M T.
XX (DELG/) DELGADO F D.
XX (CLEU/) CLEUZIAZ P.
XX (RODR/) RODRIGUE M.
XX
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2003-898044/82.
XX
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX in a biological sample comprises performing in vitro nucleic acid
XX amplification and detection of amplified products.
XX
XX Claim 1; SEQ ID NO 24; 20pp; English.
XX
XX The present invention relates to a method of detecting Mycobacterium
XX species present in a biological sample comprises performing an in vitro
XX amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
XX detecting the amplified Mycobacterium nucleic acid. The present sequence
XX is Mycobacterium amplifying PCR primer.
XX
XX Sequence 19 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 86.4%; Score 19; DB 10; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 11;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 4 GAACGGAAGGCGCTTTCGG 22
XX Db 1 GAACGGAAGGCGCTTTCGG 19
XX
XX RESULT 16
XX AEA08230
XX ID AEA08230 standard; DNA; 19 BP.
XX
XX AC AEA08230;
XX
XX 14-JUL-2005 (first entry)
XX
XX Mycobacterium xenopi 16SrRNA amplifying non-T7 primer, SEQ ID NO: 24.
XX
XX DNA amplification; microorganism detection; 16s ribosomal RNA; 16s rRNA;
XX PCR; primer; ss.
XX
XX Mycobacterium xenopi; ATCC 19250.
XX
XX US2005100915-A1.
XX
XX 12-MAY-2005.
XX
XX 18-SEP-2003; 2003US-00665708.
XX
XX 17-DEC-1999; 99US-0172190P.
XX 15-DEC-2000; 2000US-00738274.
XX
XX (BREN/) BRENTANO S T.
XX (JUCK/) JUCKER M T.
XX (DELG/) DELGADO F D.
XX (CLEU/) CLEUZIAZ P.
XX (RODR/) RODRIGUE M.
XX
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2005-345392/35.
XX
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX in a biological sample, comprises using in vitro nucleic acid

```

PT amplification and detection of amplified products.
PS Claim 1; SEQ ID NO 24; 21pp; English.
XX
CC The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample. The method involves using in
CC vitro nucleic acid amplification and detection of amplified products. The
CC invention is useful for diagnostic detection of pathogenic bacteria such
CC as Mycobacterium species. The present sequence is the Mycobacterium
CC xenopi (ATCC 19250) 16S ribosomal RNA (16SrRNA) amplifying non-T7 PCR
CC primer.
XX
SQ Sequence 19 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 86.4%; Score 19; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GAACGGAAGGCTTCGG 22
Db 1 GAACGGAAGGCTTCGG 19
RESULT 17
ADP94057
ID ADP94057 standard; DNA; 50 BP.
XX
XX
AC ADP94057;
XX
XX 11-MAR-2004 (first entry)
XX
DE Microorganism detection probe, SEQ ID 150.
XX
XX Probe; detection; identification; microorganism; food; drug;
KW 16S rRNA V1 region; 16S rRNA V2 region; 16S rRNA V3 region; ss.
XX
XX Mycobacterium gordonae.
XX
XX W02003106676-A1.
XX
PD 24-DEC-2003.
XX
XX 16-JUN-2003; 2003WO-JP007620.
XX
PF 14-JUN-2002; 2002JP-00174564.
XX
XX (HISF) HITACHI SOFTWARE ENG CO LTD.
PA (MITS-) MITSUBISHI KAGAKU BIO-CLINICAL LAB INC.
XX
XX Hashida J, Ueno S, Muto I, Naruse K, Tamura M, Matsuda K;
PI Shimadzu M, Kobayashi I, Ishiko H;
XX
XX WPI; 2004-071565/07.
XX
XX 20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a
PT microorganism for specific detection and identification of the
PT microorganism in foods and drug compositions.
XX
PS Claim 2; SEQ ID NO 150; 150pp; Japanese.
XX
XX The present invention relates to probes (ADP93908-ADP94059) for the
CC specific detection and identification of harmful microorganisms in
CC samples of foods and drug compositions. The probe sequences are derived
CC from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism,
CC or its complementary sequence. Detection and identification of the
CC microorganism is by amplification of the complete 16S rRNA gene using
CC primers ADP94060 and ADP94061, labelling the amplification product (a
CC fluorescence label is preferred), and hybridising to the probe or probes
CC of the invention. The probes may be immobilised on a DNA chip. The
CC microorganism is selected from Actinobacillus actinomycetocombitans,
CC Acinetobacter calcoaceticus, Haemophilus influenzae, Stenotrophomonas
CC maltophilia, Proteus mirabilis, Streptococcus pneumoniae, Pseudomonas
CC aeruginosa, Citrobacter freundii, Veillonella parvula, Providencia

CC stuartii, Neisseria gonorrhoeae, Streptococcus agalactiae, Morganella
CC morganii, Bacteroides fragilis, Staphylococcus hominis, Staphylococcus
CC warneri, Staphylococcus epidermidis, Enterobacter cloacae, Enterobacter
CC aerogenes, Staphylococcus epidermidis, Streptococcus constellatus,
CC Serratia marcescens, Streptococcus anginosus, Escherichia coli,
CC Klebsiella pneumoniae, Enterococcus faecalis, Enterococcus faecium,
CC Streptococcus sanguis, Streptococcus mitis, Streptococcus intermedius,
CC Listeria monocytogenes, Clostridium perfringens, Corynebacterium
CC aquarium, Streptococcus oralis, Staphylococcus aureus, Neisseria
CC meningitidis, Campylobacter fetus, Enterococcus gallinarum, Enterococcus
CC casseliflavus, Aeromonas hydrophila, Salmonella paratyphi, Salmonella
CC typhi, Streptococcus equisimilis, Streptococcus canis, Klebsiella
CC oxytoca, Staphylococcus saprophyticus, Pasteurella multocida, Eikenella
CC corrodens, Streptococcus pyogenes, Moraxella catarrhalis, Legionella
CC pneumophila, Mycobacterium tuberculosis, Mycobacterium avium,
CC Mycobacterium intracellulare, Mycobacterium kansasii or Mycobacterium
CC gordonae.
XX
SQ Sequence 50 BP; 12 A; 11 C; 19 G; 8 T; 0 U; 0 Other;
Query Match 85.5%; Score 18.8; DB 12; Length 50;
Best Local Similarity 90.9%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GTCGAACGGAAGGCTTCGG 22
Db 7 GTCGAACGGAAGGCTTCGG 28
RESULT 18
AAX32481
ID AAX32481 standard; DNA; 166 BP.
XX
XX AAX32481;
XX
DT 22-JUN-1999 (first entry)
XX
DE Preferred probe of the invention.
XX
KW 16S rRNA; maduromycetes; hybridisation; streptomycetes; probe; ss.
XX
XX Synthetic.
OS Streptomyces ambofaciens.
XX
XX W09914361-A1.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-EP006038.
XX
XX 18-SEP-1997; 97US-0059295P.
PR 16-DEC-1997; 97US-0069748P.
XX
XX (MERI) MERCK SHARP & DOHME ESPANA SAE.
XX
XX Genilloud O, Mellado RP, Parro V, Rodriguez V;
XX WPI; 1999-229548/19.
XX
XX New probes used for detection of maduromycetes bacteria and to
PT differentiate between maduromycetes and streptomycetes.
XX
PS Disclosure; Fig 1; 22pp; English.
XX
XX The invention relates to a novel nucleic acid probe hybridises to a
CC nucleic acid encoding a portion of 16S rRNA of maduromycetes bacteria
CC under hybridisation conditions, and does not hybridise to nucleic acids
CC encoding a portion of 16S rRNA of streptomycetes under identical
CC hybridisation conditions. The probes can be used for detecting the
CC presence of maduromycetes bacteria in a sample and for differentiating
CC between maduromycetes and streptomycetes bacteria in a sample. The
CC present sequence represents a preferred probe of the invention
XX

SQ Sequence 166 BP; 39 A; 43 C; 55 G; 29 T; 0 U; 0 Other;

Query Match 85.5%; Score 18.8; DB 2; Length 166;
Best Local Similarity 90.9%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCTTTCGG 22
Db 60 GTCGACGGAAGGCTTTCGG 81

RESULT 19
ABZ76674
ID ABZ76674 standard; DNA; 460 BP.
XX AC ABZ76674;
XX DT 30-APR-2003 (first entry)
XX DE Microtrasporea recticata IF014525 DNA sequence SEQ ID NO:5.
XX KW Streptomyces sp. TM-7; pravastatin; compactin; hyperlipidaemia;
XX KW antilipaeamic; microorganism; gene; ds.
XX OS Nonomuraea recticata.
XX PN WO200299109-A1.
XX PD 12-DEC-2002.
XX PF 30-MAY-2002; 2002WO-JP005252.
XX PR 01-JUN-2001; 2001JP-00166412.
XX PA (SAOC) MERCIAN CORP.
XX PI Fujii T, Hirose S, Aritoku Y, Morimiya T, Johdo O, Ieshiki K;
XX WPI; 2003-148672/14.
XX PT Novel Streptomyces sp. produced polypeptide for hydroxylation of
PT compactin at 6beta-position and its encoded DNA, applicable in
PT constructing transformant microbes to synthesize pravastatin for treating
PT hyperlipedemia.
XX PS Disclosure; Page 50-51; 67pp; Japanese.
XX CC The present invention describes a DNA sequence which contains a base
CC sequence from bases 544-1758 in the sequence of (1) with 1992 base pairs,
CC or a DNA hybridisable with the DNA under stringent conditions and
CC encoding a polypeptide with hydroxylase activity on compactin at 6beta-
CC position. Also described: (1) DNA containing base sequences from bases
CC 544-1758 and from bases 1782-1970 in the sequence of (1) or a DNA
CC hybridisable with the DNA under stringent conditions and encoding a
CC polypeptide with hydroxylase activity on compactin at the 6beta-position;
CC (2) a polypeptide encoded by any of the DNA or containing an amino acid
CC sequence based on the polypeptide but with some amino acids deleted,
CC substituted or added and having hydroxylase activity on compactin at the
CC 6beta-position; (3) a recombinant DNA obtained by integrating with any of
CC the DNA; (4) a microorganism transferred with the recombinant DNA; (5) a
CC process for producing pravastatin by culturing the transformant
CC microorganism before isolating the culture liquor or cells, and addition
CC of compactin for reaction to give pravastatin for recovery; and (6)
CC Streptomyces sp. TM-6 (FERM BP-8002) or TM-7 (FERM BP-8003). (1) has
CC antilipaeamic activity. The polypeptide and its encoded DNA are applicable
CC in constructing transformant microorganisms to synthesise pravastatin for
CC treating hyperlipidaemia. With the recombinant microorganisms,
CC pravastatin can be produced efficiently, with much less galpha
CC hydroxylated epimer formed. The present sequence represents a
CC Microtrasporea recticata IF014525 nucleotide sequence, which is given
CC in the exemplification of the present invention
XX SQ Sequence 460 BP; 97 A; 119 C; 166 G; 78 T; 0 U; 0 Other;

Query Match 85.5%; Score 18.8; DB 2; Length 166;
Best Local Similarity 90.9%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCTTTCGG 22
Db 60 GTCGACGGAAGGCTTTCGG 81

RESULT 20
ABZ76673
ID AEB72673 standard; DNA; 497 BP.
XX AC AEB72673;
XX DT 06-OCT-2005 (first entry)
XX DE Streptosporangium sp. AF935 16S rDNA, SEQ ID 2.
XX KW cyclosporin; cyclosporin A; ds.
XX OS Streptosporangium sp.
XX PN JP2005198543-A.
XX PD 28-JUL-2005.
XX PF 15-JAN-2004; 2004JP-00007488.
XX PR 15-JAN-2004; 2004JP-00007488.
XX PA (SAOC) MERCIAN CORP.
XX PI Ota K, Uematsu H, Kaneko K, Tsuchida T;
XX WPI; 2005-537020/55.
XX PT Producing cyclosporin derivative useful as reference standard for
PT quantitative measurement of cyclosporin A in blood, by incubating
PT cyclosporin A in presence of Dactyloporangium and extracting cyclosporin
PT derivative.
XX PS Disclosure; SEQ ID NO 2; 12pp; Japanese.
XX CC The invention relates to a novel method for producing a cyclosporin
CC derivative. The method involves incubating cyclosporin A in the presence
CC of a strain belonging to Dactyloporangium, Streptomyces, Nocardia,
CC Pseudonocardia or Streptosporangium or its cultured microbial cells and
CC extracting the cyclosporin derivative from the incubated liquid. The
CC cyclosporin derivative is used as a reference standard for quantitative
CC measurement of cyclosporin A and its metabolite in blood and urine. This
CC polynucleotide represents a Streptosporangium 16S rDNA sequence used in
CC the cyclosporin production method of the invention.
XX SQ Sequence 497 BP; 105 A; 121 C; 178 G; 93 T; 0 U; 0 Other;

Query Match 85.5%; Score 18.8; DB 14; Length 497;
Best Local Similarity 90.9%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCTTTCGG 22
Db 57 GTCGACGGAAGGCTTTCGG 78

RESULT 21
AED64356
ID AED64356 standard; DNA; 500 BP.
XX AC AED64356;
XX DT 12-JAN-2006 (first entry)

XX Rhodococcus sp. 16S rDNA, SEQ ID 1.
 XX 16S ribosomal RNA; 16S rRNA; ds.
 XX Rhodococcus sp.; 2-35-1 strain.
 XX JP2005304498-A.
 XX 04-NOV-2005.
 XX 22-MAR-2005; 2005JP-00081977.
 XX 23-MAR-2004; 2004JP-00083956.
 XX (SANY-) SANYO FINE KK.
 XX Isobe K, Matsura A, Sakaguchi T;
 XX WPI; 2005-762911/78.
 XX Producing alpha-L- or -D-amino adipic acid semialdehyde derivative or its
 PT salt, involves oxidatively deaminating aminomethyl group of alpha-amino
 PT protecting group of L- or D-lysine, by utilizing oxidase derived from
 PT Rhodococcus.
 XX Disclosure; SEQ ID NO 1; 30pp; Japanese.
 XX The present invention relates to a method (M1) for producing alpha-L- or
 CC -D-amino adipic acid semialdehyde derivatives. The method involves
 CC oxidatively deaminating the aminomethyl group of the alpha-amino
 CC protecting group of L- or D-lysine into an aldehyde group, by utilizing
 CC an oxidase derived from Rhodococcus. The present sequence was used to
 CC illustrate the invention.
 XX Sequence 500 BP; 113 A; 120 C; 173 G; 88 T; 0 U; 6 Other;
 SQ Query Match 85.5%; Score 18.8; DB 14; Length 500;
 Best Local Similarity 90.9%; Pred. No. 20;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GTCGAACGGAAGGCTTTTCGG 22
 Db 57 GTCGAGCGGTAAAGGCTTTTCGG 78
 RESULT 22
 AD080217/c
 ID AD080217 standard; DNA; 1343 BP.
 XX AC AD080217;
 XX 29-JUL-2004 (first entry)
 XX Rhodococcus sp. GR-002 strain 16S rDNA.
 XX cyclic hydrocarbon degrading agent; Rhodococcus; gram positive bacillus;
 KW catalase test positive; nitrate-reduction ability positive;
 KW pyrazinamidase negative; pyrrolidonyl allyl amidase negative;
 KW alkali phosphatase positive; beta-glucuronidase negative;
 KW beta-galactosidase negative; alpha-glucosidase positive;
 KW N-acetyl-beta-glucosaminidase negative; urease positive; GR-002 strain;
 KW FERM P-18804; waste engine oil; aromatic hydrocarbon;
 KW cycloaliphatic hydrocarbon; polycyclic aromatic hydrocarbon; ds.
 XX Rhodococcus sp.
 XX JP2004113197-A.
 XX 15-APR-2004.
 XX 27-SEP-2002; 2002JP-00284521.
 XX

PR 27-SEP-2002; 2002JP-00284521.
 XX (GEIT-) GEITO KK.
 XX WPI; 2004-322544/30.
 XX Novel cyclic hydrocarbon degrading Rhodococcus species GR-002 strain
 PT having biochemical properties e.g. gram positive bacillus, catalase test
 PT positive, pyrazinamidase negative, useful for degrading waste engine oil.
 XX Claim 2; SEQ ID NO 1; 13pp; Japanese.
 XX The invention relates to a novel cyclic hydrocarbon degrading agent from
 CC the Rhodococcus genus. The cyclic hydrocarbon degrading agent having
 CC biochemical properties such as: gram positive bacillus, catalase test
 CC positive, nitrate-reduction ability positive, pyrazinamidase negative,
 CC pyrrolidonyl allyl amidase negative, alkali phosphatase positive, beta-
 CC glucuronidase negative, beta-galactosidase negative, alpha-glucosidase
 CC positive, N-acetyl-beta-glucosaminidase negative, urease positive. The
 CC novel Rhodococcus microorganism is Rhodococcus sp. GR-002 strain having
 CC the accession number FERM P-18804. The cyclic hydrocarbon degrading agent
 CC is useful for processing a cyclic hydrocarbon-containing substance, such
 CC as a waste engine oil. The novel Rhodococcus microorganism is useful for
 CC degrading cyclic hydrocarbons containing aromatic hydrocarbons, such
 CC cycloaliphatic hydrocarbons, and/or polycyclic aromatic hydrocarbons.
 CC This polynucleotide represents the novel Rhodococcus microorganism 16S
 CC rDNA sequence of the invention.
 XX Sequence 1343 BP; 263 A; 452 C; 320 G; 308 T; 0 U; 0 Other;
 SQ Query Match 85.5%; Score 18.8; DB 12; Length 1343;
 Best Local Similarity 90.9%; Pred. No. 22;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GTCGAACGGAAGGCTTTTCGG 22
 Db 1290 GTCGAGCGGTAAAGGCTTTTCGG 1269
 RESULT 23
 ADW16264
 ID ADW16264 standard; DNA; 1390 BP.
 XX AC ADW16264;
 XX 07-APR-2005 (first entry)
 XX DNA copy of the N_albus 16S ribosomal RNA EN46 isolate Seq 16.
 XX 16S ribosomal RNA; ds; 16S rRNA; medicinal plant; plant breeding;
 KW disease resistance; insect resistance; crop improvement;
 KW plant growth factor; antibacterial; antimicrobial; fungicide;
 KW insecticide; nematocide.
 XX Nocardioides albus.
 XX WO2005003328-A1.
 XX 13-JAN-2005.
 XX 07-JUL-2004; 2004WO-AU000914.
 XX 07-JUL-2003; 2003US-0485241P.
 XX 22-SEP-2003; 2003US-0504703P.
 XX (FLIN-) FLINDERS TECHNOLOGIES PTY LTD.
 XX Franco CMM, Coombs JT;
 XX WPI; 2005-091806/10.
 XX Improving plant productivity comprises introducing into the plant or
 PT propagation material an endophytic actinomycete that facilitates


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XX
SQ Sequence 1427 BP; 326 A; 351 C; 471 G; 277 T; 0 U; 2 Other;

Query Match      85.5%; Score 18.8; DB 14; Length 1427;
Best Local Similarity 90.9%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCGACGGGAAGGCCCTTTCGG 22
   ||||| ||||| ||||| ||||| |||||
Db 28 GTCGACGGGAAGGCCCTTTCGG 49

RESULT 26
ADZ35975
ID ADZ35975 standard; DNA; 1440 BP.
XX
AC ADZ35975;
XX
DT 30-JUN-2005 (first entry)
DE Verrucosisspora sp. AB-18-032 16S rRNA gene.
XX
KW ds; antibiotic; antimalarial; protozoacide; 16S rRNA;
KW polycyclic macrolactone; abyssomicin; p-Aminobenzoic acid; folic acid;
KW vitamin; abyssomicin B; abyssomicin C; abyssomicin D;
KW Staphylococcus aureus infection; protozoal infection;
KW Plasmodium infection; Leishmania infection; chagas disease;
KW Gram positive bacteria infection; mrsa infection .
XX
OS Verrucosisspora sp. AB-18-032.
XX
PN WO2005033114-A1.
XX
PD 14-APR-2005.
XX
PF 23-SEP-2004; 2004WO-EP010661.
XX
PR 01-OCT-2003; 2003DE-01047472.
XX
PR 11-NOV-2003; 2003DE-01053300.
XX
PA (UYTU-) UNIV TUBINGEN.
XX
PI Fiedler H, Suessmuth R, Zaehner H, Bull A;
XX
WPI; 2005-296122/30.
XX
New abyssomicin polycyclic macrolactone compounds, useful as antibiotics
and antiprotozoal agents effective against multiresistant strains,
prepared using bacteria of genus Verrucosisspora.
XX
Disclosure; SEQ ID NO 1; 47pp; German.
XX
This invention describes novel polycyclic macrolactones and their
derivatives , prepared using bacteria of genus Verrucosisspora and
designated abyssomicins. The polycyclic macrolactones have at least one
oxa-bicyclo system as a partial structure and at least one Michael system
as double bond system. The polycyclic macrolactones are prepared by
culturing Verrucosisspora strain AB 18-032, recovering a culture
supernatant from the culture, optionally preparing a culture filtrate and
optionally isolating one or more polycyclic macrolactones from the
supernatant and/or filtrate. Alternatively the microorganism is cultured
followed by isolating one or more polycyclic macrolactones from the
microorganism. The Verrucosisspora strain AB 18-032 was isolated from
marine sediment collected at a depth of 1000m in Sagami bay in the
Japanese sea and is deposited as DSM No. 15899. The polycyclic
macrolactones inhibit the biosynthesis of p-Aminobenzoic acid, (an
essential component in the biosynthesis of folic acid) from chorismic
acid, thus inhibiting folic acid biosynthesis. The vitamin folic acid is
essential to the life of microorganisms, especially prokaryotes and
protozoa. The polycyclic macrolactones do not inhibit the biosynthesis of
folic acid in mammals (including humans), and thus have no adverse
effects on mammalian cells. Three polycyclic macrolactones are
specifically claimed, i.e. abyssomicin B, abyssomicin C and abyssomicin

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CC D. Abyssomicin C strongly inhibited growth of methicillin-resistant
CC Staphylococcus aureus strain N315 and vancomycin-resistant Staphylococcus
CC aureus strain Mu50. The products of the invention are useful as
CC antibiotics (especially effective against Gram positive bacteria) and
CC antiprotozoal agents, specifically effective against bacteria and
CC protozoa resistant (especially multi-resistant) to conventional
CC antibiotics. Typically polycyclic macrolactones are useful for combating
CC tropical protozoal diseases (e.g. malaria, leishmaniasis, sleeping
CC sickness and Chagas disease) and infections caused by resistant Gram
CC positive bacteria such as methicillin- and vancomycin-resistant
CC Staphylococcus aureus strains. Polycyclic macrolactones are also useful
CC as disinfectants (especially in hospitals and other medical
CC establishments) and as lead structures for the development of further
CC active agents. This sequence represents the Verrucosisspora strain AB 18-
CC 032 16S rRNA DNA which is used to phylogenically classify the bacterial
CC strain.
XX
SQ Sequence 1440 BP; 313 A; 363 C; 500 G; 264 T; 0 U; 0 Other;

Query Match      85.5%; Score 18.8; DB 14; Length 1440;
Best Local Similarity 90.9%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCGAACGGGAAGGCCCTTTCGG 22
   ||||| ||||| ||||| ||||| |||||
Db 4 GTCGACGGGAAGGCCCTTTCGG 25

RESULT 27
ADX38843
ID ADX38843 standard; DNA; 1443 BP.
XX
AC ADX38843;
XX
DT 05-MAY-2005 (first entry)
DE Microbispora 16S rDNA.
XX
KW antibiotic; bacterial infection; animal growth; 16S rDNA; ds;
KW antibacterial; anabolic.
XX
OS Microbispora sp. ATCC PTA-5024.
XX
PN WO2005014628-A1.
XX
PD 17-FEB-2005.
XX
PF 12-JUL-2004; 2004WO-EP007658.
XX
PR 18-JUL-2003; 2003EP-00016306.
XX
PA (VICU-) VICURON PHARM INC.
XX
PI Lazzarini A, Gastaldo L, Candiani G, Ciciliato I, Losi D;
XX
PI Marinelli F, Selva E, Parenti F;
XX
WPI; 2005-173079/18.
XX
New antibiotic 107891 complex comprising Factor A1 and Factor A2 and
having specified physico-chemical characteristics, used to form
PT medicament for the treatment or prevention of bacterial infections, or
PT used as animal growth promoter.
XX
Disclosure; SEQ ID NO 1; 85pp; English.
XX
The invention relates to an antibiotic 107891 complex comprising Factor
CC A1 and Factor A2. The antibiotic is used to form a pharmaceutical
CC composition used as medicament for the treatment or prevention of
CC bacterial infections, or as animal growth promoter. The present sequence
CC represents the Microbispora 16S rDNA.
XX
SQ Sequence 1443 BP; 308 A; 352 C; 504 G; 279 T; 0 U; 0 Other;

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XX	Sequence 1461 BP; 319 A; 350 C; 500 G; 292 T; 0 U; 0 Other;
SQ	
	Query Match 85.5%; Score 18.8; DB 14; Length 1461;
	Best Local Similarity 90.9%; Pred. No. 22;
	Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1 GTCGAACGGAAGGCGCTTTCGG 22
DB	24 GTCGAACGTAAGGCCCTTCGG 45
RESULT 29	
AED35651	
ID	AED35651 standard; DNA; 1483 BP.
XX	
AC	AED35651;
XX	
DT	15-DEC-2005 (first entry)
XX	
DE	Pseudonocardia sp. 727713 melanocortin receptor modulator WS727713.
XX	
KW	ds; melanocortin receptor; cosmetics; brain injury; cerebroprotective;
KW	inflammation; renal disease; nephrotropic; ischemia;
KW	cardiovascular disease; Vasotropic; reperfusion injury; inflammation;
KW	hepatitis; Hepatotropic; Virucide; sepsis; septic shock; Antibacterial;
KW	Immunosuppressive; respiratory distress syndrome; Respiratory-Gen.;
KW	respiratory disease; rheumatoid arthritis; arthritis; Antirheumatic;
KW	Antiarthritic; immune disorder; gout; Antigout; osteoarthritis;
KW	osteopathic; nephritis; genitourinary disease; nephrotropic;
KW	hypersensitivity; Antiallergic; inflammatory bowel disease;
KW	Gastrointestinal-Gen.; gastrointestinal disease; Endocrine-Gen.;
KW	genitourinary disease; female sexual dysfunction;
KW	male sexual dysfunction; Gynecological; transplant rejection; Analgesic;
KW	pain; neurological disease; HIV infection; Anti-HIV; hypopigmentation;
KW	Dermatological; dermatological disease; tinea; Fungicide;
KW	diabetes mellitus; Antidiabetic; metabolic disorder; anorexia nervosa;
KW	Eating-Disorders-General.; Cardiovascular-Gen.; Anorectic;
KW	nutritional disorder; psychiatric disorder; fever; Antipyretic;
KW	temperature disorder; functional bowel disorder; obesity; pancreatitis;
KW	fibroid; scar tissue; keloid; scleroderma; graft versus host disease;
KW	liver cirrhosis; pulmonary fibrosis; nephropathy; Ophthalmological;
KW	uveitis; Behcets disease; hematological disease; sarcoidosis; vasculitis;
KW	infection; antimicrobial; celiac disease; melanoma; neoplasm; Cytostatic;
KW	Anabolic.
XX	
OS	Pseudonocardia sp. 727713.
XX	
PN	WO2005097973-A1.
XX	
PD	20-OCT-2005.
XX	
PF	22-MAR-2005; 2005WO-JP005653.
XX	
PR	08-APR-2004; 2004AU-00901919.
XX	
PA	(FUJI) FUJISAWA PHARM CO LTD.
XX	
PI	Otsuka T, Ueda H, Fujie K, Muramatsu H, Hashimoto M, Takase S;
XX	
DR	WPI; 2005-703551/72.
XX	
PT	New pure WS727713 compound which is a melanocortin receptor modulator
PT	useful as antiinflammatory and for treating e.g. hypoxic shock, acute
PT	respiratory distress syndrome, rheumatic arthritis and melanoma invasion.
XX	
PS	Disclosure; SEQ ID NO 1; 41pp; English.
XX	
CC	This invention describes a novel compound WS727713 isolated from
CC	Pseudonocardia sp. 727713 in a leaf litter sample. The compound is
CC	capable of modulating the melanocortin receptor and has a potent anti-
CC	inflammatory effect. The compound ca be used as a medicament or a
CC	cosmetic for treating or preventing ischemic reperfusion injury, brain

XX	Sequence 1461 BP; 319 A; 350 C; 500 G; 292 T; 0 U; 0 Other;
SQ	
	Query Match 85.5%; Score 18.8; DB 14; Length 1443;
	Best Local Similarity 90.9%; Pred. No. 22;
	Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1 GTCGAACGGAAGGCGCTTTCGG 22
DB	34 GTCGAGCGGAAGGCGCTTTCGG 55
RESULT 28	
AEA22406	
ID	AEA22406 standard; DNA; 1461 BP.
XX	
AC	AEA22406;
XX	
DT	25-AUG-2005 (first entry)
XX	
DE	Mycobacterium gordonae 16S rRNA sequence SEQ ID NO:7.
XX	
KW	microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
XX	
OS	Mycobacterium gordonae.
XX	
PN	US2005130168-A1.
XX	
PD	16-JUN-2005.
XX	
PP	31-OCT-2003; 2003US-00697802.
XX	
PR	31-OCT-2003; 2003US-00697802.
XX	
PA	(HANX/) HAN X.
PA	(PHAM/) PHAM A S.
PI	Han X, Pham AS;
XX	
DR	WPI; 2005-424597/43.
XX	
PT	Determining a bacterium species comprises providing oligonucleotide
PT	primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
XX	
PS	Disclosure; SEQ ID NO 7; 74pp; English.
XX	
CC	The invention relates to a method (M1) for determining a bacterium
CC	species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
CC	extracting a genomic nucleotide from the bacterium to provide a
CC	nucleotide template; (c) annealing a region of a nucleotide template to a
CC	specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
CC	complimentary fashion; the primer set designed to provide a product
CC	having a predetermined size dictated by a complementary primer set; (d)
CC	amplifying the region of the nucleotide template to produce the product;
CC	and (e) determining a species of a bacterium in a nucleotide sequence of
CC	the product. Also described is an alternative method (M2) for determining
CC	a bacterium species comprising: (a) providing a specimen or a sample
CC	having a template; (b) providing a pair of primers selected from: (i) a
CC	first forward primer having consecutive bases of an AFB-f comprising any
CC	of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
CC	or variations and a first reverse primer having consecutive bases of an
CC	AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
CC	or their fragments or variations, (ii) a second forward primer having
CC	consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
CC	bp (AEA22489-AEA22516) or their fragments or variations and a second
CC	reverse primer having consecutive bases of an UB-r comprising any of the
CC	28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
CC	variations, or (iii) a first forward primer having consecutive bases of
CC	an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
CC	second reverse primer having consecutive bases of an UB-r of AEA22517-
CC	AEA22544 or their fragments or variations; (c) the specimen; and (d)
CC	comparing the product from the specimen with a nucleotide sequence from a
CC	database to determine the bacterium species present in the specimen. The
CC	methods are useful for determining a bacterium species. The present
CC	sequence represents a Mycobacterium gordonae 16S rRNA nucleotide
CC	sequence, which is used in the exemplification of the present invention.

CC and renal inflammatory diseases, hepatitis, sepsis/septic shock, hypoxic
CC shock, acute respiratory distress syndrome (ARDS), rheumatic arthritis,
CC gouty arthritis, aortic regurgitation, juvenile chronic arthritis,
CC osteoarthritis, nephritis, induction of tolerance, contact
CC hypersensitivity, inflammatory bowel disease, sexual dysfunction,
CC transplantation, pain, disease progression of HIV, post inflammatory hypo
CC pigmentation, tinea versicolor, idiopathic guttate hypomelanosis, fever,
CC functional bowel disease, obesity, satiety effect, diabetes mellitus,
CC modulation of dermal exocrine function, canities (canities
CC circumscripta), gray hair, pancreatitis, fibrotic disorders (hypertrophic
CC scars, keloids, localized scleroderma, systematic sclerosis, sclerodermic
CC graft versus host disease of the skin, cirrhosis of the liver, idiopathic
CC and bleomycin induced lung fibrosis, cyclosporin induced nephropathy),
CC uveitis (especially in Behcet's syndrome and sarcoidosis), vasculitis,
CC microbial infections, celiac disease, vulvar vestibulitis syndrome,
CC melanoma invasion or anorexia in human or an animal.
XX
SQ Sequence 1483 BP; 320 A; 360 C; 509 G; 289 T; 0 U; 5 Other;

Query Match 85.5%; Score 18.8; DB 14; Length 1483;
Best Local Similarity 90.9%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTTTCGG 22
||||| ||| |||||||||
Db 35 GTCGAGCGGTAAAGCCTTTTCGG 56

RESULT 30
ADR90327
ID ADR90327 standard; DNA; 1511 BP.
XX
AC ADR90327;
XX
DT 16-DEC-2004 (first entry)
XX
DE Rhodococcus sp. M-15 bioremediation-related 16S rDNA.
XX
KW alkane; petroleum; bioremediation; 16S ribosomal RNA; 16S rRNA; ds.
XX
OS Rhodococcus sp.
XX
PN JP2004261126-A.
XX
PD 24-SEP-2004.
XX
PF 03-MAR-2003; 2003JP-00056155.
XX
PR 03-MAR-2003; 2003JP-00056155.
XX
PA (EBAR) EBARA CORP.
XX
XX WPI; 2004-665486/65.
XX
PT Evaluating the ability of an environmental sample to degrade alkanes for
PT providing alkane degrading bacteria, comprises measuring alkane degrading
PT bacteria having high resolving power of alkane present in petroleum.
XX
FS Claim 1; SEQ ID NO 3; 33pp; Japanese.
XX
CC The invention relates to a novel method for evaluating the ability of an
CC environmental sample to degrade alkanes. The method comprises measuring
CC the number of alkane-degrading bacteria present in the sample, where the
CC bacteria have high resolving power of a type of alkane present in
CC petroleum and gyrB (gyrase beta subunit) DNA and 16S rDNA. The method of
CC the invention may be useful for evaluating the ability of an
CC environmental sample to degrade alkanes and thus, for providing alkane-
CC degrading bacteria to be utilised in bioremediation of an environment
CC contaminated with petroleum. The method is rapid and simple. The current
CC sequence is that of the Rhodococcus sp. M-15 bioremediation-related 16S
CC ribosomal RNA gene (rDNA) of the invention.
XX
SQ Sequence 1511 BP; 342 A; 362 C; 510 G; 297 T; 0 U; 0 Other;

Query Match 85.5%; Score 18.8; DB 13; Length 1511;
Best Local Similarity 90.9%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTTTCGG 22
||||| ||| |||||||||
Db 54 GTCGAGCGGTAAAGCCTTTTCGG 75

RESULT 32
AED11327
ID AED11327 standard; DNA; 1511 BP.
XX
AC AED11327;
XX
DT 01-DEC-2005 (first entry)
XX

Query Match 85.5%; Score 18.8; DB 13; Length 1511;
Best Local Similarity 90.9%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTTTCGG 22
||||| ||| |||||||||
Db 54 GTCGAGCGGTAAAGCCTTTTCGG 75

RESULT 31
ADR90325
ID ADR90325 standard; DNA; 1511 BP.
XX
AC ADR90325;
XX
DT 16-DEC-2004 (first entry)
XX
DE Rhodococcus sp. M-13 bioremediation-related 16S rDNA.
XX
KW alkane; petroleum; bioremediation; 16S ribosomal RNA; 16S rRNA; ds.
XX
OS Rhodococcus sp.
XX
PN JP2004261126-A.
XX
PD 24-SEP-2004.
XX
PF 03-MAR-2003; 2003JP-00056155.
XX
PR 03-MAR-2003; 2003JP-00056155.
XX
PA (EBAR) EBARA CORP.
XX
XX WPI; 2004-665486/65.
XX
PT Evaluating the ability of an environmental sample to degrade alkanes for
PT providing alkane degrading bacteria, comprises measuring alkane degrading
PT bacteria having high resolving power of alkane present in petroleum.
XX
FS Claim 1; SEQ ID NO 1; 33pp; Japanese.
XX
CC The invention relates to a novel method for evaluating the ability of an
CC environmental sample to degrade alkanes. The method comprises measuring
CC the number of alkane-degrading bacteria present in the sample, where the
CC bacteria have high resolving power of a type of alkane present in
CC petroleum and gyrB (gyrase beta subunit) DNA and 16S rDNA. The method of
CC the invention may be useful for evaluating the ability of an
CC environmental sample to degrade alkanes and thus, for providing alkane-
CC degrading bacteria to be utilised in bioremediation of an environment
CC contaminated with petroleum. The method is rapid and simple. The current
CC sequence is that of the Rhodococcus sp. M-13 bioremediation-related 16S
CC ribosomal RNA gene (rDNA) of the invention.
XX
SQ Sequence 1511 BP; 343 A; 367 C; 507 G; 294 T; 0 U; 0 Other;

Query Match 85.5%; Score 18.8; DB 13; Length 1511;
Best Local Similarity 90.9%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTTTCGG 22
||||| ||| |||||||||
Db 54 GTCGAGCGGTAAAGCCTTTTCGG 75

RESULT 32
AED11327
ID AED11327 standard; DNA; 1511 BP.
XX
AC AED11327;
XX
DT 01-DEC-2005 (first entry)
XX

DE Aliphatic hydrocarbon degrading R. erythropolis strain 16S rRNA gene.
 XX degradation; aliphatic hydrocarbon; bioremediation; oil degradation;
 KW pollutant; degradation; groundwater decontamination; 16S rRNA;
 KW 16S ribosomal RNA; gene; ds.
 OS Rhodococcus erythropolis.
 XX JP2005261218-A.
 PN 29-SEP-2005.
 PD 16-MAR-2004; 2004JP-00074370.
 PF 16-MAR-2004; 2004JP-00074370.
 PR (EBAR) EBARA CORP.
 XX Karube M, Tamatsubo K, Miya A;
 PI WPI; 2005-678804/70.
 DR Novel Rhodococcus erythropolis M-13 strain capable of degrading aliphatic
 XX hydrocarbon, useful for bioremediation of oil-polluted environment such
 PT as river water, underground water, ocean, sea cost.
 PT Claim 1; SEQ ID NO 1; 14pp; Japanese.
 PS The invention relates to a novel Rhodococcus erythropolis M-13 strain
 XX capable of degrading aliphatic hydrocarbons. The invention further
 CC provides the 16S rRNA gene of the novel strain showing 98% or more
 CC homology with a nucleotide sequence of a fully defined 1511 nucleotide
 CC (AED11327) sequence given in specification. The novel strain is useful
 CC for the bioremediation of an oil-polluted environment, such as river
 CC water, underground water, ocean, sea cost, etc. The novel strain degrades
 CC linear or branched aliphatic hydrocarbons efficiently. This
 CC polynucleotide sequence represents the DNA of the novel Rhodococcus
 CC erythropolis M-13 strain 16S rRNA gene of the invention.
 XX
 SQ Sequence 1511 BP; 343 A; 367 C; 507 G; 294 T; 0 U; 0 Other;
 Query Match 85.5%; Score 18.8; DB 14; Length 1511;
 Best Local Similarity 90.9%; Pred. No. 22;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GTCGAACGGAAGGCTTTTCGG 22
 DB 54 GTCGAGCGTAAGGCTTTTCGG 75
 RESULT 33
 ADE41084
 ID ADE41084 standard; rRNA; 1584 BP.
 XX ADE41084;
 AC 29-JAN-2004 (first entry)
 DT . corallina partial 16S rRNA sequence.
 XX Antibiotic; ss; 16S rRNA; MF-BA-1768alpal; MF-BA-1768betal;
 KW Staphylococcus; Enterococcus; Streptococcus; Haemophilus; Escherichia;
 KW bacterial infection.
 XX Microbispora corallina; strain NRRL 30420.
 OS US6551591-B1.
 XX 22-APR-2003.
 PD 07-SEP-2001; 2001US-00949230.
 PF 07-SEP-2001; 2001US-00949230.
 XX 07-SEP-2001; 2001US-00949230.
 PR

XX (ESSE-) ESSENTIAL THERAPEUTICS INC.
 PA Lee MD;
 PI WPI; 2003-895156/82.
 DR Novel antibiotics isolated from fermentation broth of novel strain of
 XX Microbispora corallina, useful for treating a wide range of bacterial
 PT infections.
 PT Disclosure; SEQ ID NO 1; 20pp; English.
 PS The invention relates to antibiotic MF-BA-1768alpal or MF-BA-1768-betal
 XX or its pharmaceutically acceptable salt, having physicochemical
 CC characteristics in the non-salt form as detailed in the specification.
 CC The antibiotics are isolated from a novel strain of Microbispora
 CC corallina designated NRRL 30420. Also included are producing the above
 CC antibiotic (by cultivating Microbispora corallina NRRL 30420, or an
 CC antibiotic MF-BA-1768alpal or MF-BA-1768betal -producing mutant,
 CC variant or its recombinant form, in a culture medium containing
 CC assimilable sources of carbon, nitrogen and inorganic salts under aerobic
 CC fermentation conditions until the antibiotic is produced and then
 CC recovering the antibiotic) and a composition comprising the above
 CC antibiotic or its salt. The antibiotics are useful for treating a
 CC bacterial infection caused by Staphylococcus (e.g. S. aureus, S. epidermis
 CC, S. haemolyticus), Enterococcus (e.g. E. faecalis, E. faecium),
 CC Streptococcus (e.g. S. pneumoniae, S. pyogenes), Haemophilus (e.g.
 CC H. influenzae) or Escherichia (e.g. E. coli) in a patient. The present
 CC sequence is partial 16S rRNA sequence from M. corallina NRRL 30420, which
 CC identifies the strain.
 XX
 SQ Sequence 1584 BP; 339 A; 384 C; 525 G; 320 T; 0 U; 16 Other;
 Query Match 85.5%; Score 18.8; DB 10; Length 1584;
 Best Local Similarity 90.9%; Pred. No. 22;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GTCGAACGGAAGGCTTTTCGG 22
 DB 128 GTCGAGCGGAAGGCTTTTCGG 149
 RESULT 34
 AED48445/C
 ID AED48445 standard; DNA; 84222 BP.
 XX AED48445;
 AC 15-DEC-2005 (first entry)
 XX M. echinospora gentamycin biosynthetic gene cluster DNA.
 DT ds; gene; antibiotic; virucide; aminoglycoside; bacterial infection;
 DE viral infection; gentamycin; genP; gmrB; genB1; genQ; genD3; gmrA;
 KW genS1; genC; genD2; genM2; genD1; genS2; genB4; genB3; genK;
 KW genB2; genX; genU; genT; genE; genY; genA; genF; genG; genH; genI; genJ;
 KW genL; genN; DNA polymerase beta chain; integral membrane protein;
 KW agglutinin; esterase; Trp-trRNA ligase;
 KW quinine/archaeosine tRNA-ribosyltransferase; ribosomal methyltransferase;
 KW gentamicin (hexosaminyl-6-)aminotransferase I; gentamicin oxidoreductase;
 KW (N-acetyl-) hexosaminyltransferase; ribosomal methyltransferase;
 KW L-glutamine:ketocyclitol; 2-deoxy-scyllitol-inosose synthase;
 KW gentamicin glycosyltransferase II; gentamicin aminotransferase I;
 KW gentamicin production protein; gentamicin aminotransferase IV;
 KW aminoglycoside 3'-phosphotransferase; gentamicin aminotransferase III;
 KW gentamicin C-methyltransferase; gentamicin aminotransferase II;
 KW gentamicin exporter; aminocyclitol 1-dehydrogenase; cation transporter;
 KW gentamicin methyltransferase; two-component system histidine kinase;
 KW two-component system response regulator; serine protease;
 KW DNA polymerase III epsilon subunit; RNA polymerase sigma factor;
 KW subunitase; transcriptional regulator; acetyltransferase;
 KW ATP-binding protein; ABC-transporter, permease component.


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FT      /tag= aj
FT      /product= "putative gentamicin production protein"
FT      /gene= "genA"
FT      CDS      49734..50381
FT      /tag= ak
FT      /gene= "genF"
FT      /product= "putative gentamicin production protein"
FT      /tag= al
FT      CDS      50381..50734
FT      /product= "putative gentamicin production protein"
FT      /gene= "genG"
FT      /tag= am
FT      CDS      complement(50813..54229)
FT      /product= "putative gentamicin exporter"
FT      /gene= "genH"
FT      /tag= an
FT      CDS      complement(54226..56163)
FT      /gene= "genI"
FT      /product= "putative gentamicin exporter"
FT      /tag= ao
FT      CDS      complement(56689..57627)
FT      /gene= "genJ"
FT      /product= "putative gentamicin production protein"
FT      /tag= ap
FT      CDS      58121..58741
FT      /product= "putative gentamicin production protein"

Query Match      85.5%; Score 18.8; DB 14; Length 84222;
Best Local Similarity 90.9%; Pred. No. 34;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1      GTCGACGGAAAGGCTTTCG 22
Db      15392      GTCGACGGAAAGGCTTTCG 15371

RESULT 35
ID      AAD57239/c
AC      AAD57239;
XX
XX      06-NOV-2003 (first entry)
XX      Human CGDD-19 cDNA.
XX
XX      Human; cell growth, differentiation and death protein; CGDD; leukaemia;
XX      neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;
XX      muscular disorder; myotonic dystrophy; catatonia; endocrine disorder;
XX      diabetes; Grave's disease; cancer; immunological disorder; scleroderma;
XX      systemic lupus erythematosus; allergy; Crohn's disease; renal disorder;
XX      gastrointestinal disorder; Goodpasture's syndrome; infection; cirrhosis;
XX      cardiovascular disorder; atherosclerosis; hepatic disease; transgenic;
XX      transgenic animal; gene therapy; neuroprotective; relaxant; cycostatic;
XX      dermatological; immunosuppressive; cerebroprotective; anticonvulsant;
XX      antibacterial; antiparasitic; fungicide; virucide; uropathic; cardiant;
XX      protozoacide; nootropic; gene; ss.
XX
XX      Homo sapiens.
XX
XX      Key      Location/Qualifiers
XX      CDS      112..687
XX      /tag= a
XX      /product= "Human CGDD-19 protein"
XX
XX      WO2003050253-A2.
XX
XX      19-JUN-2003.
XX
XX      04-DEC-2002; 2002WO-US039133.
XX
XX      07-DEC-2001; 2001US-0340747P.
XX      20-DEC-2001; 2001US-0342761P.

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PR      15-JAN-2002; 2002US-0349705P.
PR      06-FEB-2002; 2002US-0354764P.
PR      12-FEB-2002; 2002US-0356216P.
XX
XX      (INCY-) INCYTE GENOMICS INC.
XX
XX      Griffin JA, Rankumar J, Emerling BM, Kable AE, Elliott VS,
XX      Marquis JP, Baughn MR, Gorvad AE, Yue H, Lee EA, Becha SD, Tang YT,
XX      Tran UK, Swarnakar A, Lee S, Ison CH, Hafalia AJA, Tran B,
XX      Sprague WW, Lee SY, Khate R, Gandhi AR, Gietzen KJ, Bhatia U,
XX      Burriil JD, Blake JJ, Ho A, Zheng W;
XX
XX      WPI; 2003-532903/50.
XX      P-PSDB; AAE37930.
XX
XX      New CGDD polypeptides, useful for diagnosing, preventing, and treating
XX      disorders associated with an abnormal expression or activity of CGDD,
XX      e.g. neuromuscular, immunological, cardiovascular disorders, cancer
XX      and/or infections.
XX
XX      Claim 5; Page 283; 299pp; English.
XX
XX      The present invention relates to novel cell growth, differentiation and
XX      death (CGDD) proteins and polynucleotides encoding them. The sequences of
XX      the invention are useful in diagnosing, preventing and treating disorders
XX      associated with an abnormal expression or activity of CGDD such as
XX      neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's
XX      disease), muscular disorders (e.g. myotonic dystrophy, catatonia),
XX      endocrine disorders (e.g. diabetes, Grave's disease), cancers (e.g.
XX      leukaemia, cervical or breast cancers), immunological disorders (e.g.
XX      scleroderma, systemic lupus erythematosus, allergies), gastrointestinal
XX      disorders (e.g. Crohn's disease), renal disorders (e.g. Goodpasture's
XX      syndrome), infections (e.g. viral, bacterial, fungal, parasitic,
XX      protozoal, helminthic), cardiovascular disorders (e.g. atherosclerosis)
XX      and hepatic diseases (e.g. cirrhosis). The polynucleotides can be used to
XX      create humanised animals or transgenic animals to model human diseases.
XX      The invention is also used in gene therapy. The present sequence is human
XX      CGDD-19 cDNA
XX
XX      Sequence 1137 BP; 317 A; 274 C; 296 G; 250 T; 0 U; 0 Other;

Query Match      81.8%; Score 18; DB 9; Length 1137;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3      CGAACGGAAAGGCTTTC 20
Db      1071      CGAACGGAAAGGCTTTC 1054

RESULT 36
ADCG1232
ID      ADGC61232 standard; DNA; 1439 BP.
XX
XX      AC      ADGC61232;
XX
XX      18-DEC-2003 (first entry)
XX
XX      DE      Baeyer-Villiger enzyme 16s rDNA gene from Rhodococcus erythropolis AN12.
XX      Baeyer-Villiger; BV; monooxygenase; ketone substrate; lactone; ester;
XX      16s rDNA; ds.
XX
XX      OS      Rhodococcus erythropolis.
XX
XX      PN      WO2003020890-A2.
XX      PD      13-MAR-2003.
XX
XX      PF      29-AUG-2002; 2002WO-US027549.
XX      PR      29-AUG-2001; 2001US-0315546P.
XX

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PA (DUPO ) DU FONT DE NEMOURS & CO E I.
XX
PI Bramucci MG, Brzostowicz PC, Kostichka KN, Nagarajan V;
PI Rouviere PE, Thomas SM;
XX
DR WPI; 2003-313085/30.
XX
PT Novel nucleic acid fragment useful for converting ketone substrates to
XX the corresponding lactone or ester, is isolated from Rhodococcus,
PT Arthrobacter or Acidovorax, encoding Baeyer-Villiger monooxygenase
PT polypeptide.
XX
PS Claim 54; SEQ ID NO 6; 225pp; English.
XX
XX The invention relates to a novel isolated nucleic acid fragment
CC comprising a fragment encoding a Baeyer-Villiger (BV) monooxygenase
CC polypeptide having a sequence of 542, 541, 439, 518, 462, 523, 493, 539,
CC 649, 494, 499, 545, 532 or 538 amino acids defined in the specification;
CC a nucleic acid molecule that hybridises with the above sequence under the
CC hybridisation conditions; or their complements. The BV monooxygenase
CC fragment is useful for obtaining a nucleic acid fragment encoding a BV
CC monooxygenase polypeptide, by probing a genomic library with the
CC fragment, identifying a DNA clone that hybridises with the fragment, and
CC sequencing the genomic fragment that comprises the above identified
CC clone, where the sequenced genomic fragment encodes a BV monooxygenase
CC polypeptide. The genes and their products are useful for converting
CC suitable ketone substrates to the corresponding lactone or ester. This
CC polynucleotide sequence represents the 16S rRNA gene from Arthrobacter
CC sp. BP2 relating to the Baeyer-Villiger enzymes of the invention.
XX
SQ Sequence 1439 BP; 333 A; 357 C; 465 G; 283 T; 0 U; 1 Other;

Query Match 80.9%; Score 17.8; DB 10; Length 1439;
Best Local Similarity 90.5%; Pred. No. 71;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTCCG 22
Db 36 TCGAGCGGTAAGGCGCTTTCCG 56

RESULT 37
AAV24418
ID AAV24418 standard; preRNA; 25 BP.
AC
AC AAV24418;
XX
XX 24-AUG-1998 (first entry)
XX
XX Target sequence #2 for M. simiae specific probe.
XX
DE Probe; target sequence; hybridisation; mycobacterial cell sensitivity;
XX antimicrobial agent; pre-rRNA detection; ss.
XX
OS Synthetic.
OS Mycobacterium simiae.
XX
XX US5770373-A.
XX
XX 23-JUN-1998.
XX
XX 08-NOV-1996; 96US-00745638.
XX
XX 16-JUN-1994; 94US-00261068.
XX
XX 07-JUN-1995; 95US-00485602.
XX
XX (BECT ) BECTON DICKINSON & CO.
XX
XX Cangelosi GA, Britschgi TB;
XX
XX WPI; 1998-376792/32.
XX
XX Mycobacterial sensitivity and drug screening assays - involving release

of pre-rRNA by lysis.
XX
XX Example 4; Col 17-18; 50pp; English.
XX
CC This sequence represents a target sequence for mycobacterial probes. This
CC sequence represents a precursor RNA fragment that is released during the
CC method of the invention. The method is for the determination of
CC mycobacterial cell sensitivity to an antimicrobial agent, and comprises:
CC (a) culturing the cells in the presence of the antimicrobial agent; (b)
CC treating the cells by enzymatic or mechanical means to expose the cell
CC membrane to lysis reagents, and contacting the cells with a lysis reagent
CC under conditions such that pre-rRNA is released from the cells but not
CC degraded; and (c) detecting the pre-rRNA with an oligonucleotide probe
CC capable of hybridising to a region of the pre-rRNA that is not present in
CC mature mycobacterial rRNA, where sensitivity to the antimicrobial agent
CC is indicated by an increase or decrease in pre-rRNA levels for cells
CC exposed to the antimicrobial agent compared with mycobacterial cells not
CC exposed to the antimicrobial agent. The lysis method, unlike known
CC methods, results in detectable levels of pre-rRNA
XX
SQ Sequence 25 BP; 6 A; 7 C; 7 G; 0 T; 3 U; 2 Other;

Query Match 79.1%; Score 17.4; DB 2; Length 25;
Best Local Similarity 80.0%; Pred. No. 74;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCGCTTTCCG 22
Db 1 CGAACGGAAGGCCCUCCG 20

RESULT 38
AAV13026
ID AAV13026 standard; rRNA; 25 BP.
XX
XX AAV13026;
XX
XX 17-OCT-2003 (revised)
DT 16-MAY-1998 (first entry)
XX
XX Mycobacterium habana mature rRNA target sequence SEQ ID NO:61.
XX
XX Mycobacterium; pre-rRNA; precursor ribosomal RNA; target sequence; probe;
XX hybridisation; antibiotic resistance; cell lysis; ss.
XX
XX Mycobacterium simiae.
XX
XX US5712095-A.
XX
XX 27-JAN-1998.
XX
XX 07-JUN-1995; 95US-00485602.
XX
XX 16-JUN-1994; 94US-00261068.
XX
XX (BECT ) BECTON DICKINSON CO.
XX
XX Cangelosi GA, Britschgi TB;
XX
XX WPI; 1998-119975/11.
XX
XX Assay for pre-ribosomal RNA in mycobacterium cells - by hybridisation
XX with specific probes after cell lysis.
XX
XX Disclosure; Col 18; 54pp; English.
XX
XX The present sequence represents a mycobacterial mature ribosomal RNA
XX target sequence. The present invention describes a method for detecting
XX pre-rRNA in cells of a mycobacterial sample. The method comprises: (a)
XX treating the cells to release pre-rRNA by: (i) pretreating the cells by
XX enzymatic degradation using both lysozyme and protease until their cell
XX walls are rendered porous to expose their cell membranes, making the
XX cells susceptible to lysis; (ii) contacting the pretreated cells with a
```

CC combination of a magnesium chelator, a nonionic detergent and an anionic
 CC detergent; and (iii) heating the cells to 75-99 degrees Celsius until the
 CC mycobacterial cells are lysed; and (b) detecting the pre-rRNA using at
 CC least one oligonucleotide probe which is capable of selectively
 CC hybridizing to a region of the pre-rRNA that is not present in a mature
 CC mycobacterial rRNA. The probes can be used to identify many Mycobacterium
 CC spp. including M. tuberculosis, M. leprae, M. habana, M. avium, M. bovis,
 CC M. luteo, M. paratuberculosis, M. marinum, M. simiae and/or M.
 CC intracellular. The probes may also be used to measure mycobacterial
 CC response to inhibitors of RNA and protein synthesis and may therefore be
 CC used to screen new antimycobacterial drugs. Mycobacteria have a slow
 CC growth rate. By using the probes, drug developers can now identify
 CC compounds that are more effective, but less stable than those previously
 CC identified. (Updated on 17-OCT-2003 to standardise OS field.)
 XX
 SQ Sequence 25 BP; 6 A; 7 C; 7 G; 0 T; 3 U; 2 Other;

Query Match 79.1%; Score 17.4; DB 2; Length 25;
 Best Local Similarity 80.0%; Pred. No. 74;
 Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCTTTTCGG 22
 ||||| ||||| || :|||
 Db 1 CGAACGGAAGGCTTTTCGG 20

RESULT 39
 AAS30718
 ID AAS30718 standard; DNA; 25 BP.
 XX
 AC AAS30718;
 XX
 DT 06-AUG-2003 (revised)
 DT 04-DEC-2001 (first entry)
 DE Mycobacterium species-specific probe #24.
 XX
 XX Mycobacterium; species-specific bacterial identification; primer; ss.
 KW Mycobacterium chelonae.
 OS
 OS Mycobacterium chelonae.
 XX
 FN WO200166797-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 01-MAR-2001; 2001WO-US006731.
 XX
 XX 03-MAR-2000; 2000US-0186840P.
 PR (BECI) BECKMAN COULTER INC.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (USSH) US NAT INST OF HEALTH.
 XX
 FI Fischer SH, Rampal JB, Fahle GA, Conville PS;
 XX
 DR WPI; 2001-514847/56.
 XX
 XX Species-specific bacterial identification, used particularly to identify
 PT Mycobacterium species, involves hybridizing bacterial genus-selective or
 PT specific primers to a sample.
 XX
 PS Claim 28; Page 21; 43pp; English.

XX The invention relates to a method of species-specific bacterial
 CC identification, comprising hybridising a bacterial genus-selective or
 CC specific primer to a sample and amplifying nucleic acids. This is
 CC followed by hybridising the amplified nucleic acid to a solid phase array
 CC comprising bacterial species specific probe oligonucleotides chemically
 CC linked to a polymeric support in a predetermined pattern. This method is
 CC used for species-specific identification of a bacterium, particularly a
 CC Mycobacterium, especially M. gordonae, M. intracellulare, M. avium, M.
 CC tuberculosis, M. marinum, or M. kansasii. The method provides rapid
 CC identification of multiple species of Mycobacterium. AAS30686-AAS30720

CC represent Mycobacterium species-specific primers and probes used in the
 CC method of the invention. (Updated on 06-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 25 BP; 5 A; 6 C; 10 G; 4 T; 0 U; 0 Other;
 Query Match 79.1%; Score 17.4; DB 4; Length 25;
 Best Local Similarity 94.7%; Pred. No. 74;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 GAACGGAAGGCTTTTCGG 22
 ||||| ||||| |||||
 Db 1 GAACGGAAGGCTTTTCGG 19
 RESULT 40
 AAS30716
 ID AAS30716 standard; DNA; 25 BP.
 XX
 AC AAS30716;
 XX
 DT 06-AUG-2003 (revised)
 DT 04-DEC-2001 (first entry)
 DE Mycobacterium species-specific probe #22.
 XX
 XX Mycobacterium; species-specific bacterial identification; primer; ss.
 KW Mycobacterium chelonae.
 OS
 OS Mycobacterium chelonae.
 XX
 FN WO200166797-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 01-MAR-2001; 2001WO-US006731.
 XX
 XX 03-MAR-2000; 2000US-0186840P.
 PR (BECI) BECKMAN COULTER INC.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (USSH) US NAT INST OF HEALTH.
 XX
 FI Fischer SH, Rampal JB, Fahle GA, Conville PS;
 XX
 DR WPI; 2001-514847/56.
 XX
 XX Species-specific bacterial identification, used particularly to identify
 PT Mycobacterium species, involves hybridizing bacterial genus-selective or
 PT specific primers to a sample.
 XX
 PS Claim 28; Page 21; 43pp; English.

XX The invention relates to a method of species-specific bacterial
 CC identification, comprising hybridising a bacterial genus-selective or
 CC specific primer to a sample and amplifying nucleic acids. This is
 CC followed by hybridising the amplified nucleic acid to a solid phase array
 CC comprising bacterial species specific probe oligonucleotides chemically
 CC linked to a polymeric support in a predetermined pattern. This method is
 CC used for species-specific identification of a bacterium, particularly a
 CC Mycobacterium, especially M. gordonae, M. intracellulare, M. avium, M.
 CC tuberculosis, M. marinum, or M. kansasii. The method provides rapid
 CC identification of multiple species of Mycobacterium. AAS30686-AAS30720
 CC represent Mycobacterium species-specific primers and probes used in the
 CC method of the invention. (Updated on 06-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 25 BP; 6 A; 6 C; 9 G; 4 T; 0 U; 0 Other;
 Query Match 79.1%; Score 17.4; DB 4; Length 25;
 Best Local Similarity 94.7%; Pred. No. 74;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 GAACGGAAGGCTTTTCGG 22
 ||||| ||||| |||||
 Db 1 GAACGGAAGGCTTTTCGG 19

```

RESULT 41
AAD11024/c
ID  AAD11024 standard; DNA; 32 BP.
XX
XX  AAD11024;
XX
XX  24-SEP-2001 (first entry)
XX
DE  Probe #4 to detect amplified MAC 16S rRNA or DNA encoding 16S rRNA.
XX
XX  Mycobacterium avium complex; MAC; 16S ribosomal RNA; pathogenic bacteria;
XX  in vitro amplification; MAC infection; probe; ss.
XX
OS  Mycobacterium sp.
XX
XX  WO200144511-A2.
XX
XX  21-JUN-2001.
XX
XX  15-DEC-2000; 2000WO-US033872.
XX
XX  15-DEC-1999; 99US-0171202P.
XX
XX  (GENP-) GEN-PROBE INC.
XX  (BREN/) BRENTANO S T.
XX  (LANK/) LANKFORD R L.
XX
XX  Brentano ST, Lankford RL;
XX  WPI; 2001-398171/42.
XX
XX  Detecting Mycobacterium avium complex organisms, comprises using in vitro
XX  nucleic acid amplification with amplification oligonucleotides specific
XX  for 16S ribosomal RNA or DNA encoding 16S rRNA from the bacterial
XX  species.
XX
XX  Claim 11; Page 27; 27pp; English.
XX
XX  The present invention relates to a method for detecting Mycobacterium
XX  avium complex (MAC) organisms (eg. M. avium, M. intracellulare, M.
XX  tuberculosis, M. paratuberculosis) present in a biological sample. The
XX  method comprises amplifying a 16S ribosomal RNA (rRNA) or DNA encoding
XX  16S rRNA obtained from a biological sample containing nucleic acid from a
XX  MAC species in an in vitro nucleic acid amplification mixture comprising
XX  a polymerase activity and a pair of primers to produce an amplified
XX  nucleic acid and detecting amplified nucleic acid. The method is useful
XX  for in vitro diagnostic detection of pathogenic bacteria, particularly
XX  detecting infections caused by MAC organisms, distinguished from other
XX  closely-related Mycobacterium species. The present sequence is a probe
XX  used to detect amplified MAC 16S rRNA sequence or DNA encoding 16S rRNA
XX
XX  Sequence 32 BP; 5 A; 11 C; 7 G; 9 T; 0 U; 0 Other;
XX
XX  Query Match 79.1%; Score 17.4; DB 4; Length 32;
XX  Best Local Similarity 94.7%; Pred. No. 76;
XX  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19
    |||||
Db 28 GTCGAACGGAAGGCCTCT 10

RESULT 42
AAD11017
ID  AAD11017 standard; DNA; 32 BP.
XX
XX  AAD11017;
XX
XX  24-SEP-2001 (first entry)
XX
DE  PCR primer #4 used for in vitro amplification of MAC rRNA.
XX
XX  Mycobacterium avium complex; MAC; 16S ribosomal RNA; pathogenic bacteria;
XX  in vitro amplification; MAC infection; PCR primer; ss.
XX
XX  Mycobacterium sp.
XX
XX  WO200144511-A2.
XX
XX  21-JUN-2001.
XX
XX  15-DEC-2000; 2000WO-US033872.
XX
XX  15-DEC-1999; 99US-0171202P.
XX
XX  (GENP-) GEN-PROBE INC.
XX  (BREN/) BRENTANO S T.
XX  (LANK/) LANKFORD R L.
XX
XX  Brentano ST, Lankford RL;
XX  WPI; 2001-398171/42.
XX
XX  Detecting Mycobacterium avium complex organisms, comprises using in vitro
XX  nucleic acid amplification with amplification oligonucleotides specific
XX  for 16S ribosomal RNA or DNA encoding 16S rRNA from the bacterial
XX  species.
XX
XX  Claim 11; Page 27; 27pp; English.
XX
XX  The present invention relates to a method for detecting Mycobacterium
XX  avium complex (MAC) organisms (eg. M. avium, M. intracellulare, M.
XX  tuberculosis, M. paratuberculosis) present in a biological sample. The
XX  method comprises amplifying a 16S ribosomal RNA (rRNA) or DNA encoding
XX  16S rRNA obtained from a biological sample containing nucleic acid from a
XX  MAC species in an in vitro nucleic acid amplification mixture comprising
XX  a polymerase activity and a pair of primers to produce an amplified
XX  nucleic acid and detecting amplified nucleic acid. The method is useful
XX  for in vitro diagnostic detection of pathogenic bacteria, particularly
XX  detecting infections caused by MAC organisms, distinguished from other
XX  closely-related Mycobacterium species. The present sequence is a probe
XX  used to detect amplified MAC 16S rRNA sequence or DNA encoding 16S rRNA
XX
XX  Sequence 32 BP; 5 A; 11 C; 7 G; 9 T; 0 U; 0 Other;
XX
XX  Query Match 79.1%; Score 17.4; DB 4; Length 32;
XX  Best Local Similarity 94.7%; Pred. No. 76;
XX  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19
    |||||
Db 28 GTCGAACGGAAGGCCTCT 10

RESULT 43
AAx99195
ID  AAx99195 standard; DNA; 50 BP.
XX
XX  AAx99195;
XX
XX  28-SEP-1999 (first entry)
XX
XX  M. avium 16S rRNA gene fragment.
XX
XX  Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA;
XX  shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.
XX
XX  Mycobacterium avium.
XX
XX  WO9935284-A1.
XX
XX  15-JUL-1999.
XX
XX  30-DEC-1997; 97WO-BR000087.

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XX PR 30-DEC-1997; 97WO-BR000087.
 XX PA (UYMI-) UNIV FEDERAL MINAS GERAIS.
 XX PI Peregrino Ferreira PC, Geessien Kroon E;
 XX PI Bernardes Margutti Pinto ME, Aleixo AW;
 XX DR WPI; 1999-444201/37.
 XX PT Detection of mycobacteria by shift mobility assay.
 XX PS Disclosure; Fig 7; 20pp; English.
 XX CC The invention describes a new method for diagnosis, identification and
 CC characterisation of Mycobacterium tuberculosis or any other mycobacteria
 CC by using polymerase chain reaction (PCR) and shift mobility assay (SMA)
 CC in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,
 CC DNA amplification and shift mobility assay. The method is based on
 CC divergence in sequences found in 16S rRNA to identify mycobacteria
 CC species, since a remarkable shift of heteroduplex bands are obtained
 CC between single stranded and homoduplex bands in UPAGE. The method is
 CC fast, simple and can produce information not easily obtained when
 CC compared with other detection methods. The sensitivity of other assays
 CC suffer due to the tendency of the denatured PCR product strands to
 CC reassociate and exclude oligonucleotide probes, and stearic interference
 CC between the bound oligonucleotides and the solid support which impede
 CC hybridization to nucleic acids in solution. Sequences AAX99193-237
 CC represent 16S rRNA gene regions of some mycobacterial species
 XX SQ Sequence 50 BP; 15 A; 12 C; 14 G; 9 T; 0 U; 0 Other;
 Query Match 79.1%; Score 17.4; DB 2; Length 50;
 Best Local Similarity 94.7%; Pred. No. 80;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GTCGAACGGAAAGGCTTT 19
 Db 13 GTCGAACGGAAAGGCTCT 31
 RESULT 44
 ID AAX99196
 AC AAX99196 standard; DNA; 50 BP.
 AC AAX99196;
 DT 28-SEP-1999 (first entry)
 XX M. fortuitum 16S rRNA gene fragment.
 XX Mycobacterium tuberculosis; polymerase chain reaction; PCR: SMA;
 XX shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.
 XX Mycobacterium fortuitum.
 XX WO9935284-A1.
 XX 15-JUL-1999.
 XX 30-DEC-1997; 97WO-BR000087.
 XX 30-DEC-1997; 97WO-BR000087.
 XX (UYMI-) UNIV FEDERAL MINAS GERAIS.
 XX Peregrino Ferreira PC, Geessien Kroon E;
 XX PI Bernardes Margutti Pinto ME, Aleixo AW;
 XX DR WPI; 1999-444201/37.
 XX PT Detection of mycobacteria by shift mobility assay.
 XX

PS Disclosure; Fig 7; 20pp; English.
 XX The invention describes a new method for diagnosis, identification and
 CC characterisation of Mycobacterium tuberculosis or any other mycobacteria
 CC by using polymerase chain reaction (PCR) and shift mobility assay (SMA)
 CC in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,
 CC DNA amplification and shift mobility assay. The method is based on
 CC divergence in sequences found in 16S rRNA to identify mycobacteria
 CC species, since a remarkable shift of heteroduplex bands are obtained
 CC between single stranded and homoduplex bands in UPAGE. The method is
 CC fast, simple and can produce information not easily obtained when
 CC compared with other detection methods. The sensitivity of other assays
 CC suffer due to the tendency of the denatured PCR product strands to
 CC reassociate and exclude oligonucleotide probes, and stearic interference
 CC between the bound oligonucleotides and the solid support which impede
 CC hybridization to nucleic acids in solution. Sequences AAX99193-237
 CC represent 16S rRNA gene regions of some mycobacterial species
 XX SQ Sequence 50 BP; 14 A; 12 C; 14 G; 9 T; 0 U; 1 Other;
 Query Match 79.1%; Score 17.4; DB 2; Length 50;
 Best Local Similarity 94.7%; Pred. No. 80;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GTCGAACGGAAAGGCTTT 19
 Db 13 GTCGAACGGAAAGGCTCT 31
 RESULT 45
 ID ADF94050
 AC ADF94050 standard; DNA; 50 BP.
 AC ADF94050;
 DT 11-MAR-2004 (first entry)
 XX Microorganism detection probe, SEQ ID 143.
 DE Probe; detection; identification; microorganism; food; drug;
 KW 16S rRNA V1 region; 16S rRNA V2 region; 16S rRNA V3 region; ss.
 XX Mycobacterium avium.
 OS WO2003106676-A1.
 XX 24-DEC-2003.
 XX 16-JUN-2003; 2003WO-JP007620.
 XX 14-JUN-2002; 2002JP-00174564.
 XX (HISF) HITACHI SOFTWARE ENG CO LTD.
 PA (MITS-) MITSUBISHI KAGAKU BIO-CLINICAL LAB INC.
 XX Hashida J, Ueno S, Muto I, Naruse K, Tamura M, Matsuda K;
 PI Shimadzu M, Kobayashi I, Ishiko H;
 XX WPI; 2004-071565/07.
 XX 20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a
 PT microorganism for specific detection and identification of the
 PT microorganism in foods and drug compositions.
 XX Claim 2; SEQ ID NO 143; 150pp; Japanese.
 XX The present invention relates to probes (ADF93908-ADF94059) for the
 CC specific detection and identification of harmful microorganisms in
 CC samples of foods and drug compositions. The probe sequences are derived
 CC from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism,
 CC or its complementary sequence. Detection and identification of the
 CC microorganism is by amplification of the complete 16S rRNA gene using
 CC primers ADF94060 and ADF94061, labelling the amplification product (a

CC fluorescence label is preferred), and hybridising to the probe or probes
 CC of the invention. The probes may be immobilised on a DNA chip. The
 CC microorganism is selected from Actinobacillus actinomycetocornitans,
 CC Acinetobacter calcoaceticus, Haemophilus influenzae, Stenotrophomonas
 CC maltophilia, Proteus mirabilis, Streptococcus pneumoniae, Pseudomonas
 CC aeruginosa, Citrobacter freundii, Veillonella parvula, Providencia
 CC stuartii, Neisseria gonorrhoeae, Streptococcus agalactiae, Morganella
 CC morganii, Bacteroides fragilis, Staphylococcus hominis, Staphylococcus
 CC warneri, Staphylococcus haemolyticus, Enterobacter cloacae, Enterobacter
 CC aerogenes, Staphylococcus epidermidis, Streptococcus constellatus,
 CC Serratia marcescens, Streptococcus anginosus, Escherichia coli,
 CC Klebsiella pneumoniae, Enterococcus faecalis, Enterococcus faecium,
 CC Streptococcus sanguinis, Streptococcus mitis, Streptococcus intermedius,
 CC Listeria monocytogenes, Clostridium perfringens, Corynebacterium
 CC aquaticum, Streptococcus oralis, Staphylococcus aureus, Neisseria
 CC meningitidis, Campylobacter fetus, Enterococcus gallinarum, Enterococcus
 CC casseliflavus, Aeromonas hydrophila, Salmonella paratyphi, Salmonella
 CC typhi, Streptococcus equisimilis, Streptococcus canis, Klebsiella
 CC oxytoca, Staphylococcus saprophyticus, Pasteurella multocida, Eikenella
 CC corrodens, Streptococcus pyogenes, Moraxella catarrhalis, Legionella
 CC pneumophila, Mycobacterium tuberculosis, Mycobacterium avium,
 CC Mycobacterium intracellulare, Mycobacterium kansasii or Mycobacterium
 CC gordonae.
 XX
 SQ Sequence 50 BP; 12 A; 11 C; 19 G; 8 T; 0 U; 0 Other;

Query Match 79.1%; Score 17.4; DB 12; Length 50;
 Best Local Similarity 94.7%; Pred. No. 80;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19
 |||||
 Db 5 GTCGAACGGAAGGCCTCT 23

RESULT 46
 AEB98762
 ID AEB98762 standard; DNA; 209 BP.
 XX
 AC AEB98762;
 XX
 DT 06-OCT-2005 (first entry)
 XX
 DE Mycobacterium avium partial 16S rDNA sequence, SEQ ID 4.
 XX
 KW microorganism detection; mycobacterium infection; antibacterial; ds.
 XX
 OS Mycobacterium avium.
 XX
 PN JP2005204582-A.
 XX
 PD 04-AUG-2005.
 XX
 PF 23-JAN-2004; 2004JP-00015195.
 XX
 PR 23-JAN-2004; 2004JP-00015195.
 XX
 XX (ASAH) ASahi KASEI KK.
 PA
 XX Oda N;
 XX
 XX WPI; 2005-526965/54.
 XX
 PT New single-stranded oligonucleotide, useful for amplifying the nucleic
 PT acid of Mycobacterium avium, Mycobacterium intracellulare, and
 PT Mycobacterium kansasii.
 XX
 XX Example 1; SEQ ID NO 4; 14pp; Japanese.
 XX
 CC The invention relates to a novel single-stranded oligonucleotide used in
 CC a detection method of an atypical mycobacteria group. The invention
 CC further includes: amplifying the nucleic acid of Mycobacterium avium by a
 CC loop-mediated isothermal amplification (LAMP) method; amplifying the

CC nucleic acid of M. intracellulare by a LAMP method; amplifying the
 CC nucleic acid of M. kansasii by a LAMP method; and a kit for detecting the
 CC nucleic acid of M. avium by a LAMP method; detecting the nucleic acid of
 CC M. intracellulare by a LAMP method; or detecting the nucleic acid of M.
 CC kansasii by a LAMP method. The single-stranded oligonucleotide is useful
 CC in medical applications. This polynucleotide represents a Mycobacterium
 CC avium partial 16S rDNA sequence amplified by the LAMP method of the
 CC invention.
 XX
 SQ Sequence 209 BP; 48 A; 48 C; 70 G; 43 T; 0 U; 0 Other;

Query Match 79.1%; Score 17.4; DB 14; Length 209;
 Best Local Similarity 94.7%; Pred. No. 93;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19
 |||||
 Db 43 GTCGAACGGAAGGCCTCT 61

RESULT 47
 ABT23571
 ID ABT23571 standard; DNA; 560 BP.

XX AC ABT23571;
 XX
 DT 22-MAY-2003 (first entry)
 XX
 DE Stabilising reagent method related oligo SEQ ID No 23.
 XX
 KW Stabilising reaction reagent; PCR; primer; RNaseH; long-term storage;
 KW specific amplification; pathogenic microorganism; chimeric;
 KW genetic engineering; clinical medicine; ss.
 XX
 OS Mycobacterium avium.
 XX
 PN WO2002101042-A1.
 XX
 PD 19-DEC-2002.
 XX
 PF 12-JUN-2002; 2002WO-JP005832.
 XX
 PR 12-JUN-2001; 2001JP-00177737.
 PR 20-AUG-2001; 2001JP-00249689.
 XX
 XX (TAKI) TAKARA BIO INC.
 PA
 XX Sagawa H, Uemori T, Mukai H, Yamamoto J, Tomono J, Kobayashi E;
 PI Enoki T, Asada K, Kato I;
 PI
 XX WPI; 2003-148805/14.
 DR
 XX Method for stabilizing and storing reaction reagents for specific
 PT amplification and detection of nucleic acids particularly in e.g.
 PT identifying pathogenic microorganisms or viruses in sample.
 XX
 PS Example 15; Page 109; 177pp; Japanese.
 XX
 CC The invention relates to a novel stabilising reaction reagent for use in
 CC the amplification and/or detection of a target nucleic acid comprising:
 CC preparing a reaction mixture with e.g. a nucleic acid as template, at
 CC least 1 primer and RNaseH; and incubation of the reaction mixture for a
 CC defined period of time to form a reaction product during the
 CC amplification of such target nucleic acid. The method is useful for
 CC stabilising and long-term storage of reaction reagents for highly
 CC sensitive and specific amplification and detection of nucleic acids
 CC particularly in identifying pathogenic microorganisms or viruses in a
 CC sample using chimeric oligonucleotide primers, which is useful in genetic
 CC engineering and clinical medicine. This polynucleotide sequence
 CC represents an oligo relating to the novel stabilising reaction reagent
 CC method of the invention
 XX
 SQ Sequence 560 BP; 117 A; 134 C; 198 G; 111 T; 0 U; 0 Other;

Query Match 79.1%; Score 17.4; DB 10; Length 560;
Best Local Similarity 94.7%; Pred. No. 1.e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTT 19
| | | | | | | | | | | | | | | | | | | | | |
Db 34 GTCGAACGGAAGGCCTCT 52

RESULT 48
AEA22411
ID AEA22411 standard; DNA; 1421 BP.
XX AC AEA22411;
XX DT 25-AUG-2005 (first entry)
XX DE Mycobacterium lentiflavum 16S rRNA sequence SEQ ID NO:12.
XX KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
XX OS Mycobacterium lentiflavum.
XX PN US2005130168-A1.
XX PD 16-JUN-2005.
XX PF 31-OCT-2003; 2003US-00697802.
XX PR 31-OCT-2003; 2003US-00697802.
XX (HANX/) HAN X.
XX PA (PHAM/) PHAM A S.
XX PI Han X, Pham AS;
XX DR WPI; 2005-424597/43.
XX Determining a bacterium species comprises providing oligonucleotide
primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
XX Disclosure; SEQ ID NO 12; 74pp; English.

The invention relates to a method (M1) for determining a bacterium species. (M1) comprises: (a) culturing a bacterium from a specimen; (b) extracting a genomic nucleotide from the bacterium to provide a nucleotide template; (c) annealing a region of a nucleotide template to a specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion, the primer set designed to provide a product amplifying the region of the nucleotide template to produce the product; and (e) determining a species of a bacterium in a nucleotide sequence of the product. Also described is an alternative method (M2) for determining a bacterium species comprising: (a) providing a specimen or a sample having a template; (b) providing a pair of primers selected from: (i) a first forward primer having consecutive bases of an AFB-f comprising any of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments or variations and a first reverse primer having consecutive bases of an AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488) or their fragments or variations, (ii) a second forward primer having consecutive bases of an UB-f comprising any of the 28 sequences of 15-21 bp (AEA22489-AEA22516) or their fragments or variations and a second reverse primer having consecutive bases of an UB-r comprising any of the 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or variations, or (iii) a first forward primer having consecutive bases of an AFB-f of AEA22417-AEA22452 or their fragments or variations and a second reverse primer having consecutive bases of an UB-r of AEA22517-AEA22544 or their fragments or variations; (c) the specimen; and (d) comparing the product from the specimen with a nucleotide sequence from a database to determine the bacterium species present in the specimen. The methods are useful for determining a bacterium species. The present sequence represents a Mycobacterium lentiflavum 16S rRNA nucleotide

CC sequence, which is used in the exemplification of the present invention.
XX Sequence 1421 BP; 306 A; 344 C; 487 G; 284 T; 0 U; 0 Other;
SQ

Query Match 79.1%; Score 17.4; DB 14; Length 1421;
Best Local Similarity 94.7%; Pred. No. 1.e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTT 19
| | | | | | | | | | | | | | | | | | | | | |
Db 24 GTCGAACGGAAGGCCTCT 42

RESULT 49
ADK66476
ID ADK66476 standard; RNA; 1431 BP.
XX AC ADK66476;
XX DT 06-MAY-2004 (first entry)
XX DE Corynebacterium 16S rRNA sequence.
XX KW ss; 16S rRNA; microorganism detection; clinical sample;
XX PN pharmaceutical composition.
XX OS Corynebacterium sp.
XX PN W02004009839-A2.
XX PD 29-JAN-2004.
XX PF 16-JUL-2003; 2003WO-EP007717.
XX PR 18-JUL-2002; 2002DE-01032776.
XX PR 14-FEB-2003; 2003DE-01007732.
XX (HENK) HENKEL KGAA.
XX PA (VERM-) VERMICON AG.
XX PI Stettler A, Jasoy C, Scholtyssek R, Maienschein V, Nieveler S;
XX PI Weiss A, Trebesius K, Beimfohr C, Ludwig W, Bamberg RR, Schleifer K;
XX PI Muehlner S, Adomat C, Bergmaier I;
XX DR WPI; 2004-123402/12.
XX New oligonucleotides for specific detection of microorganisms, useful
e.g. for detecting or quantifying microbes on the skin, in foods,
PT clinical samples or water, by in situ hybridization.
XX Disclosure; Page 66-67; 67pp; German.
XX The present invention provides a number of oligonucleotides for the
specific detection of microorganisms. The oligonucleotides are used to
detect and/or quantify microorganisms, especially on the skin, in foods
or the environment (water, soil and air), from waste waters or biofilms,
CC in clinical samples (body fluids or tissues), and in pharmaceutical or
CC cosmetic compositions. The present sequence is a Corynebacterium 16S rRNA
CC sequence.
XX Sequence 1431 BP; 308 A; 327 C; 488 G; 0 T; 307 U; 1 Other;
SQ

Query Match 79.1%; Score 17.4; DB 12; Length 1431;
Best Local Similarity 78.9%; Pred. No. 1.e+02;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTT 19
| | | | | | | | | | | | | | | | | | | | | |
Db 34 GUCGAACGGAAGGCCTCU 52

RESULT 50
ADK66445

```

ID ADK66445 standard; rRNA; 1431 BP.
XX
AC ADK66445;
XX
DT 06-MAY-2004 (first entry)
XX
DE Corynebacterium 16S rRNA sequence.
XX
KW ss; 16S rRNA; microorganism detection; skin; acne.
XX
OS Corynebacterium sp.
XX
PN WC2004009843-A2.
XX
PD 29-JAN-2004.
XX
PF 16-JUL-2003; 2003WO-EP007718.
XX
PR 18-JUL-2002; 2002DE-01032775.
XX
PR 14-FEB-2003; 2003DE-01006616.
XX
PA (HENK ) HENKEL KGAA.
XX
PI Saettler A, Jassoy C, Scholtyssek R, Maienschein V, Nievelev S;
PI Weiss A, Trebesius K, Beimfohr C, Ludwig W, Bamberg RR, Schleifer K;
PI Mueller S, Adomat C, Bergmaier I;
XX
DR WPI; 2004-123405/12.
XX
XX Kit for detection of microorganisms on skin, useful e.g. for diagnosis of
XX infection, comprises specific oligonucleotides for in situ hybridization.
XX
PS Disclosure; Page 62-63; 63pp; German.
XX
CC The present invention relates to a kit for detecting microorganisms that
CC contains at least one oligonucleotide specific for at least one species,
CC or group of species, that is present on the skin. The kit is used to
CC detect and/or quantify microorganisms that are present on the skin; e.g.
CC for early diagnosis of secondary infection in cases of acne. The present
CC sequence is a Corynebacterium 16S rRNA sequence.
XX
SQ Sequence 1431 BP; 308 A; 327 C; 488 G; 0 T; 307 U; 1 Other;

Query Match 79.1%; Score 17.4; DB 12; Length 1431;
Best Local Similarity 78.9%; Pred. No. 1.1e+02;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19
Db 34 GUCGAACGGAAGGCCUCU 52

RESULT 51
AAQ37639
ID AAQ37639 standard; rRNA; 1449 BP.
XX
AC AAQ37639;
XX
DT 25-MAR-2003 (revised)
DT 18-JUN-1993 (first entry)
XX
DE Mycobacterium genavense 16S rRNA.
XX
KW Detection; rapid; immunosuppressed patients; AIDS; ss.
XX
OS Mycobacterium genavense.
XX
PN EP529985-A1.
XX
PD 03-MAR-1993.
XX
PF 21-AUG-1992; 92EP-00307690.
XX

Query Match 79.1%; Score 17.4; DB 2; Length 1449;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19
Db 51 GTCGAACGGAAGGCCTCT 69

RESULT 52
AEA22401
ID AEA22401 standard; DNA; 1454 BP.
XX
AC AEA22401;
XX
DT 25-AUG-2005 (first entry)
XX
DE Mycobacterium avium 16S rRNA sequence SEQ ID NO:2.
XX
KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
XX
OS Mycobacterium avium.
XX
PN US2005130168-A1.
XX
PD 16-JUN-2005.
XX
PF 31-OCT-2003; 2003US-00697802.
XX
PR 31-OCT-2003; 2003US-00697802.
XX
PA (HANX/) HAN X.
PA (PHAM/) PHAM A S.
XX
PI Han X, Pham AS;
XX
DR WPI; 2005-424597/43.
XX
XX Determining a bacterium species comprises providing oligonucleotide
XX primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
XX
PS Disclosure; SEQ ID NO 2; 74pp; English.
XX
XX The invention relates to a method (M1) for determining a bacterium
XX species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)

```

CC extracting a genomic nucleotide from the bacterium to provide a
 CC nucleotide template; (c) annealing a region of a nucleotide template to a
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
 CC complementary fashion, the primer set designed to provide a product
 CC having a predetermined size dictated by a complementary primer set; (d)
 CC amplifying the region of the nucleotide template to produce the product;
 CC and (e) determining a species of a bacterium in a nucleotide sequence of
 CC the product. Also described is an alternative method (M2) for determining
 CC a bacterium species comprising: (a) providing a specimen or a sample
 CC having a template; (b) providing a pair of primers selected from: (i) a
 CC first forward primer having consecutive bases of an AFB-f comprising any
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
 CC or variations and a first reverse primer having consecutive bases of an
 CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
 CC or their fragments or variations, (ii) a second forward primer having
 CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
 CC bp (AEA22489-AEA22516) or their fragments or variations and a second
 CC reverse primer having consecutive bases of an UB-r comprising any of the
 CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
 CC variations, or (iii) a first forward primer having consecutive bases of
 CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
 CC second reverse primer having consecutive bases of an UB-r of AEA22517-
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)
 CC comparing the product from the specimen with a nucleotide sequence from a
 CC database to determine the bacterium species present in the specimen. The
 CC methods are useful for determining a bacterium species. The present
 CC sequence represents a Mycobacterium avium 16S rRNA nucleotide sequence,
 CC which is used in the exemplification of the present invention.

XX
 SQ Sequence 1454 BP; 316 A; 348 C; 494 G; 296 T; 0 U; 0 Other;

Query Match 79.1%; Score 17.4; DB 14; Length 1454;
 Best Local Similarity 94.7%; Pred. No. 1.1e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCCTTT 19
 |||||
 Db 34 GTCGACGGAAGGCCTCT 52

RESULT 53
 ADB61680
 ID ADB61680 standard; DNA; 1465 BP.

XX AC ADB61680;

XX DT 04-DEC-2003 (first entry)

XX DE 16S rRNA of Mycobacterium avium DNA sequence.

XX enriching mRNA; high quality bacterial mRNA; bacterial gene expression;
 XX poly-A tail; mRNA purification; oligo-dT capture;
 XX prokaryote mRNA purification; bridging oligonucleotide; targeting region;
 XX capture oligonucleotide; prokaryotic 16S rRNA; prokaryotic 23S rRNA;
 XX eukaryotic 17S rRNA; eukaryotic 18S rRNA; eukaryotic 28S rRNA;
 XX 28S eukaryotic rRNA bridging oligonucleotide; ds.

XX OS Mycobacterium avium.

XX XX WO2003054162-A2.

XX PD 03-JUL-2003.

XX PF 19-DEC-2002; 2002WO-US041014.

XX PR 20-DEC-2001; 2001US-00029397.

XX XX (AMB1-) AMBION INC.

XX PI Murphy GL, Whitley JP;

XX XX WPI; 2003-663255/62.

XX

PT Depleting or isolating targeted nucleic acids e.g. rRNA, involves using a
 PT bridging oligonucleotide comprising bridging region and a targeting
 PT region complementary to a targeted nucleic acid, and a capture
 PT oligonucleotide.

XX Claim 4; Page 168; 209pp; English.

XX This invention relates to a novel method for isolating, depleting or
 CC separating a targeted nucleic acid, such as rRNA, from a sample
 CC comprising targeted and non-targeted nucleic acids. It effects a way of
 CC enriching for non-targeted nucleic acids such as mRNAs. Isolating
 CC sufficient quantities of high quality bacterial mRNA is a demanding
 CC process which impedes analysis of bacterial gene expression in the
 CC presence of host cells. A small percentage of bacterial mRNAs may be poly
 CC -A tailed, but these are targeted for degradation and tend to be
 CC unstable. As a result, the commonly employed method for mRNA purification
 CC with eukaryotic cells, oligo-dT capture, is ineffective. The present
 CC invention provides an alternative, more suitable method for mRNA
 CC purification from prokaryotes. The method of the invention comprises the
 CC incubation of a sample with a bridging oligonucleotide (containing a
 CC targeting region) and subsequently incubating with a capture
 CC oligonucleotide allowing the isolation of the target from the sample. The
 CC method is useful for depleting or isolating targeted nucleic acid, for
 CC example rRNA such as prokaryotic 16S or prokaryotic 23S, eukaryotic 17S
 CC or 18S or eukaryotic 28S rRNA, from a sample. The rRNA sequence may
 CC comprise any one of 64 fully defined sequences as given in the
 CC specification. The present sequence is that of a DNA sequence which
 CC represents the sequence of 16S rRNA of Mycobacterium avium related to the
 CC invention.

XX SQ Sequence 1465 BP; 321 A; 345 C; 496 G; 298 T; 0 U; 5 Other;

Query Match 79.1%; Score 17.4; DB 10; Length 1465;

Best Local Similarity 94.7%; Pred. No. 1.1e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCCTTT 19
 |||||
 Db 24 GTCGACGGAAGGCCTCT 42

RESULT 54

ADR90572

ID ADR90572 standard; DNA; 1472 BP.

XX AC ADR90572;

XX DT 02-DEC-2004 (first entry)

XX DE M avium 16S rRNA gene sequence SeqID1.

XX KW acid-fast bacterium; differentiation; 16S rRNA; M avium complex; MAC;
 KW taxonomic-tree analysis; atypical-mycobacteria; gene; ds.

XX OS Mycobacterium avium.

XX FH Key Location/Qualifiers

FT variation 893

FT /*tag= a

FT variation 1312

FT /*tag= b

FT variation 1393

FT /*tag= c

XX XX JP2004254591-A.

XX PD 16-SEP-2004.

XX XX 26-FEB-2003; 2003JP-00048654.

XX XX 26-FEB-2003; 2003JP-00048654.

XX XX (MITP) MITSUBISHI YUKA BCL KK.

PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 21-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140655P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.

PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159233P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 78.2%; Score 17.2; DB 3; Length 788;
Best Local Similarity 86.4%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 GTCGAACGGAAGGCTTTTCGG 22
Db 333 GTCGACGTTAAGGCTTTTCGG 354

RESULT 57
ADFS6670
ID ADF56670 standard; DNA; 1437 BP.
XX
XX
AC ADF56670;
XX
XX 12-FEB-2004 (first entry)
XX
DE YS-44442 16S rDNA, SEQ ID 1.
XX
KW Pravastatin; HMG-CoA reductase inhibitor;
KW 3-hydroxy-3-methyl glutaryl-CoA reductase inhibitor; 16S rDNA; ds.
XX
OS Saccharothrix sp.
XX
XX JP2003250532-A.
PN
XX
PD 09-SEP-2003.
XX
PF 22-FEB-2002; 2002JP-00046750.
XX
PR 22-FEB-2002; 2002JP-00046750.
XX
PA (YUNG-) YUNG SHIN PHARM IND CO LTD.
XX
XX WPI; 2004-046768/05.
XX
XX Microorganisms Saccharothrix genus YS-44442 and YS-45494 and their
PT mutants useful for producing pravastatin.
XX
PS Example 1; SEQ ID NO 1; 18pp; Japanese.
XX
CC The present invention relates to microorganisms (I) Saccharothrix genus
CC YS-44442 and YS-45494 strains and their mutants. Also claimed is a method
CC (M1) for producing pravastatin by using (I) and isolating (M2) 3-hydroxy-
CC 3-methyl glutaryl (HMG)-CoA reductase inhibitors.
XX
SQ Sequence 1437 BP; 320 A; 362 C; 495 G; 260 T; 0 U; 0 Other;

Query Match 78.2%; Score 17.2; DB 12; Length 1437;
Best Local Similarity 86.4%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCTTTTCGG 22
Db 34 GTCGACGTTAAGGCTTTTCGG 55

RESULT 58
ADG64519
ID ADG64519 standard; DNA; 1437 BP.
XX
XX
AC ADG64519;
XX
XX 11-MAR-2004 (first entry)
XX
DE Saccharothrix strain YS-44442 16S rDNA sequence.
XX
XX Microorganism; Saccharothrix; YS-44442; YS-45494;
KW 3-hydroxy-3-methylglutaryl-CoA reductase inhibitor; HMG-CoA reductase;
KW pravastatin; fermentation; compactin; lovastatin;
KW blood cholesterol level; antilipemic; 16S rDNA; ds.
XX
XX Saccharothrix sp.
OS
XX
PN US2003199047-A1.
XX
PD 23-OCT-2003.

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XX 27-FEB-2002; 2002US-00085871.
PF
XX 27-FEB-2002; 2002US-00085871.
PR
XX
XX (LEEF/) LEE F.
PA (LEEM/) LEE M.
PA (HONG/) HONG A C.
PA (CHIU/) CHIU S.
XX
XX Lee F, Lee M, Hong AC, Chiu S;
PI WPI; 2004-041353/04.
XX
DR Novel microorganism strains YS-44442 and YS-45494 of Saccharothrix,
PT useful for producing pravastatin.
XX
XX Example 1; SEQ ID NO 1; 16pp; English.
XX
CC The present invention relates to the isolation of novel microorganism
CC strains of Saccharothrix designated YS-44442 and YS-45494. Also disclosed
CC is a method for isolating 3-hydroxy-3-methylglutaryl (HMG)-CoA reductase
CC inhibitors such as pravastatin. The Saccharothrix strains YS-44442 and YS
CC -45494 are useful for producing pravastatin. The method involves
CC cultivating the strains at a suitable condition to generate a
CC fermentation broth, feeding compactin into the broth, fermenting the
CC broth for a period of time to convert the compactin to pravastatin, and
CC isolating the pravastatin from the broth. The fermentation broth is
CC cultivated for less than 2 days, preferably for 18 hours. The
CC fermentation broth is derived from a seed culture of the microorganism
CC which is cultivated at a suitable condition for 18-48 hours before
CC inoculation into the broth. The broth is fermented for less than 5 days,
CC preferably 3 days, most preferably less than 24 hours. The method of the
CC invention is useful for isolating HMG-CoA reductase inhibitor. Such as
CC pravastatin, compactin or lovastatin, preferably pravastatin. The
CC pravastatin or HMG-CoA reductase inhibitors are useful for reducing blood
CC cholesterol levels. The present sequence represents Saccharothrix strain
CC YS-44442 16S rDNA sequence.
XX
SQ Sequence 1437 BP; 320 A; 362 C; 495 G; 260 T; 0 U; 0 Other;

Query Match 78.2%; Score 17.2; DB 12; Length 1437;
Best Local Similarity 86.4%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCTTTTCGG 22
Db 34 GTCGACGTTAAGGCTTTTCGG 55

RESULT 59
ADY86147
ID ADY86147 standard; DNA; 1437 BP.
XX
XX
AC ADY86147;
XX
XX 02-JUN-2005 (first entry)
XX
DE Saccharothrix YS-44442 16S rDNA, SEQ ID NO: 1.
XX
KW Microorganism; fermentation; hypercholesterolemia; 16S rDNA; antilipemic;
KW metabolic disorder; ds.
XX
XX Saccharothrix; YS-44442.
OS
XX
XX US2005064566-A1.
PN
XX
XX 24-MAR-2005.
PD
XX
XX 03-DEC-2003; 2003US-00727643.
PF
XX 27-FEB-2002; 2002US-00085871.
XX
XX

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```
PA (LEEF/) LEE F.  
PA (LEEM/) LEE M.  
PA (HONG/) HONG A C.  
PA (CHIU/) CHIU S.  
PI Lee F, Lee M, Hong AC, Chiu S;  
XX WPI; 2005-252680/26.  
XX  
XX Isolation of pravastatin, used to treat hypercholesterolemia, comprises  
XX adding ammonium sulfate into a first solution to form precipitate, and  
XX isolating and dissolving the precipitate to form a second solution and  
XX followed by extracting.  
XX  
XX Example 1; SEQ ID NO 1; 19pp; English.  
XX  
XX The present invention relates to two new microorganism strains of  
XX Saccharothrix, designated as YS-4442 and YS-45494. The invention also  
XX provides a method of isolating pravastatin from Saccharothrix sp and an  
XX improved process for isolation of 3-hydroxy-3-methylglutaryl-Coenzyme A  
XX (HMG CoA) reductase inhibitor. The invention is useful for the  
XX preparation of pravastatin which is useful in the treatment of  
XX hypercholesterolemia. The present sequence is the Saccharothrix YS-44442  
XX 16S rDNA.  
SQ Sequence 1437 BP; 320 A; 362 C; 495 G; 260 T; 0 U; 0 Other;  
Query Match 78.2%; Score 17.2; DB 14; Length 1437;  
Best Local Similarity 86.4%; Pred. No. 1.4e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 GTCGAACGGAAAGCGCTTTTCGG 22  
Db 34 GTCGAGCGGTAAGGCCCTTCGG 55  
RESULT 60  
ID ADF56671 standard; DNA; 1471 BP.  
AC ADF56671;  
XX  
XX 12-FEB-2004 (first entry)  
XX  
XX YS-45494 16S rDNA, SEQ ID 2.  
XX  
XX Pravastatin; HMG-CoA reductase inhibitor;  
XX 3-hydroxy-3-methyl glutaryl-CoA reductase inhibitor; 16S rDNA; ds.  
XX  
XX Saccharothrix sp.  
XX  
XX JP2003250532-A.  
XX  
XX 09-SEP-2003.  
XX  
XX 22-FEB-2002; 2002JP-00046750.  
XX  
XX 22-FEB-2002; 2002JP-00046750.  
XX  
XX (YUNG-) YUNG SHIN PHARM IND CO LTD.  
XX  
XX WPI; 2004-046768/05.  
XX  
XX Microorganisms Saccharothrix genus YS-4442 and YS-45494 and their  
XX mutants useful for producing pravastatin.  
XX  
XX Example 1; SEQ ID NO 2; 18pp; Japanese.  
XX  
XX The present invention relates to microorganisms (I) Saccharothrix genus  
XX YS-4442 and YS-45494 strains and their mutants. Also claimed is a method  
XX (M1) for producing pravastatin by using (I) and isolating (M2) 3-hydroxy-  
XX 3-methyl glutaryl (HMG)-CoA reductase inhibitors.  
SQ Sequence 1471 BP; 331 A; 369 C; 506 G; 265 T; 0 U; 0 Other;  
Query Match 78.2%; Score 17.2; DB 12; Length 1471;  
Best Local Similarity 86.4%; Pred. No. 1.4e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 GTCGAACGGAAAGCGCTTTTCGG 22  
Db 34 GTCGAGCGGTAAGGCCCTTCGG 55  
RESULT 61  
ID ADG64520 standard; DNA; 1471 BP.  
XX  
XX ADG64520;  
XX  
XX 11-MAR-2004 (first entry)  
XX  
XX Saccharothrix strain YS-45494 16S rDNA sequence.  
XX  
XX Microorganism; Saccharothrix; YS-4442; YS-45494;  
XX 3-hydroxy-3-methylglutaryl-CoA reductase inhibitor; HMG-CoA reductase;  
XX pravastatin; fermentation; compactin; lovastatin;  
XX blood cholesterol level; antilipemic; 16S rDNA; ds.  
XX  
XX Saccharothrix sp.  
XX  
XX US2003199047-A1.  
XX  
XX 23-OCT-2003.  
XX  
XX 27-FEB-2002; 2002US-00085871.  
XX  
XX 27-FEB-2002; 2002US-00085871.  
XX  
XX (LEEF/) LEE F.  
XX (LEEM/) LEE M.  
XX (HONG/) HONG A C.  
XX (CHIU/) CHIU S.  
XX  
XX Lee F, Lee M, Hong AC, Chiu S;  
XX  
XX WPI; 2004-041353/04.  
XX  
XX Novel microorganism strains YS-4442 and YS-45494 of Saccharothrix,  
XX useful for producing pravastatin.  
XX  
XX Example 1; SEQ ID NO 2; 16pp; English.  
XX  
XX The present invention relates to the isolation of novel microorganism  
XX strains of Saccharothrix designated YS-4442 and YS-45494. Also disclosed  
XX is a method for isolating 3-hydroxy-3-methylglutaryl (HMG)-CoA reductase  
XX inhibitors such as pravastatin. The Saccharothrix strains YS-4442 and YS  
XX -45494 are useful for producing pravastatin. The method involves  
XX cultivating the strains at a suitable condition to generate a  
XX fermentation broth, feeding compactin into the broth, fermenting the  
XX broth for a period of time to convert the compactin to pravastatin, and  
XX isolating the pravastatin from the broth. The fermentation broth is  
XX cultivated for less than 2 days, preferably for 18 hours. The  
XX fermentation broth is derived from a seed culture of the microorganism  
XX which is cultivated at a suitable condition for 18-48 hours before  
XX inoculation into the broth. The broth is fermented for less than 5 days,  
XX preferably 3 days, most preferably less than 24 hours. The method of the  
XX invention is useful for isolating HMG-CoA reductase inhibitor such as  
XX pravastatin, compactin or lovastatin, preferably pravastatin. The  
XX pravastatin or HMG-CoA reductase inhibitors are useful for reducing blood  
XX cholesterol levels. The present sequence represents Saccharothrix strain  
XX YS-45494 16S rDNA sequence.  
SQ Sequence 1471 BP; 331 A; 369 C; 506 G; 265 T; 0 U; 0 Other;  
Query Match 78.2%; Score 17.2; DB 12; Length 1471;
```



```

Best Local Similarity 86.4%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTCGG 22
Db 34 GTCGAGCGGTAAGGCCCTTCGG 55

RESULT 62
ADY86148
ID ADY86148 standard; DNA; 1471 BP.
XX AC
XX ADY86148;
DT 02-JUN-2005 (first entry)
XX DE
XX Saccharothrix YS-45494 16s rDNA, SEQ ID NO: 2.
DE DE
XX Microorganism; fermentation; hypercholesterolemia; 16s rDNA; antilipemic;
KW KW metabolic disorder; ds.
XX OS
XX Saccharothrix; YS-45494.
XX US2005064566-A1.
XX PN
XX 24-MAR-2005.
XX PD
XX 03-DEC-2003; 2003US-00727643.
XX PF
XX 27-FEB-2002; 2002US-00085871.
XX PR
XX (LEEF/) LEE F.
XX PA
XX (LEEM/) LEE M.
XX PA
XX (HONG/) HONG A. C.
XX PA
XX (CHIU/) CHIU S.
XX PI
XX Lee F, Lee M, Hong AC, Chiu S;
XX WPI; 2005-252680/26.
XX DR
XX Isolation of pravastatin, used to treat hypercholesterolemia, comprises
PT adding ammonium sulfate into a first solution to form precipitate,
PT isolating and dissolving the precipitate to form a second solution and
PT followed by extracting.
XX PS
XX Example 1; SEQ ID NO 2; 19pp; English.
XX CC
XX The present invention relates to two new microorganism strains of
CC Saccharothrix, designated as YS-4442 and YS-45494. The invention also
CC provides a method of isolating pravastatin from Saccharothrix sp and an
CC improved process for isolation of 3-hydroxy-3-methylglutaryl-Coenzyme A
CC (HMG CoA) reductase inhibitor. The invention is useful for the
CC preparation of pravastatin which is useful in the treatment of
CC hypercholesterolemia. The present sequence is the Saccharothrix YS-45494
XX 16s rDNA.
XX CC
SQ Sequence 1471 BP; 331 A; 369 C; 506 G; 265 T; 0 U; 0 Other;

Query Match 78.2%; Score 17.2; DB 14; Length 1471;
Best Local Similarity 86.4%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTCGG 22
Db 34 GTCGAGCGGTAAGGCCCTTCGG 55

RESULT 63
AED47485
ID AED47485 standard; DNA; 1477 BP.
XX AC
XX AED47485;
XX XX

Best Local Similarity 86.4%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTCGG 22
Db 51 GTCGAGCGGTAAGGCCCTTCGG 72

RESULT 64
ADS17269
ID ADS17269 standard; DNA; 1488 BP.
XX AC
XX ADS17269;
XX CC
DT 02-DEC-2004 (first entry)
XX DE
XX Lechevalieria aerocolonigenes strain VK-A9 16S rDNA.
XX KW
XX Plant protectant; antibiotic; thiobutacin; antifungal; antioomycete;
XX KW phytophthora blight; gene; ds; ribosomal DNA; rDNA.
XX OS
XX Lechevalieria aerocolonigenes.
XX US2004180960-A1.
XX PN
XX 16-SEP-2004.
XX PD

15-DEC-2005 (first entry)
XX DE
XX Nocardia sp. TP-A0674 16S ribosomal DNA, SEQ ID 1.
XX KW
XX Analgesic; Nootropic; Antiparkinsonian; Antiasthmatic; Respiratory-Gen.;
KW Uropathic; binding inhibitor; muscarinic acetylcholine receptor;
KW analgesic; Parkinsons disease; asthma;
KW chronic obstructive pulmonary disease; bladder disease;
KW micturition disorder; 16S ribosomal RNA; 16S rRNA; gene; ds.
XX OS
XX Nocardia sp.
XX JP2005289890-A.
XX PN
XX 20-OCT-2005.
XX PD
XX 31-MAR-2004; 2004JP-00107929.
XX PF
XX 31-MAR-2004; 2004JP-00107929.
XX PR
XX (YOSH ) YOSHITOMI PHARM IND KK.
XX PA
XX Furumai T, Igarashi Y, Onaka H, Ikeda Y, Nonaka H;
XX WPI; 2005-738172/76.
XX DR
XX Binding inhibitor of muscarinic acetylcholine receptor subtype 4 or 3
PT useful for treating diseases e.g. asthma, contains chelate having TPU
PT 0052A-F compound derived from Nocardia species TP-A0674 and metal ion.
XX PT
XX Disclosure; SEQ ID NO 1; 22pp; Japanese.
XX PS
XX The invention relates to a novel binding inhibitor of muscarinic
CC acetylcholine receptor subtype 4 or 3, comprising a chelate having a TPU
CC 0052A-F compound or its salt and a metal ion. The invention further
CC comprises a method and a microorganism for producing the novel binding
CC inhibitor. The binding inhibitor and compound are useful as central
CC analgesics and memory improving drugs, for treating Parkinson's disease,
CC asthma, chronic obstructive pulmonary disease, overactive bladder,
CC frequent urination and urinary incontinence. This polynucleotide sequence
CC represents the 16S ribosomal DNA of a Nocardia sp. TP-A0674
CC microorganism, useful in producing a muscarinic acetylcholine receptor
CC binding inhibitor compound of the invention.
XX CC
SQ Sequence 1477 BP; 341 A; 357 C; 494 G; 285 T; 0 U; 0 Other;

Query Match 78.2%; Score 17.2; DB 14; Length 1477;
Best Local Similarity 86.4%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTCGG 22
Db 51 GTCGAGCGGTAAGGCCCTTCGG 72

RESULT 65
ADS17269
ID ADS17269 standard; DNA; 1488 BP.
XX AC
XX ADS17269;
XX CC
DT 02-DEC-2004 (first entry)
XX DE
XX Lechevalieria aerocolonigenes strain VK-A9 16S rDNA.
XX KW
XX Plant protectant; antibiotic; thiobutacin; antifungal; antioomycete;
XX KW phytophthora blight; gene; ds; ribosomal DNA; rDNA.
XX OS
XX Lechevalieria aerocolonigenes.
XX US2004180960-A1.
XX PN
XX 16-SEP-2004.
XX PD

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XX 13-JAN-2004; 2004US-00756683.
XX
XX
XX 13-MAR-2003; 2003KR-00015628.
XX
XX 13-MAR-2003; 2003KR-00015629.
XX
XX (HWAN/) HWANG B K.
XX (LBEJ/) LEE J Y.
XX
XX Hwang BK, Lee JY;
XX
XX WPI; 2004-661528/64.
XX
XX EMBL; AY196703.
XX
XX New antibiotic compound, thiobutacin, is used to treat plant disease e.g.
XX phytophthora blight and to control plant diseases caused by pathogens
XX e.g. Phytophthora capsici and Botrytis cinerea.
XX
XX Example 2; SEQ ID NO 1; 17pp; English.
XX
XX The invention relates to an antibiotic compound thiobutacin and
XX antifungal and antioomycete compositions comprising thiobutacin.
XX Thiobutacin is used to treat plant disease such as phytophthora blight
XX and to control plant diseases caused by pathogens e.g. Phytophthora
XX capsici and Botrytis cinerea. The present sequence is the lechevalieria
XX aerocolonigenes strain VK-A9 16S ribosomal DNA (rDNA). L. aerocolonigenes
XX strain VK-A9 has strong antifungal and antimicrobial activity and it can
XX inhibit the growth of Phytophthora capsici.
XX
XX Sequence 1488 BP; 339 A; 369 C; 508 G; 272 T; 0 U; 0 Other;
XX
XX Query Match 78.2%; Score 17.2; DB 13; Length 1488;
XX Best Local Similarity 86.4%; Pred. No. 1.4e+02;
XX Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
Qy 1 GTCGAACGGGAAGCCCTTCGG 22
Db 46 GTCGAGCGGTAAAGCCCTTCGG 67
XX
XX RESULT 65
XX ADW12667
XX ID ADW12667 standard; DNA; 1514 BP.
XX
XX AC ADW12667;
XX
XX 07-APR-2005 (first entry)
XX
XX Rhodococcus opacus 16S rDNA, SEQ ID NO:2.
XX
XX Stereoselective synthesis; enantiomeric enrichment;
XX beta-amino acid synthesis; cell culture; 16S ribosomal RNA; 16S rRNA; ds.
XX
XX Rhodococcus opacus.
XX
XX US2005009151-A1.
XX
XX 13-JAN-2005.
XX
XX 22-JUN-2004; 2004US-00875161.
XX
XX 10-JUL-2003; 2003US-0486032P.
XX
XX 02-SEP-2003; 2003US-0499622P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Chase M, Clayton R, Landis B, Banerjee A;
XX
XX WPI; 2005-110890/12.
XX
XX Stereoselective synthesis of beta-amino acid such as D-beta- or L-beta-
XX phenylalanine, by contacting amino donor and amino acceptor in presence
XX of beta-amino acid transaminase to form beta-amino acid enantiomer, from
XX
XX amino acceptor.
XX
XX Claim 78; SEQ ID NO 2; 44pp; English.
XX
XX The invention relates to methods for the stereoselective synthesis and
XX for the enantiomeric enrichment of a beta-amino acid or its salt. The
XX methods involve contacting an amino donor and an amino acceptor in the
XX presence of a stereoselective beta-amino acid transaminase to form a beta
XX -amino acid enantiomer (or its salt) from the amino acceptor. The
XX invention also relates to purified stereoselective D-beta-transaminases
XX derived from a microorganism of the genera Variovorax, Nocardia,
XX Comamonas, Rhodococcus or Pseudomonas; purified stereoselective L-beta-
XX transaminases derived from a microorganism of the genus Alcaligenes;
XX methods of selecting and culturing microorganisms which express a beta-
XX transaminase; purified cultures of Variovorax paradoxus or Rhodococcus
XX opacus; the 16S ribosomal RNA gene (rDNA) of Variovorax paradoxus or
XX Rhodococcus opacus (ADW12666 and ADW12667, respectively); and a method of
XX detecting these 16S rDNA sequences. The methods of the invention are
XX useful for stereoselectively synthesizing a beta-amino acid such as D-
XX beta-phenylalanine or L-beta-phenylalanine, or for enriching one or the
XX other enantiomer in a racemic mixture. In the examples of the invention,
XX microorganisms from soil samples from two different environments were
XX screened transaminase activity on DL-beta-phenylalanine. Ribosomal DNA
XX sequencing was used to facilitate the taxonomic identification of two
XX purified microorganisms from the environmental samples. The present
XX sequence represents the specifically claimed 16S rDNA sequence which was
XX identified as originating from Rhodococcus opacus.
XX
XX Sequence 1514 BP; 339 A; 368 C; 509 G; 286 T; 0 U; 12 Other;
XX
XX Query Match 78.2%; Score 17.2; DB 14; Length 1514;
XX Best Local Similarity 86.4%; Pred. No. 1.4e+02;
XX Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
Qy 1 GTCGAACGGGAAGCCCTTCGG 22
Db 57 GTCGAGCGGTAAAGCCCTTCGG 78
XX
XX RESULT 66
XX AEB98771
XX ID AEB98771 standard; DNA; 39 BP.
XX
XX AC AEB98771;
XX
XX 06-OCT-2005 (first entry)
XX
XX Mycobacterium avium identification LAMP primer, SEQ ID 13.
XX
XX microorganism detection; mycobacterium infection; antibacterial; primer;
XX PCR; ss; LAMP.
XX
XX Mycobacterium avium.
XX
XX Synthetic.
XX
XX JP2005204582-A.
XX
XX 04-AUG-2005.
XX
XX 23-JAN-2004; 2004JP-00015195.
XX
XX 23-JAN-2004; 2004JP-00015195.
XX
XX (ASAH ) ASahi KASEI KK.
XX
XX Oda N;
XX
XX WPI; 2005-526965/54.
XX
XX New single-stranded oligonucleotide, useful for amplifying the nucleic
XX acid of Mycobacterium avium, Mycobacterium intracellulare, and
XX Mycobacterium kansasii.
XX

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PS Claim 1; SEQ ID NO 13; 14pp; Japanese.

XX The invention relates to a novel single-stranded oligonucleotide used in

CC a detection method of an atypical mycobacteria group. The invention

CC further includes: amplifying the nucleic acid of Mycobacterium avium by a

CC loop-mediated isothermal amplification (LAMP) method; amplifying the

CC nucleic acid of M. intracellulare by a LAMP method; and a kit for detecting the

CC nucleic acid of M. kansasii by a LAMP method; and a kit for detecting the

CC nucleic acid of M. avium by a LAMP method; detecting the nucleic acid of

CC M. intracellulare by a LAMP method; or detecting the nucleic acid of M.

CC kansasii by a LAMP method. The single-stranded oligonucleotide is useful

CC in medical applications. This oligo sequence represents a loop-mediated

CC isothermal amplification (LAMP) primer used in the exemplification of the

XX invention.

SQ Sequence 39 BP; 10 A; 11 C; 10 G; 8 T; 0 U; 0 Other;

Query Match 77.3%; Score 17; DB 14; Length 39;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGACGGAAGGCCT 17

DB 23 GTCGACGGAAGGCCT 39

RESULT 67

AAT45276

ID AAT45276 standard; rRNA; 1391 BP.

XX AC AAT45276;

XX 12-SEP-1997 (first entry)

XX Corynebacterium diphtheriae 16S rRNA.

XX Ribosomal RNA; species specific; detection; reverse transcription;

XX primer; hybridisation probe; identification; ss.

XX Corynebacterium diphtheriae.

XX Key Location/Qualifiers

FT misc_feature 38..59

FT /*tag= a

FT /notes= "Defined as nucleotides 72-100"

FT misc_feature 153..170

FT /*tag= b

FT /notes= "Defined as nucleotides 195-215"

FT misc_feature 415..431

FT /*tag= c

FT /notes= "Defined as nucleotides 466-494"

FT misc_feature 544..567

FT /*tag= d

FT /notes= "Defined as nucleotides 544-567"

FT misc_feature 773..787

FT /*tag= e

FT /notes= "Defined as nucleotides 838-853"

FT misc_feature 793..808

FT /*tag= f

FT /notes= "Defined as nucleotides 859-875"

FT misc_feature 946..965

FT /*tag= g

FT /notes= "Defined as nucleotides 1013-1032"

XX

PN FR2733755-A1.

XX 08-NOV-1996.

XX 03-MAY-1995; 95PR-00005494.

XX 03-MAY-1995; 95FR-00005494.

XX (INMR) BIO MERIEUX.

XX Mabilat C, Ruimy R;

XX WPI; 1997-001738/01.

XX Fragments of Corynebacterium 16S RNA - useful as probes and primers for

XX identifying Corynebacterium spp.

XX Claim 1; Fig 1; 60pp; French.

XX Fragments covering 90 % of the sequence of 16S ribosomal RNA were

XX amplified from 28 strains of 25 different species of Corynebacterium by

XX PCR using primers specific for eubacteria. The amplification products

XX were sequenced and the sequences were aligned for comparison. It was

XX found that certain regions, i.e. those corresponding to nucleotides 72-

XX 100, 195-215, 466-494, 608-631, 838-853, 859-875 and 1013-1033 in the 16S

XX ribosomal RNA of C. diphtheriae (refer to features table for the present

XX sequence), vary considerably between different species. Probes and

XX primers comprising at least 5 nucleotides from one of these species-

XX specific sequences, including the present sequence, or their complements,

XX are useful to distinguish between different Corynebacterium species. DNA

XX versions of the probes and primers are also included

SQ Sequence 1391 BP; 309 A; 317 C; 464 G; 1 T; 295 U; 5 Other;

Query Match 77.3%; Score 17; DB 2; Length 1391;

Best Local Similarity 88.2%; Pred. No. 1.8e+02;

Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGACGGAAGGCCT 17

DB 33 GUCGACGGAAGGCCU 49

RESULT 68

ABN86276

ID ABN86276 standard; DNA; 1457 BP.

XX AC ABN86276;

XX 08-OCT-2002 (first entry)

XX G. polyisoprenivorans P8219 16S rDNA sequence #2.

XX Microorganism; environmental; hormone; phthalic acid; alkyl ester; ds.

XX Gordonia polyisoprenivorans.

XX JP2002142754-A.

XX 21-MAY-2002.

XX 08-NOV-2000; 2000JP-00341214.

XX 08-NOV-2000; 2000JP-00341214.

XX (IMBI-) IMB KK.

XX WPI; 2002-561124/60.

XX A Gordonia sp. microorganism, useful in the eradication of the

XX environmental hormone of phthalic acid esters for environmental

XX protection.

XX Disclosure; Fig 2A-D; 21pp; Japanese.

XX The invention relates to a Gordonia sp. microorganism, capable of

XX eradication of the environmental hormone of phthalic acid alkyl esters.

XX The microorganism is used in the eradication of phthalic acid esters for

XX environmental protection. The present sequence represents an alternate G.

XX polyisoprenivorans P8219 16S rDNA sequence

SQ Sequence 1457 BP; 323 A; 348 C; 493 G; 291 T; 0 U; 2 Other;

Query Match 76.4%; Score 16.8; DB 6; Length 1457;
 Best Local Similarity 90.0%; Pred. No. 2.3e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCCCTTC 20
 |||||
 Db 44 GTCGACGGAAGGCCCTGC 63

RESULT 69

ABN86275

ID ABN86275 standard; DNA; 1457 BP.

XX AC

XX AC

XX 08-OCT-2002 (first entry)

XX

XX

XX G. polyisoprenivorans P8219 16S rDNA sequence.

XX

XX Microorganism; environmental; hormone; phthalic acid; alkyl ester; ds.

XX

XX Gordonia polyisoprenivorans.

XX

XX JP2002142754-A.

XX

XX 21-MAY-2002.

XX

XX 08-NOV-2000; 2000JP-00341214.

XX

XX 08-NOV-2000; 2000JP-00341214.

XX

XX (IMBI-) IMB KK.

XX

XX WPI; 2002-561124/60.

XX

XX A Gordonia sp. microorganism, useful in the eradication of the
 PT environmental hormone of phthalic acid esters for environmental
 PT protection.

XX

XX Disclosure; Fig 2A-D; 2lpp; Japanese.

XX

XX The invention relates to a Gordonia sp. microorganism, capable of
 CC eradication of the environmental hormone of phthalic acid alkyl esters.
 CC The microorganism is used in the eradication of phthalic acid esters for
 CC environmental protection. The present sequence represents a G.
 CC polyisoprenivorans P8219 16S rDNA sequence

XX

SQ Sequence 1457 BP; 322 A; 349 C; 496 G; 290 T; 0 U; 0 Other;

Query Match 76.4%; Score 16.8; DB 6; Length 1457;
 Best Local Similarity 90.0%; Pred. No. 2.3e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCCCTTC 20
 |||||
 Db 44 GTCGACGGAAGGCCCTGC 63

RESULT 70

AAS59540/c

ID AAS59540 standard; DNA; 2743 BP.

XX

XX AC

XX AAS59540;

XX

XX 13-FEB-2002 (first entry)

XX

XX Propionibacterium acnes immunogenic protein encoding DNA #35.

XX

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant; ds.

XX Propionibacterium acnes.
 OS WO200181581-A2.
 PN
 XX
 PD 01-NOV-2001.
 XX
 XX 20-APR-2001; 2001WO-US012865.
 XX
 XX 21-APR-2000; 2000US-0199047P.
 PR
 PR 02-JUN-2000; 2000US-0208841P.
 PR
 PR 07-JUL-2000; 2000US-0216747P.
 XX
 XX (CORI-) CORIXA CORP.

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XX WO2003033515-A1.
 XX 24-APR-2003.
 XX 11-OCT-2002; 2002WO-US032727.
 XX 15-OCT-2001; 2001US-00978825.
 XX (CORI-) CORIXA CORP.
 XX Mitcham JL, Skeiky YAM, Persing DH, Bhatia A, Maisonneuve JL;
 PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
 PI Barth B, Vallieue-Dougllass J;
 XX WPI; 2003-381789/36.
 XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX Claim 1; SEQ ID NO 35; 1481pp; English.
 XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a P. acnes DNA config which is specifically claimed
 CC in the invention. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 2743 BP; 645 A; 999 C; 546 G; 551 T; 0 U; 2 Other;
 Query Match 76.4%; Score 16.8; DB 8; Length 2743;
 Best Local Similarity 90.0%; Pred. No. 2.5e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GTCGACGGAAAGCCCTTC 20
 Db 2589 GTCGACGGAAAGCCCTGC 2570
 RESULT 72
 ABV75558
 ID ABV75558 standard; DNA; 36538 BP.
 XX AC ABV75558;
 XX DT 22-JAN-2003 (first entry)
 XX Saccharopolyspora butenyl-spinosyn biosynthetic gene cluster 2.
 DE Butenyl; biosynthetic enzyme; PKS; polyketide synthetase; macrolide;
 XX metabolite; spinosyn; gene; ds.
 KW

XX Saccharopolyspora sp.
 OS
 XX
 FH Location/Qualifiers
 CDS complement(114..938)
 FT /tag= a
 FT /product= "busp"
 FT /note= "No start codon given"
 FT 1389..2561
 FT /tag= b
 FT /product= "busG"
 FT 2601..3353
 FT /tag= c
 FT /product= "bush"
 FT complement(3359..4546)
 FT /tag= d
 FT /product= "busI"
 FT 4684..6303
 FT /tag= e
 FT /product= "busJ"
 FT 6317..7510
 FT /tag= f
 FT /product= "busK"
 FT 7555..8406
 FT /tag= g
 FT /product= "busL"
 FT /note= "No start codon given"
 FT 8640..9572
 FT /tag= h
 FT /product= "busM"
 FT /note= "No start codon given"
 FT complement(9668..10666)
 FT /tag= i
 FT /product= "busN"
 FT complement(10675..12135)
 FT /tag= j
 FT /product= "busO"
 FT complement(12864..14177)
 FT /tag= k
 FT /product= "busP"
 FT 14627..15970
 FT /tag= l
 FT /product= "busQ"
 FT /note= "No start codon given"
 FT 16008..17144
 FT /tag= m
 FT /product= "busR"
 FT /note= "No start codon given"
 FT 17168..17917
 FT /tag= n
 FT /product= "busS"
 FT complement(18520..19932)
 FT /tag= o
 FT /product= "ORF LI"
 FT complement(19978..20488)
 FT /tag= p
 FT /product= "ORF LII"
 FT /note= "No start codon given"
 FT complement(20536..21033)
 FT /tag= q
 FT /product= "ORF LIII"
 FT /note= "No start codon given"
 FT 21179..21925
 FT /tag= r
 FT /product= "ORF LIV"
 FT complement(22671..23453)
 FT /tag= s
 FT /product= "ORF LVI"
 FT complement(23687..24886)
 FT /tag= t
 FT /product= "ORF LVII"
 FT complement(26177..26923)
 FT /tag= u

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FT FT /product= "ORF LVIII"
FT FT /note= "No start codon given"
FT CDS 27646. .28476
FT FT /*tag= v
FT FT /product= "ORF LIX"
FT FT /note= "No start codon given"
XX
XX
XX WO200279477-A2.
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009968.
XX
XX 30-MAR-2001; 2001US-0280175P.
XX
XX (DOWC ) DOW AGROSCIENCES LLC.
XX
XX Hahn DR, Jackson JD, Bullard BS, Gustafson GD, Waldron C;
XX Mitchell JC;
XX
XX WPI; 2003-058434/05.
XX P-PSDB; ABP57683, ABP57684, ABP57685, ABP57686, ABP57687, ABP57688,
XX ABP57689, ABP57690, ABP57691, ABP57692, ABP57693, ABP57694, ABP57695,
XX ABP57696, ABP57697, ABP57698, ABP57699, ABP57700, ABP57701, ABP57702,
XX ABP57703, ABP57704.
XX
XX New butenyl-spinosyn biosynthetic genes, useful for increasing the
XX production of butenyl-spinosyn insecticidal macrolides, or for changing
XX the metabolites or products produced by spinosyn-producing
XX microorganisms.
XX
XX Claim 2; Page 99-119; 218pp; English.
XX
XX The invention relates to a novel DNA molecule comprising a DNA sequence
XX that encodes a butenyl-spinosyn biosynthetic enzyme, a butenyl-spinosyn
XX PKS (polyketide synthetase) domain, or a spinosyn PKS module. The butenyl-
XX -spinosyn biosynthetic genes are useful for increasing the production of
XX butenyl-spinosyn insecticidal macrolides. The genes are also useful for
XX changing the metabolites or products produced by spinosyn-producing
XX microorganisms. The present sequence represents a DNA molecule encoding
XX butenyl-spinosyn biosynthetic enzymes
XX
XX SQ Sequence 36538 BP; 6867 A; 12266 C; 11182 G; 6223 T; 0 U; 0 Other;
XX
XX Query Match 76.4%; Score 16.8; DB 10; Length 36538;
XX Best Local Similarity 90.0%; Pred. No. 3.2e+02;
XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 1 GTCGAACGGAAGGCTTTC 20
XX ||||| |||||
XX 7521 GTCGAACGACACAGGCTTTC 7540
XX
XX RESULT 73
XX AAV24413
XX ID AAV24413 standard; preRNA; 23 BP.
XX
XX AC AAV24413;
XX
XX 24-AUG-1998 (first entry)
XX
XX Target sequence #2 for M. intracellulare specific probe.
XX
XX Probe; target sequence; hybridisation; mycobacterial cell sensitivity;
XX antimicrobial agent; pre-rRNA detection; ss.
XX
XX Synthetic.
XX OS Mycobacterium intracellulare.
XX
XX US5770373-A.
XX
XX 23-JUN-1998.
XX

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PF 08-NOV-1996; 96US-00745638.
XX
XX 16-JUN-1994; 94US-00261068.
XX 07-JUN-1995; 95US-00485602.
XX
XX (BECT ) BECTON DICKINSON & CO.
XX
XX Cangelosi GA, Britschgi TB;
XX WPI; 1998-376792/32.
XX
XX Mycobacterial sensitivity and drug screening assays - involving release
XX of pre-rRNA by lysis.
XX
XX Example 4; Col 17-18; 50pp; English.
XX
XX This sequence represents a target sequence for mycobacterial probes. This
XX sequence represents a precursor RNA fragment that is released during the
XX method of the invention. The method is for the determination of
XX mycobacterial cell sensitivity to an antimicrobial agent, and comprises:
XX (a) culturing the cells in the presence of the antimicrobial agent; (b)
XX treating the cells by enzymatic or mechanical means to expose the cell
XX membrane to lysis reagents, and contacting the cells with a lysis reagent
XX under conditions such that pre-rRNA is released from the cells but not
XX degraded; and (c) detecting the pre-rRNA with an oligonucleotide probe
XX capable of hybridising to a region of the pre-rRNA that is not present in
XX mature mycobacterial rRNA, where sensitivity to the antimicrobial agent
XX is indicated by an increase or decrease in pre-rRNA levels for cells
XX exposed to the antimicrobial agent compared with mycobacterial cells not
XX exposed to the antimicrobial agent. The lysis method, unlike known
XX methods, results in detectable levels of pre-rRNA
XX
XX SQ Sequence 23 BP; 6 A; 6 C; 7 G; 0 T; 3 U; 1 Other;
XX
XX Query Match 74.5%; Score 16.4; DB 2; Length 23;
XX Best Local Similarity 78.9%; Pred. No. 2.4e+02;
XX Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 4 GAACGGAAGGCTTTCGG 22
XX ||||| |||||
XX 1 GAACGGAAGNCCUUCGG 19
XX
XX Db
XX
XX RESULT 74
XX AAV13021
XX ID AAV13021 standard; rRNA; 23 BP.
XX
XX AC AAV13021;
XX
XX 18-MAY-1998 (first entry)
XX
XX Mycobacterium intracellulare mature rRNA target sequence SEQ ID NO:56.
XX
XX Mycobacterium; pre-rRNA; precursor ribosomal RNA; target sequence; probe;
XX hybridisation; antibiotic resistance; cell lysis; ss.
XX
XX OS Mycobacterium intracellulare.
XX
XX US5712095-A.
XX
XX 27-JAN-1998.
XX
XX 07-JUN-1995; 95US-00485602.
XX
XX 16-JUN-1994; 94US-00261068.
XX
XX (BECT ) BECTON DICKINSON CO.
XX
XX Cangelosi GA, Britschgi TB;
XX WPI; 1998-119975/11.
XX
XX Assay for pre-ribosomal RNA in mycobacterium cells - by hybridisation
XX

```

PT with specific probes after cell lysis.
 XX Disclosure; Col 18; 54pp; English.
 XX
 CC The present sequence represents a mycobacterial mature ribosomal RNA
 CC target sequence. The present invention describes a method for detecting
 CC pre-rRNA in cells of a mycobacterial sample. The method comprises: (a)
 CC treating the cells to release pre-rRNA by: (i) pretreating the cells by
 CC enzymatic degradation using both lysozyme and protease until their cell
 CC walls are rendered porous to expose their cell membranes, making the
 CC cells susceptible to lysis; (ii) contacting the pretreated cells with a
 CC combination of a magnesium chelator, a nonionic detergent and an anionic
 CC detergent; and (iii) heating the cells to 75-99 degrees Celsius until the
 CC mycobacterial cells are lysed; and (b) detecting the pre-rRNA using at
 CC least one oligonucleotide probe which is capable of selectively
 CC hybridizing to a region of the pre-rRNA that is not present in a mature
 CC mycobacterial RNA. The probes can be used to identify many Mycobacterium
 CC spp. including M. tuberculosis, M. leprae, M. habana, M. avium, M. bovis,
 CC M. lufu, M. paratuberculosis, M. marinum, M. simiae and/or M.
 CC intracellulare. The probes may also be used to measure mycobacterial
 CC response to inhibitors of RNA and protein synthesis and may therefore be
 CC used to screen new antimycobacterial drugs. Mycobacteria have a slow
 CC growth rate. By using the probes, drug developers can now identify
 CC compounds that are more effective, but less stable than those previously
 CC identified
 XX
 SQ Sequence 23 BP; 6 A; 6 C; 7 G; 0 T; 3 U; 1 Other;
 Query Match 74.5%; Score 16.4; DB 2; Length 23;
 Best Local Similarity 78.9%; Pred. No. 2.4e+02;
 Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 4 GAACGGGAAGCCTTCGG 22
 ||||| :|||
 Db 1 GAACGGGAAGCCTTCGG 19
 RESULT 75
 AAX99198
 ID AAX99198 standard; DNA; 50 BP.
 AC AAX99198;
 XX
 DT 28-SEP-1999 (first entry)
 XX
 DE M. smegmatis 16S rRNA gene fragment.
 XX
 KW Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA;
 KW shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.
 XX
 OS Mycobacterium smegmatis.
 XX
 FN WO9935284-A1.
 XX
 PD 15-JUL-1999.
 XX
 PF 30-DEC-1997; 97WO-BR000087.
 XX
 PR 30-DEC-1997; 97WO-BR000087.
 XX
 PA (UYMI-) UNIV FEDERAL MINAS GERAIS.
 XX
 PI Peregrino Ferreira PC, Geessien Kroon E;
 PI Bernardes Margutti Pinto ME, Aleixo AW;
 XX
 DR WPI; 1999-444201/37.
 XX
 PT Detection of mycobacteria by shift mobility assay.
 XX
 PS Disclosure; Fig 7; 20pp; English.
 XX
 PA (UYMI-) UNIV FEDERAL MINAS GERAIS.
 XX
 PI Peregrino Ferreira PC, Geessien Kroon E;
 PI Bernardes Margutti Pinto ME, Aleixo AW;
 XX
 DR WPI; 1999-444201/37.
 XX
 PT Detection of mycobacteria by shift mobility assay.
 XX
 PS Disclosure; Fig 7; 20pp; English.
 XX
 CC The invention describes a new method for diagnosis, identification and
 CC characterisation of Mycobacterium tuberculosis or any other mycobacteria

CC by using polymerase chain reaction (PCR) and shift mobility assay (SMA)
 CC in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,
 CC DNA amplification and Shift mobility assay. The method is based on
 CC divergence in sequences found in 16S rRNA to identify mycobacteria
 CC species, since a remarkable shift of heteroduplex bands are obtained
 CC between single stranded and homoduplex bands in UPAGE. The method is
 CC fast, simple and can produce information not easily obtained when
 CC compared with other detection methods. The sensitivity of other assays
 CC suffer due to the tendency of the denatured PCR product strands to
 CC reassociate and exclude oligonucleotide probes, and steric interference
 CC between the bound oligonucleotides and the solid support which impede
 CC hybridization to nucleic acids in solution. Sequences AAX99193-237
 CC represent 16S rRNA gene regions of some mycobacterial species
 XX
 SQ Sequence 50 BP; 13 A; 12 C; 15 G; 9 T; 0 U; 1 Other;
 Query Match 74.5%; Score 16.4; DB 2; Length 50;
 Best Local Similarity 89.5%; Pred. No. 2.6e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GTCGAACGGAAGGCCTTT 19
 ||||| :|||
 Db 13 GTCGAACGGAAGGCCTTT 31
 RESULT 76
 AAX99201
 ID AAX99201 standard; DNA; 50 BP.
 AC AAX99201;
 XX
 DT 27-AUG-2003 (revised)
 DT 28-SEP-1999 (first entry)
 XX
 DE M. simium 16S rRNA gene fragment.
 XX
 KW Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA;
 KW shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.
 XX
 OS Mycobacterium simiae.
 XX
 FN WO9935284-A1.
 XX
 PD 15-JUL-1999.
 XX
 PF 30-DEC-1997; 97WO-BR000087.
 XX
 PR 30-DEC-1997; 97WO-BR000087.
 XX
 PA (UYMI-) UNIV FEDERAL MINAS GERAIS.
 XX
 PI Peregrino Ferreira PC, Geessien Kroon E;
 PI Bernardes Margutti Pinto ME, Aleixo AW;
 XX
 DR WPI; 1999-444201/37.
 XX
 PT Detection of mycobacteria by shift mobility assay.
 XX
 PS Disclosure; Fig 7; 20pp; English.
 XX
 PA The invention describes a new method for diagnosis, identification and
 CC characterisation of Mycobacterium tuberculosis or any other mycobacteria
 CC by using polymerase chain reaction (PCR) and shift mobility assay (SMA)
 CC in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,
 CC DNA amplification and Shift mobility assay. The method is based on
 CC divergence in sequences found in 16S rRNA to identify mycobacteria
 CC species, since a remarkable shift of heteroduplex bands are obtained
 CC between single stranded and homoduplex bands in UPAGE. The method is
 CC fast, simple and can produce information not easily obtained when
 CC compared with other detection methods. The sensitivity of other assays
 CC suffer due to the tendency of the denatured PCR product strands to
 CC reassociate and exclude oligonucleotide probes, and steric interference
 CC between the bound oligonucleotides and the solid support which impede

CC hybridization to nucleic acids in solution. Sequences AAX99193-237
 CC represent 16S rRNA gene regions of some mycobacterial species. (Updated
 CC on 27-AUG-2003 to correct OS field.)

XX Sequence 50 BP; 14 A; 11 C; 13 G; 9 T; 0 U; 3 Other;
 SQ

Query Match 74.5%; Score 16.4; DB 2; Length 50;
 Best Local Similarity 89.5%; Pred. NO. 2.6e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GTCGAACGGAAGGCTTT 19
 |||||
 Db 13 GTCGAACGGAAGNCCTT 31
 |||||

RESULT 77

ID ADA68711/c
 ID ADA68711 standard; DNA; 765 BP.

AC ADA68711;

XX 20-NOV-2003 (first entry)

XX Rice gene, SEQ ID 2034.

XX Plant; bacterial infection; fungal infection; viral infection; rice;
 KW gene; ds.

XX Oryza sativa.

XX WO2003000898-A1.

PN 03-JAN-2003.

XX 22-JUN-2001; 2001WO-1B001105.

XX 22-JUN-2001; 2001WO-1B001105.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
 PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;

XX WPI; 2003-175290/17.

XX Identifying at least one gene involved in plant resistance or response to
 PT pathogenic infection for conferring resistance or tolerance to a plant to
 PT bacterial, fungal or viral infection by determining or detecting plant
 PT gene expression.

XX Claim 6; SEQ ID NO 2034; 899pp; English.

XX The present invention relates to a method (M1) for identifying genes
 CC involved in plant resistance or response to pathogenic infection. M1
 CC comprises identifying a gene whose expression is significantly altered in
 CC the incompatible interaction of plant gene expression relative to
 CC expression of the gene in an uninfected plant, in a mutant plant that
 CC does not express a gene associated with response to pathogenic infection,
 CC or in a corresponding incompatible or compatible interaction. (M1) is
 CC useful for conferring resistance to resistance or tolerance to a plant to
 CC bacterial, fungal or viral infection. The present or tolerance was used to
 CC illustrate the invention.

SQ Sequence 765 BP; 207 A; 171 C; 153 G; 216 T; 0 U; 18 Other;

Query Match 73.6%; Score 16.2; DB 8; Length 765;
 Best Local Similarity 78.9%; Pred. NO. 4.3e+02;
 Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 4 GAACGGAAGGCTTTTCGG 22
 |||||

Db 725 GAAYGGAAGTCTTTCGR 707
 |||||

RESULT 78

ID ADW16249

XX ADW16249 standard; DNA; 1158 BP.

AC ADW16249;

XX 07-APR-2005 (first entry)

XX DNA copy of the Microbispora 16S ribosomal RNA EN2 isolate Seq 1.
 XX 16S ribosomal RNA; ds; 16S rRNA; medicinal plant; plant breeding;
 KW disease resistance; insect resistance; crop improvement;
 KW plant growth factor; antibacterial; antimicrobial; fungicide;
 KW insecticide; nematocide.

XX Microbispora.

XX WO2005003328-A1.

PN 13-JAN-2005.

XX 07-JUL-2004; 2004WO-AU000914.

XX 07-JUL-2003; 2003US-0485241P.

XX 22-SEP-2003; 2003US-0504703P.

XX (FLIN-) FLINDERS TECHNOLOGIES PTY LTD.

XX Franco CHM, Coombs JT;

XX WPI; 2005-091806/10.

XX Improving plant productivity comprises introducing into the plant or
 PT propagation material an endophytic actinomycete that facilitates
 PT induction of at least one characteristic related to improved
 PT productivity.

XX Claim 1; SEQ ID NO 1; 235pp; English.

XX This invention relates to a novel method for improving plant
 CC productivity. Specifically, it refers to introducing into the plant or
 CC propagation material an endophytic actinomycetes or variant thereof,
 CC where the actinomycetes facilitate induction of a characteristic related
 CC to improved productivity. The present invention further describes
 CC metabolites of the actinomycetes microorganism such as auxin, gibberellin
 CC or cytokinin that are able to induce disease resistance in plants i.e.
 CC provide disease bio-control capabilities against pathogen infection.
 CC Accordingly, the method facilitates the improvement of cereal crop
 CC productivity including increasing germination by up-regulating plant
 CC growth promoting activities, as well as improving plant vigor or flower
 CC and fruit yield. Furthermore, the new actinomycete or metabolite is
 CC useful in the manufacture of a medicament for the therapeutic and/or
 CC prophylactic treatment of a mammalian or non-mammalian subject i.e.
 CC plant. As such, this method provides plant protectants and plant growth
 CC stimulants that exhibit antibacterial, antimicrobial, fungicide,
 CC insecticide and nematocide activities. This polynucleotide is the DNA
 CC sequence of an actinomycetes 16S ribosomal RNA sequence of the invention.

XX Sequence 1158 BP; 247 A; 265 C; 379 G; 234 T; 0 U; 33 Other;

Query Match 73.6%; Score 16.2; DB 14; Length 1158;
 Best Local Similarity 85.7%; Pred. NO. 4.5e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 TCGAACGGAAGGCTTTTCGG 22
 |||||

Db 16 TCAAGCGGAAGGCTTTTCGG 36
 |||||

RESULT 79

ID AAD11277

XX AAD11277 standard; DNA; 23 BP.


```

XX AC AAD11277;
XX DT 24-SEP-2001 (first entry)
XX DE Mycobacterium 16S rRNA amplifying primer #21.
XX DE Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
XX KW Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
XX OS Mycobacterium sp.
XX PN WO200144510-A2.
XX PD 21-JUN-2001.
XX PF 17-DEC-1999; 99WO-US030346.
XX PR 17-DEC-1999; 99WO-US030346.
XX PA (GENP-) GEN-PROBE INC.
XX PA (INMR ) BIOMERIEUX SA.
XX PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX DR WPI; 2001-398170/42.
XX DT Detecting Mycobacterium species, involves in vitro amplification of 16S
XX PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using
XX PT specific primers, and detecting the amplified nucleic acid.
XX PS Claim 1; Page 37; 44pp; English.
XX CC The invention relates to a method of detecting Mycobacterium species,
XX CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
XX CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture
XX CC comprising a polymerase, and at least two primers, and then detecting the
XX CC amplified nucleic acid. The method is relatively simple and useful for
XX CC detecting the presence of various Mycobacterium species in a biological
XX CC sample, and thus important for diagnosis of infections resulting from
XX CC them. The method is especially important for screening opportunistic
XX CC infections caused by M. tuberculosis or a Mycobacterium other than
XX CC tuberculosis (MOTT). The present sequence is a PCR primer used for
XX CC amplifying Mycobacterium 16S rRNA
XX SQ Sequence 23 BP; 7 A; 7 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 72.7%; Score 16; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GTCGACGGAAAGGCC 16
Db 4 GTCGACGGAAAGGCC 19
RESULT 80
ADG88358
ID ADG88358 standard; DNA; 23 BP.
XX AC ADG88358;
XX DT 11-MAR-2004 (first entry)
XX DE Mycobacterium amplifying PCR primer #27.
XX KW In vitro amplification; PCR; primer; ss.
XX OS Mycobacterium xenopi.
XX PN US2003165824-A1.
XX PD 04-SEP-2003.

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XX PF 15-DEC-2000; 2000US-00738274.
XX PR 17-DEC-1999; 99US-0172190P.
XX PA (BREN/) BRENTANO S T.
XX PA (JUCK/) JUCKER M T.
XX PA (DELG/) DELGADO F D.
XX PA (CLEU/) CLEUZIAT P.
XX PA (RODR/) RODRIGUE M.
XX PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX DR WPI; 2003-898044/82.
XX DT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX PT in a biological sample comprises performing in vitro nucleic acid
XX PT amplification and detection of amplified products.
XX PS Claim 1; SEQ ID NO 27; 20pp; English.
XX CC The present invention relates to a method of detecting Mycobacterium
XX CC species present in a biological sample comprises performing an in vitro
XX CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
XX CC detecting the amplified Mycobacterium nucleic acid. The present sequence
XX CC is Mycobacterium amplifying PCR primer.
XX SQ Sequence 23 BP; 7 A; 7 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 72.7%; Score 16; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GTCGACGGAAAGGCC 16
Db 4 GTCGACGGAAAGGCC 19
RESULT 81
AEA08233
ID AEA08233 standard; DNA; 23 BP.
XX AC AEA08233;
XX DT 14-JUL-2005 (first entry)
XX DE Mycobacterium xenopi 16SrRNA amplifying non-T7 primer, SEQ ID NO: 27.
XX KW Microorganism detection; DNA amplification; 16S ribosomal RNA; 16S rRNA;
XX KW PCR; primer; ss.
XX OS Mycobacterium xenopi; ATCC 19250.
XX PN US2005100915-A1.
XX PD 12-MAY-2005.
XX PF 18-SEP-2003; 2003US-00665708.
XX PR 17-DEC-1999; 99US-0172190P.
XX PR 15-DEC-2000; 2000US-00738274.
XX PA (BREN/) BRENTANO S T.
XX PA (JUCK/) JUCKER M T.
XX PA (DELG/) DELGADO F D.
XX PA (CLEU/) CLEUZIAT P.
XX PA (RODR/) RODRIGUE M.
XX PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX DR WPI; 2005-345392/35.
XX PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present

```

PT in a biological sample, comprises using in vitro nucleic acid
 XX amplification and detection of amplified products.

PS Example 3; SEQ ID NO 27; 21pp; English.

CC The present invention relates to a method of detecting Mycobacterium
 CC species present in a biological sample. The method involves using in
 CC vitro nucleic acid amplification and detection of amplified products. The
 CC invention is useful for diagnostic detection of pathogenic bacteria such
 CC as Mycobacterium species. The present sequence is the Mycobacterium
 CC xenopi (ATCC 19250) 16S ribosomal RNA (16SrRNA) amplifying non-T7 PCR
 CC primer.

XX Sequence 23 BP; 7 A; 7 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 72.7%; Score 16; DB 14; Length 23;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16
 Db 4 GTCGAACGGAAGGCC 19

RESULT 82

ID AAD11278 standard; DNA; 26 BP.

AC AAD11278;

DT 24-SEP-2001 (first entry)

DE Mycobacterium 16S rRNA amplifying primer #22.

KW Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
 KW Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.

OS Mycobacterium sp.

XX WO200144510-A2.

XX 21-JUN-2001.

PF 17-DEC-1999; 99WO-US030346.

PR 17-DEC-1999; 99WO-US030346.

XX (GENP-) GEN-PROBE INC.
 XX (INNR) BIOMERIEUX SA.

PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;

DR WPI; 2001-398170/42.

XX Detecting Mycobacterium species, involves in vitro amplification of 16S
 PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using
 PT specific primers, and detecting the amplified nucleic acid.

PS Claim 1; Page 37; 44pp; English.

CC The invention relates to a method of detecting Mycobacterium species,
 CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
 CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture
 CC comprising a polymerase, and at least two primers, and then detecting the
 CC amplified nucleic acid. The method is relatively simple and useful for
 CC detecting the presence of various Mycobacterium species in a biological
 CC sample, and thus important for diagnosis of infections resulting from
 CC them. The method is especially important for screening opportunistic
 CC infections caused by M. tuberculosis or a Mycobacterium other than
 CC tuberculosis (MOTT). The present sequence is a PCR primer used for
 CC amplifying Mycobacterium 16S rRNA

XX Sequence 26 BP; 5 A; 6 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 72.7%; Score 16; DB 4; Length 26;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16
 Db 1 GTCGAACGGAAGGCC 16

RESULT 83

ADG88359
 ID ADG88359 standard; DNA; 26 BP.

XX AC ADG88359;

XX 11-MAR-2004 (first entry)

XX Mycobacterium amplifying PCR primer #28.

XX In vitro amplification; PCR; primer; ss.

XX Mycobacterium xenopi.

XX US2003165824-A1.

XX 04-SEP-2003.

XX 15-DEC-2000; 2000US-00738274.

XX 17-DEC-1999; 99US-0172190P.

XX (BREN/) BRENTANO S T.

XX (JUCK/) JUCKER M T.

XX (DELG/) DELGADO F D.

XX (CLEU/) CLEUZIAZ P.

XX (RODR/) RODRIGUE M.

XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;

XX WPI; 2003-898044/82.

XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
 PT in a biological sample comprises performing in vitro nucleic acid
 PT amplification and detection of amplified products.

PS Claim 1; SEQ ID NO 28; 20pp; English.

CC The present invention relates to a method of detecting Mycobacterium
 CC species present in a biological sample comprises performing an in vitro
 CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
 CC detecting the amplified Mycobacterium nucleic acid. The present sequence
 CC is Mycobacterium amplifying PCR primer.

XX Sequence 26 BP; 5 A; 6 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 72.7%; Score 16; DB 10; Length 26;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16
 Db 1 GTCGAACGGAAGGCC 16

RESULT 84

AEA08234
 ID AEA08234 standard; DNA; 26 BP.

XX AC AEA08234;

XX 14-JUL-2005 (first entry).

XX DT XX

DE Mycobacterium xenopi 16SrRNA amplifying non-T7 PCR primer, SEQ ID NO: 28.
XX Microorganism detection; DNA amplification; 16S ribosomal RNA; 16S rRNA;
KW PCR; primer; ss.
XX
XX Mycobacterium xenopi; ATCC 19250.
XX
XX US2005100915-A1.
XX
XX 12-MAY-2005.
XX
XX 18-SEP-2003; 2003US-00665708.
XX
XX 17-DEC-1999; 99US-01721190P.
XX
XX 15-DEC-2000; 2000US-00738274.
XX
XX (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAT P.
PA (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2005-345392/35.
XX
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample, comprises using in vitro nucleic acid
PT amplification and detection of amplified products.
XX
XX Example 3; SEQ ID NO 28; 21pp; English.
XX
XX The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample. The method involves using in
CC vitro nucleic acid amplification and detection of amplified products. The
CC invention is useful for diagnostic detection of pathogenic bacteria such
CC as Mycobacterium species. The present sequence is the Mycobacterium
CC xenopi (ATCC 19250) 16S ribosomal RNA (16SrRNA) amplifying non-T7 primer.
XX
XX Sequence 26 BP; 5 A; 6 C; 8 G; 7 T; 0 U; 0 Other;
SQ

Query Match 72.7%; Score 16; DB 14; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTCGACGGAAAGGCC 16
Db 1 GTCGACGGAAAGGCC 16
RESULT 85
AEB98776
ID AEB98776 standard; DNA; 39 BP.
XX
XX AEB98776;
XX
XX 06-OCT-2005 (first entry)
DT
XX Mycobacterium intracellulare identification LAMP primer, SEQ ID 18.
DE
XX microorganism detection; mycobacterium infection; antibacterial; primer;
KW PCR; ss; LAMP.
XX
XX Mycobacterium intracellulare.
OS Synthetic.
OS
XX JP2005204582-A.
PN
XX 04-AUG-2005.
PD
XX 23-JAN-2004; 2004JP-00015195.
XX
XX 23-JAN-2004; 2004JP-00015195.
PR

XX (ASAH) ASAH KASEI KK.
PA
XX Oda N;
PI
XX WPI; 2005-526965/54.
XX
XX New single-stranded oligonucleotide, useful for amplifying the nucleic
PT acid of Mycobacterium avium, Mycobacterium intracellulare, and
PT Mycobacterium kansasii.
XX
XX Claim 2; SEQ ID NO 18; 14pp; Japanese.
XX
XX The invention relates to a novel single-stranded oligonucleotide used in
CC a detection method of an atypical mycobacteria group. The invention
CC further includes: amplifying the nucleic acid of Mycobacterium avium by a
CC loop-mediated isothermal amplification (LAMP) method; amplifying the
CC nucleic acid of M. intracellulare by a LAMP method; amplifying the
CC nucleic acid of M. kansasii by a LAMP method; and a kit for detecting the
CC nucleic acid of M. avium by a LAMP method; detecting the nucleic acid of
CC M. intracellulare by a LAMP method; or detecting the nucleic acid of M.
CC kansasii by a LAMP method. The single-stranded oligonucleotide is useful
CC in medical applications. This oligo sequence represents a loop-mediated
CC isothermal amplification (LAMP) primer used in the exemplification of the
CC invention.
XX
XX Sequence 39 BP; 10 A; 12 C; 10 G; 7 T; 0 U; 0 Other;
SQ

Query Match 72.7%; Score 16; DB 14; Length 39;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTCGACGGAAAGGCC 16
Db 23 GTCGACGGAAAGGCC 38
RESULT 86
ADF94053
ID ADF94053 standard; DNA; 50 BP.
XX
XX ADF94053;
AC
XX 11-MAR-2004 (first entry)
DT
XX Microorganism detection probe, SEQ ID 146.
DE
XX Probe; detection; identification; microorganism; food; drug;
KW 16S rRNA V1 region; 16S rRNA V2 region; 16S rRNA V3 region; ss.
KW
XX Mycobacterium intracellulare.
OS
XX WO2003106676-A1.
PN
XX 24-DEC-2003.
PD
XX 16-JUN-2003; 2003WO-JP007620.
PF
XX 14-JUN-2002; 2002JP-00174564.
PR
XX (HISF) HITACHI SOFTWARE ENG CO LTD.
PA (MITS-) MITSUBISHI KAGAKU BIO-CLINICAL LAB INC.
PA
XX Hashida J, Ueno S, Muto I, Naruse K, Tamura M, Matsuda K;
PI Shimadzu M, Kobayashi I, Ishiko H;
PI
XX WPI; 2004-071565/07.
DR
XX 20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a
XX microorganism for specific detection and identification of the
PT microorganism in foods and drug compositions.
PT
XX Claim 2; SEQ ID NO 146; 150pp; Japanese.
PS

XX The present invention relates to probes (ADP93908-ADP94059) for the
 CC specific detection and identification of harmful microorganisms in
 CC samples of foods and drug compositions. The probe sequences are derived
 CC from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism,
 CC or its complementary sequence. Detection and identification of the
 CC microorganism is by amplification of the complete 16S rRNA gene using
 CC primers ADP94060 and ADP94061, labelling the amplification product (a
 CC fluorescence label is preferred), and hybridising to the probe or probes
 CC of the invention. The probes may be immobilised on a DNA chip. The
 CC microorganism is selected from *Actinobacillus actinomycetemcomitans*,
 CC *Acinetobacter calcoaceticus*, *Haemophilus influenzae*, *Stenotrophomonas*
 CC *malophilia*, *Proteus mirabilis*, *Streptococcus pneumoniae*, *Pseudomonas*
 CC *aeruginosa*, *Citrobacter freundii*, *Veillonella parvula*, *Providencia*
 CC *stuartii*, *Neisseria gonorrhoeae*, *Streptococcus agalactiae*, *Morganella*
 CC *morganii*, *Bacteroides fragilis*, *Staphylococcus hominis*, *Staphylococcus*
 CC *warneri*, *Staphylococcus haemolyticus*, *Enterobacter cloacae*, *Enterobacter*
 CC *aerogenes*, *Staphylococcus epidermidis*, *Streptococcus constellatus*,
 CC *Serratia marcescens*, *Streptococcus anginosus*, *Escherichia coli*,
 CC *Klebsiella pneumoniae*, *Enterococcus faecalis*, *Enterococcus faecium*,
 CC *Streptococcus sanguis*, *Streptococcus mitis*, *Streptococcus intermedius*,
 CC *Listeria monocytogenes*, *Clostridium perfringens*, *Corynebacterium*
 CC *aquaticum*, *Streptococcus oxalis*, *Staphylococcus aureus*, *Neisseria*
 CC *meningitidis*, *Campylobacter fetus*, *Enterococcus gallinarum*, *Enterococcus*
 CC *caseliflavus*, *Aeromonas hydrophila*, *Salmonella paratyphi*, *Salmonella*
 CC *typhi*, *Streptococcus equisimilis*, *Streptococcus canis*, *Klebsiella*
 CC *oxytoca*, *Staphylococcus saprophyticus*, *Pasteurella multocida*, *Eikenella*
 CC *corrodens*, *Streptococcus pyogenes*, *Moraxella catarrhalis*, *Legionella*
 CC *pneumophila*, *Mycobacterium tuberculosis*, *Mycobacterium avium*,
 CC *Mycobacterium intracellulare*, *Mycobacterium kansasii* or *Mycobacterium*
 CC *gordonae*.

XX Sequence 50 BP; 11 A; 12 C; 20 G; 7 T; 0 U; 0 Other;

Query Match 72.7%; Score 16; DB 12; Length 50;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTCGACGGAAAGGCC 16
 |||||
 Db 5 GTCGACGGAAAGGCC 20

RESULT 87
 ADU66542
 ID ADU66542 standard; DNA; 80 BP.

XX AC ADU66542;

XX 27-JAN-2005 (first entry)

XX Cut base A amplicon fragment.

XX ds; mass spectroscopy; DNA cleavage; DNA sequencing; sequencing.

XX Unidentified.

XX WO2004097369-A2.

XX 11-NOV-2004.

XX 22-APR-2004; 2004WO-US012520.

XX 25-APR-2003; 2003US-0466006P.

XX (SEQU-) SEQUENOM INC.

XX (BOEC/) BOECKER S.

XX Boecker S, Van Den Boom D;

XX WPI; 2005-012656/01.

XX Obtaining sequence information from target biomolecule, by fragmenting

PT target biomolecule by partial cleavage, performing mass spectrometry,
 PT extracting information from mass spectra, constructing sequencing graph
 PT and traversing graphs.

XX Disclosure; SEQ ID NO 11; 133pp; English.

XX This invention describes a novel method for obtaining sequence
 CC information from a target biomolecule and involves fragmenting the target
 CC biomolecule into several fragments by partial cleavage, performing mass
 CC spectrometry on fragments to produce mass spectra, extracting peak
 CC information from the produced mass spectra, constructing sequencing graph
 CC using the extracted peak information and traversing the sequencing graphs
 CC to reconstruct sequence information of the target biomolecule. The target
 CC biomolecule is nucleic acid molecule such as DNA or RNA, or is a protein
 CC and the compositions of the two fragments are the base compositions or
 CC amino acid compositions. This method preferably involves subjecting the
 CC nucleic acid molecule to partial cleavage reactions with one or more
 CC specific cleavage reagents, thus generating two or more fragments that
 CC are specific cleavage products, determining the molecular weights of the
 CC two or more fragments, determining the possible base compositions of the
 CC two or more fragments, ordering the possible base compositions of the two
 CC or more fragments according to the number of specific cleavage sites that
 CC are not cleaved in each fragment, constructing one or more sequencing
 CC graphs that are a graph theoretical representation of the ordered base
 CC compositions for the two or more fragments, and traversing the one or
 CC more sequencing graph to reconstruct one or more underlying sequence
 CC candidates, where each sequencing graph corresponds to the ordered base
 CC compositions derived from a partial cleavage reaction with one base-
 CC specific cleavage reagent. This method further involves scoring the one
 CC or more underlying sequence candidates and determining the rank order of
 CC fitness, where the scoring is done by statistical analysis or maximum
 CC likelihood statistical analysis. This method determines epigenetic
 CC changes in a target nucleic acid molecule relative to reference nucleic
 CC acid molecule and allows the sequencing of large biomolecules. The
 CC invention also describes a method of producing a candidate sequence of a
 CC biomolecule which involves receiving several sequencing graphs having
 CC several vertices and edges, where each vertex represents a compomer of
 CC the biomolecule and each edge represents a cut base of the sequencing
 CC graph and generating the candidate sequence by traversing several
 CC sequencing graphs. This second method further involves traversing several
 CC sequencing graphs by tracing through each sequencing graph, starting at a
 CC source vertex. The results of each method can be read by a program
 CC product for use in a computer that executes program instructions recorded
 CC in a computer-readable media to produce a candidate sequence of a
 CC biomolecule or to obtain sequence information in a target biomolecule.
 CC The target biomolecule contains a sequence variation, which is a mutation
 CC or a polymorphism. The target is a target nucleic acid molecule from an
 CC organism chosen from eukaryotes, prokaryotes and viruses, preferably a
 CC bacterium. The specific cleavage reagent is an RNase chosen from RNase
 CC T1, RNase U2, RNase Phym, RNase A, chicken liver RNase (RNase CL3) and
 CC cusavitin, or a glycosylase. The sequence variations in the target
 CC biomolecule permit genotyping a subject, forensic analysis, disease
 CC diagnosis or disease prognosis. The novel methods are useful for de novo
 CC sequencing, to identify genetic disease or chromosome abnormality,
 CC identifying a predisposition to a disease, or condition including an
 CC obesity, atherosclerosis, or cancer, to identify an infection by an
 CC infectious agent, to identify a pathogen, determine haplotypes, analyze
 CC microsatellite sequences, and short tandem repeat (STR) loci, determine
 CC allelic variation and/or frequency, and analyze cellular methylation
 CC patterns. This sequence represents an amplicon used to illustrate the
 CC sequencing technique described in the invention.

XX Sequence 80 BP; 18 A; 20 C; 27 G; 15 T; 0 U; 0 Other;

Query Match 72.7%; Score 16; DB 14; Length 80;

Best Local Similarity 100.0%; Pred. No. 4.3e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTCGACGGAAAGGCC 16

Db 54 GTCGACGGAAAGGCC 69

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RESULT 88
AEB98763
ID AEB98763 standard; DNA; 209 BP.
XX
XX AEB98763;
AC
XX
XX 06-OCT-2005 (first entry)
DT
XX
XX Mycobacterium intracellulare partial 16S rDNA sequence, SEQ ID 5.
DE
XX
XX microorganism detection; mycobacterium infection; antibacterial; ds.
XX
XX Mycobacterium intracellulare.
OS
XX
XX JP2005204582-A.
PN
XX
XX 04-AUG-2005.
PD
XX
XX 23-JAN-2004; 2004JP-00015195.
PF
XX
XX 23-JAN-2004; 2004JP-00015195.
PR
XX
XX (ASAH ) ASahi KASEI KK.
PA
XX
XX Oda N;
PI
XX
XX WPI; 2005-526965/54.
DR
XX
XX New single-stranded oligonucleotide, useful for amplifying the nucleic
PT acid of Mycobacterium avium, Mycobacterium intracellulare, and
PT Mycobacterium kansasii.
PT
XX
XX Example 1; SEQ ID NO 5; 14pp; Japanese.
PS
XX
XX The invention relates to a novel single-stranded oligonucleotide used in
CC a detection method of an atypical mycobacteria group. The invention
CC further includes: amplifying the nucleic acid of Mycobacterium avium by a
CC loop-mediated isothermal amplification (LAMP) method; amplifying the
CC nucleic acid of M. intracellulare by a LAMP method; amplifying the
CC nucleic acid of M. kansasii by a LAMP method; and a kit for detecting the
CC nucleic acid of M. avium by a LAMP method; detecting the nucleic acid of
CC M. intracellulare by a LAMP method; or detecting the nucleic acid of M.
CC kansasii by a LAMP method. The single-stranded oligonucleotide is useful
CC in medical applications. This polynucleotide represents a Mycobacterium
CC intracellulare partial 16S rDNA sequence amplified by the LAMP method of
CC the invention.
XX
XX Sequence 209 BP; 45 A; 47 C; 73 G; 44 T; 0 U; 0 Other;
SQ
Query Match 72.7%; Score 16; DB 14; Length 209;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16
Db 43 GTCGAACGGAAGGCC 58

RESULT 89
ABT23572
ID ABT23572 standard; DNA; 560 BP.
XX
XX ABT23572;
AC
XX
XX 22-MAY-2003 (first entry)
DT
XX
XX Stabilising reagent method related oligo SEQ ID No 24.
DE
XX
XX Stabilising reagent; PCR; primer; RNaseH; long-term storage;
XX specific amplification; pathogenic microorganism; chimeric;
XX genetic engineering; clinical medicine; ss.
XX
XX Mycobacterium avium.
OS

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XX WO2002101042-A1.
PN
XX 19-DEC-2002.
PD
XX
XX 12-JUN-2002; 2002WO-JP005832.
PF
XX
XX 12-JUN-2001; 2001JP-00177737.
PR 20-AUG-2001; 2001JP-00249689.
XX
XX (TAKI ) TAKARA BIO INC.
PA
XX
XX Sagawa H, Uemori T, Mukai H, Yamamoto J, Tomono J, Kobayashi E;
PI Enoki T, Asada K, Kato I;
PI
XX WPI; 2003-148805/14.
DR
XX
XX Method for stabilizing and storing reaction reagents for specific
PT amplification and detection of nucleic acids particularly in e.g.
PT identifying pathogenic microorganisms or viruses in sample.
XX
XX Example 15; Page 110; 177pp; Japanese.
PS
XX
XX The invention relates to a novel stabilising reaction reagent for use in
CC the amplification and/or detection of a target nucleic acid comprising:
CC preparing a reaction mixture with e.g. a nucleic acid as template, at
CC least 1 primer and RNaseH; and incubation of the reaction mixture for a
CC defined period of time to form a reaction product during the
CC amplification of such target nucleic acid. The method is useful for
CC stabilising and long-term storage of reaction reagents for highly
CC sensitive and specific amplification and detection of nucleic acids
CC particularly in identifying pathogenic microorganisms or viruses in a
CC sample using chimeric oligonucleotide primers, which is useful in genetic
CC engineering and clinical medicine. This polynucleotide sequence
CC represents an oligo relating to the novel stabilising reaction reagent
CC method of the invention
XX
XX Sequence 560 BP; 117 A; 134 C; 199 G; 110 T; 0 U; 0 Other;
SQ
Query Match 72.7%; Score 16; DB 10; Length 560;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16
Db 46 GTCGAACGGAAGGCC 61

RESULT 90
AAA02278
ID AAA02278 standard; cDNA; 935 BP.
XX
XX AAA02278;
AC
XX
XX 19-MAY-2000 (first entry)
DT
XX
XX Human colon cancer cell line polynucleotide sequence SEQ ID NO:2269.
DE
XX
XX Human; colon cancer; tumour; diagnosis; gene expression product; probe;
XX detection; cancerous state; metastasis; identification; breast cancer;
XX oestrogen receptor-positive breast cancer; therapy;
XX oestrogen receptor-negative breast cancer; lung cancer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9958675-A2.
PN
XX
XX 18-NOV-1999.
PD
XX
XX 13-MAY-1999; 99WO-US010602.
PF
XX
XX 14-MAY-1998; 98US-0085426P.
PR 15-MAY-1998; 98US-0085537P.
PR

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PR 15-MAY-1998; 98US-0085696P.
PR 21-OCT-1998; 98US-0105234P.
PR 27-OCT-1998; 98US-0105877P.
XX
PA (CHIR ) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
XX
PI Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
PI Reinhard C, Giese K, Randazzo F, Kennedy GC, Pot D, Kassam A;
PI Lamson G, Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
PI Leshkowitz D, Kita D, Garcia V, Jones LW, Stache-Crain B;
XX
DR WPI; 2000-126369/11.
XX
Polynucleotide library used to determine cancerous states of mammalian
cells.
XX
Claim 1; Page 892; 1097pp; English.
XX
AAA00010 to AAA02716 represent polynucleotides isolated from cDNA
libraries constructed from human colon cancer cell lines. The present
invention also describes a method of detecting differentially expressed
genes correlated with a cancerous state of a mammalian cell, comprising
detecting at least one differentially expressed gene product in a test
sample derived from a cell suspected of being cancerous, where detection
of the differentially expressed gene product is correlated with a
cancerous state of the cell from which the test sample was derived. The
polynucleotides sequences can be used in a method for detecting
differentially expressed genes correlated with a cancerous state of a
mammalian cell. The polynucleotides can also be used as probes for
detecting and mapping related genes. They can be used in diagnosis and
prognosis of diseases and disorders (e.g. identification of pre-
metastatic or metastatic cancerous states, stages of cancer, or
responsiveness of cancer to therapy). This is particularly for breast
cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
negative breast cancer, lung cancer, and colon cancer
XX
SQ Sequence 935 BP; 300 A; 234 C; 227 G; 44 T; 0 U; 130 Other;
Query Match 72.7%; Score 16; DB 3; Length 935;
Best Local Similarity 84.2%; Pred. No. 5.6e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 4 GAACGGAAAGCCTTTCGG 22
||| ||||| ||||| |||
Db 452 GAANGGAANGCGCTTTNGG 470

RESULT 91
AEA22410
ID AEA22410 standard; DNA; 1321 BP.
XX
AC AEA22410;
XX
XX
DT 25-AUG-2005 (first entry)
XX
DE Mycobacterium kubicae 16S rRNA sequence SEQ ID NO:11.
XX
KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
XX
OS Mycobacterium kubicae.
XX
PN US2005130168-A1.
XX
XX
PD 16-JUN-2005.
XX
PF 31-OCT-2003; 2003US-00697802.
XX
PR 31-OCT-2003; 2003US-00697802.
XX
XX (HANX/) HAN X.
PA (PHAM/) PHAM A S.
XX

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```

PI Han X, Pham AS;
XX
DR WPI; 2005-424597/43.
XX
PT Determining a bacterium species comprises providing oligonucleotide
PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
XX
XX Disclosure; SEQ ID NO 11; 74pp; English.
XX
The invention relates to a method (M1) for determining a bacterium
species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
extracting a genomic nucleotide from the bacterium to provide a
nucleotide template; (c) annealing a region of a nucleotide template to a
specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
complimentary fashion, the primer set designed to provide a product
having a predetermined size dictated by a complementary primer set; (d)
amplifying the region of the nucleotide template to produce the product;
and (e) determining a species of a bacterium in a nucleotide sequence of
the product. Also described is an alternative method (M2) for determining
a bacterium species comprising: (a) providing a specimen or a sample
having a template; (b) providing a pair of primers selected from: (i) a
first forward primer having consecutive bases of an AFB-f comprising any
of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
or variations and a first reverse primer having consecutive bases of an
AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
or their fragments or variations, (ii) a second forward primer having
consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
bp (AEA22489-AEA22516) or their fragments or variations and a second
reverse primer having consecutive bases of an UB-r comprising any of the
28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
variations, or (iii) a first forward primer having consecutive bases of
an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
second reverse primer having consecutive bases of an UB-r of AEA22517-
AEA22544 or their fragments or variations; (c) the specimen; and (d)
comparing the product from the specimen with a nucleotide sequence from a
database to determine the bacterium species present in the specimen. The
methods are useful for determining a bacterium species. The present
invention represents a Mycobacterium kubicae 16S rRNA nucleotide sequence,
which is used in the exemplification of the present invention.
XX
SQ Sequence 1321 BP; 287 A; 314 C; 457 G; 263 T; 0 U; 0 Other;
Query Match 72.7%; Score 16; DB 14; Length 1321;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GTCGAACGGAAAGGCC 16
||| ||||| ||||| |||
Db 18 GTCGAACGGAAAGGCC 33

RESULT 92
ADO85868/C
ID ADO85868 standard; DNA; 1344 BP.
XX
AC ADO85868;
XX
DT 29-JUL-2004 (first entry)
XX
DE Gordononia sp. bacterium 16S rDNA.
XX
KW microorganism; Gordononia genus; gram-positive bacillus; catalase;
KW nitrate reduction; alkali phosphatase; beta-galactosidase;
KW pyrazinamidase; pyrolidonyl allyl amidase; beta-glucuronidase;
KW alpha-glucosidase; urease; gelatin-liquefaction; esculin; glucose;
KW ribose; GK-004 strain; FERM P-18806;
KW cyclic hydrocarbon degradation agent; waste engine oil; 16S rDNA; ds.
XX
OS Gordononia sp.
XX
XX JP2004121068-A.
XX
PD 22-APR-2004.

```


PI Saitoh C, Yashiro A, Tokunaga C, Ozawa K, Yokoi A, Ogata N;
 PI Ochiai K, Ando K, Katahira H;
 DR WPI; 2000-062809/05.
 XX Production of seasoning liquors with the flavor of vegetables pickled in
 PT salted rice bran.
 XX
 XX Disclosure; Page 41-43; 45pp; Japanese.
 XX The invention relates to a method of producing seasoning liquors with the
 CC flavour of vegetables pickled in salted rice bran paste by culturing a
 CC microorganism in a rice bran dispersion to produce gamma-dodecalactone
 CC and/or gamma-dodecalactone. The microorganism produces lactic acid,
 CC propionic acid, gamma-dodecalactone and/or gamma-dodecalactone. The
 CC microorganism is especially a novel strain of *Corynebacterium* (strain NK-
 CC 1, FERM BP-6329) with properties defined in the specification. This
 CC sequence represents the 16S rRNA gene from the novel *Corynebacterium*
 CC strain. The seasoning liquor is used for preparing a salted rice bran
 CC pickle bed which provides pickles
 XX
 SQ Sequence 1460 BP; 320 A; 342 C; 492 G; 305 T; 0 U; 1 Other;
 Query Match 72.7%; Score 16; DB 3; Length 1460;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTCGAACGGAAGGCC 16
 Db 42 GTCGAACGGAAGGCC 57
 RESULT 95
 AEA22415
 ID AEA22415 standard; DNA; 1462 BP.
 XX AEA22415;
 XX 25-AUG-2005 (first entry)
 DT Mycobacterium szulgai 16S rRNA sequence SEQ ID NO:16.
 DE microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
 XX Mycobacterium szulgai.
 OS US2005130168-A1.
 PN 16-JUN-2005.
 PD 31-OCT-2003; 2003US-00697802.
 PF 31-OCT-2003; 2003US-00697802.
 PR (HANX/) HAN X.
 PA (PHAM/) PHAM A S.
 XX Han X, Pham AS;
 PI WPI; 2005-424597/43.
 XX Determining a bacterium species comprises providing oligonucleotide
 PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
 XX Disclosure; SEQ ID NO 16; 74pp; English.
 XX The invention relates to a method (M1) for determining a bacterium
 CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
 CC extracting a genomic nucleotide from the bacterium to provide a
 CC nucleotide template; (c) annealing a region of a nucleotide template to a
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
 CC complimentary fashion, the primer set designed to provide a product
 CC having a predetermined size dictated by a complimentary primer set; (d)

CC amplifying the region of the nucleotide template to produce the product;
 CC and (e) determining a species of a bacterium in a nucleotide sequence of
 CC the product. Also described is an alternative method (M2) for determining
 CC a bacterium species comprising: (a) providing a specimen or a sample
 CC having a template; (b) providing a pair of primers selected from: (i) a
 CC first forward primer having consecutive bases of an AFB-f comprising any
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
 CC or variations and a first reverse primer having consecutive bases of an
 CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
 CC or their fragments or variations, (ii) a second forward primer having
 CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
 CC bp (AEA22489-AEA22516) or their fragments or variations and a second
 CC reverse primer having consecutive bases of an UB-r comprising any of the
 CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
 CC variations, or (iii) a first forward primer having consecutive bases of
 CC an APF-f of AEA22417-AEA22452 or their fragments or variations and a
 CC second reverse primer having consecutive bases of an UB-r of AEA22517-
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)
 CC comparing the product from the specimen with a nucleotide sequence from a
 CC database to determine the bacterium species present in the specimen. The
 CC methods are useful for determining a bacterium species. The present
 CC sequence represents a *Mycobacterium szulgai* 16S rRNA nucleotide sequence,
 CC which is used in the exemplification of the present invention.
 XX
 SQ Sequence 1462 BP; 314 A; 350 C; 507 G; 291 T; 0 U; 0 Other;
 Query Match 72.7%; Score 16; DB 14; Length 1462;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTCGAACGGAAGGCC 16
 Db 24 GTCGAACGGAAGGCC 39
 RESULT 96
 AEA22414
 ID AEA22414 standard; DNA; 1484 BP.
 XX AEA22414;
 XX 25-AUG-2005 (first entry)
 DT Mycobacterium simiae 16S rRNA sequence SEQ ID NO:15.
 XX microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
 DE Mycobacterium simiae.
 OS US2005130168-A1.
 PN 16-JUN-2005.
 PD 31-OCT-2003; 2003US-00697802.
 PF 31-OCT-2003; 2003US-00697802.
 PR (HANX/) HAN X.
 PA (PHAM/) PHAM A S.
 XX Han X, Pham AS;
 PI WPI; 2005-424597/43.
 XX Determining a bacterium species comprises providing oligonucleotide
 PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
 XX Disclosure; SEQ ID NO 15; 74pp; English.
 XX The invention relates to a method (M1) for determining a bacterium
 CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
 CC extracting a genomic nucleotide from the bacterium to provide a
 CC nucleotide template; (c) annealing a region of a nucleotide template to a
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
 CC complimentary fashion, the primer set designed to provide a product
 CC having a predetermined size dictated by a complimentary primer set; (d)

CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
 CC complementary fashion, the primer set designed to provide a product
 CC having a predetermined size dictated by a complementary primer set; (d)
 CC amplifying the region of the nucleotide template to produce the product;
 CC and (e) determining a species of a bacterium in a nucleotide sequence of
 CC the product. Also described is an alternative method (M2) for determining
 CC a bacterium species comprising: (a) providing a specimen or a sample
 CC having a template; (b) providing a pair of primers selected from: (i) a
 CC first forward primer having consecutive bases of an AFB-f comprising any
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
 CC or variations and a first reverse primer having consecutive bases of an
 CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
 CC or their fragments or variations, (ii) a second forward primer having
 CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
 CC bp (AEA22489-AEA22516) or their fragments or variations and a second
 CC reverse primer having consecutive bases of an UB-r comprising any of the
 CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
 CC variations, or (iii) a first forward primer having consecutive bases of
 CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
 CC second reverse primer having consecutive bases of an UB-r of AEA22517-
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)
 CC comparing the product from the specimen with a nucleotide sequence from a
 CC database to determine the bacterium species present in the specimen. The
 CC methods are useful for determining a bacterium species. The present
 CC sequence represents a Mycobacterium simiae 16S rRNA nucleotide sequence,
 CC which is used in the exemplification of the present invention.

XX
 SQ Sequence 1484 BP; 320 A; 362 C; 509 G; 293 T; 0 U; 0 Other;

Query Match 72.7%; Score 16; DB 14; Length 1484;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGGAAGGCC 16
 |||||
 Db 24 GTCGAACGGGAAGGCC 39

RESULT 97

ADW92517
 ID ADM92517 standard; DNA; 1517 BP.

XX AC ADM92517;

XX DT 03-JUN-2004 (first entry)

XX DE Gordonia genus Actinomyces DNA sequence SeqID1.

XX KW Gordonia genus; Actinomyces; ammonia; nitrous acid oxidation;
 KW purifying fresh water; purifying seawater; ayu fish; flatfish; blowfish;
 KW gold fish; ds.

XX OS Gordonia.

XX PN JP2004081109-A.

XX PD 18-MAR-2004.

XX PF 27-AUG-2002; 2002JP-00247166.

XX PR 27-AUG-2002; 2002JP-00247166.

XX PA (KANM-) KANMONKAI KK.

XX DR WPI; 2004-233309/22.

XX PT Gordonia genus Actinomyces for purifying fresh water and seawater useful
 PT in raising ayu fish, flatfish, blowfish and gold fish, has ammonia
 PT utilizing ability and nitrous acid oxidation ability.

XX PS Disclosure; SEQ ID NO 1; 16pp; Japanese.

XX CC This invention relates to a novel Gordonia genus Actinomyces which has

CC ammonia utilizing ability and nitrous acid oxidation ability. The
 CC invention may be useful for purifying fresh water and seawater, of
 CC particular use in raising ayu fish, flatfish, blowfish and gold fish. The
 CC Gordonia genus actinomyces effectively suppresses concentration of
 CC ammonia and nitrous acid in fresh water and seawater, and provides
 CC purified water that is favourable for raising fishes.

XX SQ Sequence 1517 BP; 334 A; 363 C; 515 G; 304 T; 0 U; 1 Other;

Query Match 72.7%; Score 16; DB 12; Length 1517;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGGAAGGCC 16
 |||||
 Db 57 GTCGAACGGGAAGGCC 72

RESULT 98

AD071823
 ID AD071823 standard; DNA; 1517 BP.

XX AC AD071823;

XX DT 15-JUL-2004 (first entry)

XX DE DNA of RNA isolated from Gordonia sp. Kammonkai-1129 SeqID 1.

XX KW astaxanthin; canthaxanthine; microbial; livestock fodder; fish breeding;
 KW ds.

XX OS Gordonia sp.

XX PN JP2004089015-A.

XX PD 25-MAR-2004.

XX PF 29-AUG-2002; 2002JP-00251165.

XX PR 29-AUG-2002; 2002JP-00251165.

XX PA (KANM-) KANMONKAI KK.

XX DR WPI; 2004-253025/24.

XX PT Production of astaxanthin and canthaxanthine useful as fodder and feed
 PT for livestock, domestic fowl and fish, involves cultivating Actinomyces
 PT belonging to Gordonia genus.

XX PS Disclosure; SEQ ID NO 1; 13pp; Japanese.

XX CC This invention relates to a novel method for producing astaxanthin and
 CC canthaxanthine. Specifically, it refers to the cultivation of Actinomyces
 CC microbial cells belonging to the Gordonia genus using a fresh water or
 CC sea water mineral nutrition containing culture medium. The present
 CC invention describes producing astaxanthin and canthaxanthine for use as a
 CC fodder for livestock and domestic fowl, as well as a feed for fish
 CC breeding. The production method uses natural products and is efficient at
 CC a low cost. This polynucleotide sequence is a DNA copy of RNA isolated
 CC from the Gordonia sp. Kammonkai-1129 microorganism of the invention.

XX SQ Sequence 1517 BP; 334 A; 363 C; 515 G; 304 T; 0 U; 1 Other;

Query Match 72.7%; Score 16; DB 12; Length 1517;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGGAAGGCC 16
 |||||
 Db 57 GTCGAACGGGAAGGCC 72

RESULT 99

```
AEA22407
ID AEA22407 standard; DNA; 1527 BP.
XX
XX AEA22407;
AC
XX
XX 25-AUG-2005 (first entry)
DT
XX
XX Mycobacterium heckeshornense 16S rRNA sequence SEQ ID NO:8.
DE
XX microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
KW
XX Mycobacterium heckeshornense.
XX
XX OS
XX US2005130168-A1.
XX
XX 16-JUN-2005.
XX
XX 31-OCT-2003; 2003US-00697802.
XX
XX 31-OCT-2003; 2003US-00697802.
PR
XX (HANX/) HAN X.
PA (PHAM/) PHAM A S.
XX
XX Han X, Pham AS;
PI
XX WPI; 2005-424597/43.
DR
XX
XX Determining a bacterium species comprises providing oligonucleotide
XX primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
XX
XX Disclosure; SEQ ID NO 8; 74pp; English.
XX
XX The invention relates to a method (M1) for determining a bacterium
XX species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
XX extracting a genomic nucleotide from the bacterium to provide a
XX nucleotide template; (c) annealing a region of a nucleotide template to a
XX specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
XX complimentary fashion, the primer set designed to provide a product
XX having a predetermined size dictated by a complementary primer set; (d)
XX amplifying the region of the nucleotide template to produce the product;
XX and (e) determining a species of a bacterium in a nucleotide sequence of
XX the product. Also described is an alternative method (M2) for determining
XX a bacterium species comprising: (a) providing a specimen or a sample
XX having a template; (b) providing a pair of primers selected from: (i) a
XX first forward primer having consecutive bases of an AFB-f comprising any
XX of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
XX or variations; and a first reverse primer having consecutive bases of an
XX AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
XX or their fragments or variations; (ii) a second forward primer having
XX consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
XX bp (AEA22489-AEA22516) or their fragments or variations; and a second
XX reverse primer having consecutive bases of an UB-r comprising any of the
XX variations; or (iii) a first forward primer having consecutive bases of
XX an AFB-f of AEA22417-AEA22452 or their fragments or variations; and a
XX second reverse primer having consecutive bases of an UB-r of AEA22517-
XX AEA22544 or their fragments or variations; (c) the specimen; and (d)
XX comparing the product from the specimen with a nucleotide sequence from a
XX database to determine the bacterium species present in the specimen. The
XX methods are useful for determining a bacterium species. The present
XX sequence represents a Mycobacterium heckeshornense 16S rRNA nucleotide
XX sequence, which is used in the exemplification of the present invention.
XX
XX Sequence 1527 BP; 325 A; 365 C; 534 G; 303 T; 0 U; 0 Other;
XX
XX Query Match 72.7%; Score 16; DB 14; Length 1527;
XX Best Local Similarity 100.0%; Pred. No. 5.9e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GTCGACGGAAGGCC 16
XX ||||||||||||
XX 48 GTCGACGGAAGGCC 63
XX
XX
XX RESULT 100
XX AAD11264
XX ID AAD11264 standard; DNA; 32 BP.
XX
XX AAD11264;
AC
XX
XX 24-SEP-2001 (first entry)
DT
XX
XX Mycobacterium 16S rRNA amplifying primer #8.
DE
XX Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
KW Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
XX
XX Mycobacterium sp.
XX
XX WO200144510-A2.
XX
XX 21-JUN-2001.
XX
XX 17-DEC-1999; 99WO-US030346.
XX
XX 17-DEC-1999; 99WO-US030346.
XX
XX (GENP-) GEN-PROBE INC.
XX (INMR ) BIOMERIEUX SA.
XX
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
XX WPI; 2001-398170/42.
XX
XX Detecting Mycobacterium species, involves in vitro amplification of 16S
XX rRNA or DNA encoding RNA in nucleic acid amplification mixture using
XX specific primers, and detecting the amplified nucleic acid.
XX
XX Claim 1; Page 35; 44pp; English.
XX
XX The invention relates to a method of detecting Mycobacterium species,
XX that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
XX encoding 16S rRNA in an in vitro nucleic acid amplification mixture
XX comprising a polymerase, and at least two primers, and then detecting the
XX amplified nucleic acid. The method is relatively simple and useful for
XX detecting the presence of various Mycobacterium species in a biological
XX sample, and thus important for diagnosis of infections resulting from
XX them. The method is especially important for screening opportunistic
XX infections caused by M. tuberculosis or a Mycobacterium other than
XX tuberculosis (MOTT). The present sequence is a PCR primer used for
XX amplifying Mycobacterium 16S rRNA
XX
XX Sequence 32 BP; 10 A; 6 C; 10 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 71.8%; Score 15.8; DB 4; Length 32;
XX Best Local Similarity 89.5%; Pred. No. 5e+02;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 GTCGACGGAAGGCCCTTT 19
XX ||||||||||||
XX 5 GTCGACGGAAGGCTCT 23
XX
XX Search completed: May 19, 2006, 04:19:01
XX Job time : 266.361 secs
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 02:24:46 ; Search time 1471.35 Seconds
(without alignments)
836.120 Million cell updates/sec

Title: US-10-665-708-23

Perfect score: 22
Sequence: 1 gtcgaacggaaggcttcgg 22

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 48236798 segs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

EST.*

1: gb_est1.*

2: gb_est3.*

3: gb_est4.*

4: gb_est5.*

5: gb_est6.*

6: gb_est7.*

7: gb_est8.*

8: gb_est9.*

9: gb_est10.*

10: gb_est11.*

11: gb_est12.*

12: gb_est13.*

13: gb_est14.*

14: gb_est15.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
c	1	18.8	85.5	312	7	B2241896
	2	18.8	85.5	657	8	CN208729
	3	18.4	83.6	735	5	CF882404
	4	18.4	83.6	788	4	CB908942
	5	17.8	80.9	452	4	BY275654
	6	17.8	80.9	910	9	DN561788
	7	17.8	80.9	967	13	CL447050
	8	17.8	80.9	1205	11	BZ552660
	9	17.8	80.9	1242	11	BZ559026
	10	17.4	79.1	316	4	CB603496
	11	17.4	79.1	828	7	BF240426
	12	17.2	78.2	247	1	AV314699
	13	17.2	78.2	305	7	BF172476
	14	17.2	78.2	446	5	CK234849
	15	17.2	78.2	451	6	CNS089GP
	16	17.2	78.2	461	9	DR323178
	17	17.2	78.2	515	3	BM649944
	18	17.2	78.2	538	1	AL910651
	19	17.2	78.2	563	3	BU609865

AM154744	AM154744	618	1	AM154744
AA754068	AA754068	620	1	AA754068
CR532627	CR532627	646	8	CR532627
AX618313	AX618313	649	4	AX618313
DU818647	DU818647	683	14	DU818647
DR370688	DR370688	684	10	DR370688
BM622387	BM622387	709	3	BM622387
CC605085	CC605085	724	12	CC605085
CR532626	CR532626	727	8	CR532626
BU365226	BU365226	803	3	BU365226
BE881910	BE881910	872	7	BE881910
CF885931	CF885931	945	5	CF885931
CL065269	CL065269	952	12	CL065269
BG538412	BG538412	979	12	BG538412
CC939630	CC939630	999	12	CC939630
CD122074	CD122074	356	4	CD122074
DT685074	DT685074	439	10	DT685074
BH764015	BH764015	597	11	BH764015
LBFA055F03	LBFA055F03	614	14	LBFA055F03
BH006273	BH006273	625	11	BH006273
CB378019	CB378019	630	4	CB378019
DT727398	DT727398	680	10	DT727398
DU601889	DU601889	777	14	DU601889
CF700782	CF700782	802	5	CF700782
DY361640	DY361640	824	10	DY361640
CF722314	CF722314	835	5	CF722314
CR077081	CR077081	927	10	CR077081
DT758502	DT758502	930	13	DT758502
CZ520644	CZ520644	946	10	CZ520644
DT803768	DT803768	958	14	DT803768
CNS06NEF5	CNS06NEF5	1003	14	CNS06NEF5
AL287640	AL287640	1007	13	AL287640
CL295780	CL295780	1019	14	CL295780
DU772735	DU772735	1043	14	DU772735
DU760208	DU760208	305	8	DU760208
CO684942	CO684942	412	3	CO684942
BF623830	BF623830	492	7	BF623830
BF257478	BF257478	544	7	BF257478
BF253911	BF253911	544	7	BF253911
BE571264	BE571264	585	7	BE571264
BU398878	BU398878	603	3	BU398878
BU306528	BU306528	629	7	BU306528
BF625550	BF625550	639	7	BF625550
BU283959	BU283959	643	3	BU283959
BH794488	BH794488	660	11	BH794488
BF622265	BF622265	698	7	BF622265
BU412995	BU412995	709	3	BU412995
EX855983	EX855983	740	4	EX855983
BF982698	BF982698	747	2	BF982698
BE195630	BE195630	799	7	BE195630
BU409605	BU409605	847	3	BU409605
CNS02922	CNS02922	883	14	CNS02922
CO583238	CO583238	944	8	CO583238
CC213477	CC213477	1124	12	CC213477
DR139870	DR139870	1173	9	DR139870
BZ548902	BZ548902	1330	11	BZ548902
DT975169	DT975169	1370	10	DT975169
DN730360	DN730360	1462	9	DN730360
BI529719	BI529719	182	2	BI529719
CF045077	CF045077	267	5	CF045077
CF044432	CF044432	288	5	CF044432
BW531407	BW531407	294	4	BW531407
BO980749	BO980749	298	3	BO980749
BI166846	BI166846	315	2	BI166846
CV668361	CV668361	339	8	CV668361
DY170338	DY170338	346	10	DY170338
CZ003780	CZ003780	370	13	CZ003780
AA652906	AA652906	379	1	AA652906
CK291892	CK291892	390	5	CK291892
AW400594	AW400594	399	7	AW400594
CG857155	CG857155	431	12	CG857155
BW530083	BW530083	491	4	BW530083

93	16.2	73.6	492	1	AA640643	AA640643 nr22c11.r	166	16.2	73.6	922	3	BQ888316	BQ888316
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c 95	16.2	73.6	520	1	AA798556	AA798556 vx75H03.r	c 169	16.2	73.6	925	12	CC620929	CC620929
c 96	16.2	73.6	521	11	BZ543563	BZ543563 OGAD15TC	c 169	16.2	73.6	927	14	DU793027	DU793027
c 97	16.2	73.6	537	9	CK608591	CK608591 ANR1_39_B	c 170	16.2	73.6	935	5	CK282064	CK282064
c 98	16.2	73.6	548	4	CB826166	CB826166 rw22a03.y	c 171	16.2	73.6	938	5	CK282065	CK282065
c 99	16.2	73.6	565	7	AV822903	AV822903 AV822903	c 172	16.2	73.6	940	12	CG145299	CG145299
c 100	16.2	73.6	569	13	CW966724	CW966724 ATAA-aab2	c 173	16.2	73.6	942	5	CK296945	CK296945
c 101	16.2	73.6	594	8	CN061365	CN061365 AG2_P30.p	c 174	16.2	73.6	945	12	CC712360	CC712360
c 102	16.2	73.6	605	3	BM622761	BM622761 170006874	c 175	16.2	73.6	949	12	CC678267	CC678267
c 103	16.2	73.6	622	2	BM327318	BM327318 PIC1_12_A	c 176	16.2	73.6	954	7	BE727405	BE727405
c 104	16.2	73.6	625	4	EX620074	EX620074 BX620074	c 177	16.2	73.6	955	12	CG142098	CG142098
c 105	16.2	73.6	627	5	CK282937	CK282937 EST745659	c 178	16.2	73.6	962	5	CK294576	CK294576
c 106	16.2	73.6	630	5	CK282063	CK282063 EST744785	c 179	16.2	73.6	969	5	CK293763	CK293763
c 107	16.2	73.6	632	2	EG927981	EG927981 HNC67-1-B	c 180	16.2	73.6	971	3	BQ713233	BQ713233
c 108	16.2	73.6	640	13	CW074031	CW074031 104_342.1	c 181	16.2	73.6	978	5	CK298679	CK298679
c 109	16.2	73.6	643	14	AG078845	AG078845 Pan trogl	c 182	16.2	73.6	994	12	CC620945	CC620945
c 110	16.2	73.6	654	12	CE016451	CE016451 tigr-gss-	c 183	16.2	73.6	1003	5	CK282938	CK282938
c 111	16.2	73.6	659	1	AA543680	AA543680 v183c06.r	c 184	16.2	73.6	1006	9	DR139593	DR139593
c 112	16.2	73.6	659	4	CA590992	CA590992 hab333E10.	c 185	16.2	73.6	1006	9	DR139593	DR139593
c 113	16.2	73.6	661	12	BZ688362	BZ688362 OGAD75TC	c 186	16.2	73.6	1009	12	CC712366	CC712366
c 114	16.2	73.6	665	4	BY747224	BY747224 BY747224	c 187	16.2	73.6	1018	14	DU741222	DU741222
c 115	16.2	73.6	679	2	BG498953	BG498953 602544616	c 188	16.2	73.6	1039	7	BE036789	BE036789
c 116	16.2	73.6	681	13	CZ139111	CZ139111 OA_BBa003	c 189	16.2	73.6	1115	2	BE0716050	BE0716050
c 117	16.2	73.6	686	5	CK752412	CK752412 atr02-11m	c 190	16.2	73.6	1132	9	DR141636	DR141636
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c 130	16.2	73.6	759	5	CK282940	CK282940 EST745662	c 203	16.2	72.7	736	9	CK798411	CK798411
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AUTHORS		Bryopsida; Dicranidae; Pottiaceae; Pottiaceae; Tortula.	
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JOURNAL		Oliver M.J., Dowd, S.E., Zaragosa, J., Mauget, S.A. and Payton, P.R.	
PUBMED		The rehydration transcriptome of the desiccation-tolerant bryophyte	
COMMENT		Tortula ruralis: transcript classification and analysis	
FEATURES		BMC Genomics 5 (1), 89 (2004)	
source		15546486	
Query Match		Contact: Oliver Melvin J	
Best Local Similarity		Plant Stress Lab	
Matches		USDA-ARS	
QY		3810 4th St, Lubbock, TX 79415, USA	
Db		Tel: 806-749-5560	
RESULT 3		Fax: 806-723-5272	
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AUTHORS		Hypocreales; Hypocreaceae; Hypocrea.	
TITLE		1 (bases 1 to 735)	
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PUBMED		Transcriptional regulation of biomass-degrading enzymes in the	
COMMENT		filamentous fungus Trichoderma reesei	
FEATURES		J. Biol. Chem. 278 (34), 31988-31997 (2003)	
source		12788920	
Query Match		Contact: Pamela K. Foreman	
Best Local Similarity		Genencor Intl.	
Matches		925 Page Mill Road, Palo Alto, CA 94304, USA	
QY		Tel: (650) 846-7635	
Db		Fax: (650) 621-7817	
RESULT 4		Email: pforeman@genencor.com	
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TITLE		1 (bases 1 to 788)	
JOURNAL		Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,	
PUBMED		Dunn-Coleman, N.S., Goedegebuur, F., Houfek, T.D., England, G.J.,	
COMMENT		Kelley, A.S., Meeran, H.J., Mitchell, T., Mitchinson, C.,	
FEATURES		Olivares, H.A., Teunissen, P.J., Yao, J. and Ward, M.	
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Query Match		filamentous fungus Trichoderma reesei	
Best Local Similarity		J. Biol. Chem. 278 (34), 31988-31997 (2003)	
Matches		12788920	
QY		Contact: Pamela K. Foreman	
Db		Genencor Intl.	
RESULT 4		925 Page Mill Road, Palo Alto, CA 94304, USA	
CF882404		Tel: (650) 846-7635	
LOCUS		Fax: (650) 621-7817	
DEFINITION		Email: pforeman@genencor.com	
ACCESSION		Seq primer: Lt-F1 primer.	
VERSION		Location/Qualifiers	
KEYWORDS		1. .788	
SOURCE		/organism="Hypocrea jecorina"	
ORGANISM		/mol_type="mRNA"	
REFERENCE		/strain="QM6a"	
AUTHORS		/db_xref="taxon:51453"	
TITLE		Hypocrea jecorina (anamorph: Trichoderma reesei)	
JOURNAL		Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;	
PUBMED		Hypocreales; Hypocreaceae; Hypocrea.	
COMMENT		1 (bases 1 to 735)	
FEATURES		Diener, S.E., Dunn-Coleman, N., Foreman, P., Houfek, T.D.,	
source		Transcriptional regulation of biomass-degrading enzymes in the	
Query Match		filamentous fungus Trichoderma reesei	
Best Local Similarity		J. Biol. Chem. 278 (34), 31988-31997 (2003)	
Matches		12788920	
QY		Contact: Pamela K. Foreman	
Db		Genencor Intl.	
RESULT 4		925 Page Mill Road, Palo Alto, CA 94304, USA	
CF882404		Tel: (650) 846-7635	
LOCUS		Fax: (650) 621-7817	
DEFINITION		Email: pforeman@genencor.com	
ACCESSION		Seq primer: Lt-F1 primer.	
VERSION		Location/Qualifiers	
KEYWORDS		1. .788	
SOURCE		/organism="Hypocrea jecorina"	
ORGANISM		/mol_type="mRNA"	
REFERENCE		/strain="QM6a"	
AUTHORS		/db_xref="taxon:51453"	
TITLE		Hypocrea jecorina (anamorph: Trichoderma reesei)	
JOURNAL		Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;	
PUBMED		Hypocreales; Hypocreaceae; Hypocrea.	
COMMENT		1 (bases 1 to 735)	
FEATURES		Diener, S.E., Dunn-Coleman, N., Foreman, P., Houfek, T.D.,	
source		Transcriptional regulation of biomass-degrading enzymes in the	
Query Match		filamentous fungus Trichoderma reesei	
Best Local Similarity		J. Biol. Chem. 278 (34), 31988-31997 (2003)	
Matches		12788920	
QY		Contact: Pamela K. Foreman	
Db		Genencor Intl.	
RESULT 4		925 Page Mill Road, Palo Alto, CA 94304, USA	
CF882404		Tel: (650) 846-7635	
LOCUS		Fax: (650) 621-7817	
DEFINITION		Email: pforeman@genencor.com	
ACCESSION		Seq primer: Lt-F1 primer.	
VERSION		Location/Qualifiers	
KEYWORDS		1. .788	
SOURCE		/organism="Hypocrea jecorina"	
ORGANISM		/mol_type="mRNA"	
REFERENCE		/strain="QM6a"	
AUTHORS		/db_xref="taxon:51453"	
TITLE		Hypocrea jecorina (anamorph: Trichoderma reesei)	
JOURNAL		Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;	
PUBMED		Hypocreales; Hypocreaceae; Hypocrea.	
COMMENT		1 (bases 1 to 735)	
FEATURES		Diener, S.E., Dunn-Coleman, N., Foreman, P., Houfek, T.D.,	
source		Transcriptional regulation of biomass-degrading enzymes in the	
Query Match		filamentous fungus Trichoderma reesei	
Best Local Similarity		J. Biol. Chem. 278 (34), 31988-31997 (2003)	

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/clones="tric086xm16"
/dev stages="mycellia"
/clone lib="T-reseai mycellial culture, Version 3 april"
/notes="Vector: pREP3Y; Site_1: Not I/Sal I; Mycellial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."

ORIGIN
Query Match      83.6%; Score 18.4; DB 4; Length 788;
Best Local Similarity 95.0%; Pred. No. 3.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTC 20
    |||||
Db 111 GTCGAACGGAAGGCGCTTTC 130

RESULT 5
LOCUS BY275654
DEFINITION BY275654 RIKEN full-length enriched, visual cortex Mus musculus
          cDNA clone K430314L24 5', mRNA sequence.
ACCESSION BY275654
VERSION BY275654.1 GI:26465991
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
          Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
          Sciurognathi; Muroidea; Muridae; Murinae; Mus.
          1 (bases 1 to 452)
          Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
          Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yananaka, I.,
          Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
          Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
          Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
          Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusci, V.,
          Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
          Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
          Gariboldi, M., Giassi, C., Godzik, A., Gough, J., Grimmond, S.,
          Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
          Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Kongsaya, A.,
          Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
          Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
          Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
          Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
          Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
          Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
          Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
          Verardo, R., Wagner, L.G., Wahlestedt, C., Wang, Y., Watanabe, Y.,
          Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
          Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
          Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
          Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
          Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
          Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
          Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
          Rogers, J., Birney, E. and Hayashizaki, Y.
          Analysis of the mouse transcriptome based on functional annotation
          of 60,770 full-length cDNAs
          Nature 420, 563-573 (2002)
          12466851
          Contact: Yoshihide Hayashizaki
          Laboratory for Genome Exploration Research Group, RIKEN Genomic
          Sciences Center (GSC), Yokohama Institute
          The Institute of Physical and Chemical Research (RIKEN)
          1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
          Tel: 81-45-503-9222
          Fax: 81-45-503-9216
          Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
          Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
          Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
          Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,

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Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Michela Fagiolini and Takao K. Hensch (
Laboratory for Neuronal Circuit Development Brain Science Institute
RIKEN 2-1 Hiroseawa, Wako-shi, Saitama 351-0198 Japan ) whose
assistance we gratefully acknowledge. Please visit our web site
(http://genome.gsc.riken.go.jp) for further details.

FEATURES             source
          1..452
             /organism="Mus musculus"
             /mol_type="mRNA"
             /strain="C57BL/6J"
             /db_xref="taxon:10090"
             /clone="K430314L24"
             /tissue_type="visual cortex"
             /clone_lib="RIKEN full-length enriched, visual cortex"

ORIGIN
Query Match      80.9%; Score 17.8; DB 4; Length 452;
Best Local Similarity 90.5%; Pred. No. 6.1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTCG 22
    |||||
Db 253 TCGAACGGAAGGCGCTTTCG 273

RESULT 6
LOCUS DN561788
DEFINITION 92178421 Sea Urchin primary mesenchyme cell cDNA library
          Strongylocentrotus purpuratus cDNA clone PMCSRP2-102A16 5', mRNA
          sequence.
ACCESSION DN561788
VERSION DN561788.1 GI:61120827
KEYWORDS EST.
SOURCE Strongylocentrotus purpuratus
          Strongylocentrotus purpuratus
          Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
          Echinoidea; Euechinoidea; Echinacea; Echinoida;
          Strongylocentrotidae; Strongylocentrotus.
          1 (bases 1 to 910)
          Zhu, X., Mahairas, G., Illies, M.R., Cameron, R.A., Davidson, E.H. and
          Ettensohn, C.A.
          A large scale analysis of mRNAs expressed by primary mesenchyme
          cells of the sea urchin embryo
          Development 128 (13), 2615-2627 (2001)
          11493577
          Contact: Erica Sodergren
          Human Genome Sequencing Center
          Baylor College of Medicine
          One Baylor Plaza, Houston, TX 77030, USA
          Tel: 713-798-7676
          Fax: 713-798-6977
          Email: ericas@bcm.tmc.edu
          NCBI Trace Archive: 486682679

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Qy 2 TCGAACGGAAGGCCTTTCGG 22

Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.

FEATURES

source
1. 1242
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="2-164"
/db_xref="taxon:287"
/clone="pacs2-164 1210"
/clone_lib="pacs2-164"
/note="clinical isolate 2-164 whole genomic shotgun library."

ORIGIN

Query Match 80.9%; Score 17.8; DB 11; Length 1242;
Best Local Similarity 90.5%; Pred. No. 7,1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTCCG 22
||||| ||||| ||||| ||||| |||||
Db 910 TCGAACGGAAGGCGCTTTCCG 930

RESULT 10

CB603496 316 bp mRNA linear EST 16-MAY-2003
LOCUS L843 Late-oocyst subtraction library Anopheles stephensi/Plasmodium
DEFINITION berghei mixed EST library cDNA clone L843, mRNA sequence.

ACCESSION CB603496
VERSION CB603496.1 GI:29543286
KEYWORDS EST.

SOURCE Anopheles stephensi/Plasmodium berghei mixed EST library
ORGANISM Anopheles stephensi/Plasmodium berghei mixed EST library

REFERENCE Eukaryota; mixed EST libraries.

AUTHORS 1 (bases 1 to 316)

Srinivasan, P., Eappen, A.G., Ghosh, A.K., Valenzuela, J.,
Ribeiro, J.M.C., Dimopoulos, G., Kafatos, F., Adams, J., Fujioka, H. and
Jacobs-Lorena, M.
Analysis of the Plasmodium and Anopheles transcriptomes during
oocyst differentiation

J. Biol. Chem. 279 (7), 5581-5587 (2004)

14627711
Contact: Srinivasan, P., Jacobs-Lorena, M

Case Western Reserve University
10900 Euclid Ave., 647 B., Biomedical Research Building., Dept of
Genetics., Cleveland, OH 44106, USA

Tel: 216-368-2790

Fax: 216-368-3432

Email: sxp82@cwru.edu.

Location/Qualifiers

1. 316
/organism="Anopheles stephensi/Plasmodium berghei mixed
EST library"

/mol_type="mRNA"

/db_xref="taxon:224741"

/clone="L843"

/tissue_type="Midgut"

/dev_stages="Oocyst"

/clone_lib="Late-oocyst subtraction library"

/note="Vector: pGEM-easy; Site_1: EcoRI; Site_2: EcoRI;
P.berghei ANKA 2.34; Enrichment for differentially
expressed genes during parasite development by subtractive
hybridization. The library represents A.stephensi and
P.berghei genes expressed specifically during oocyst
development (4-6 days after infectious blood meal)."

ORIGIN

Query Match 79.1%; Score 17.4; DB 4; Length 316;
Best Local Similarity 94.7%; Pred. No. 9,2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTT 19

Db 192 GTCGAACGGAAGGCGCTTT 210

RESULT 11

BF240426/c
LOCUS

DEFINITION

BF240426

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BF240426

601905978F1 NIH_MGC_54 Homo sapiens CDNA clone IMAGE:413899 5',

mRNA sequence.

BF240426

BF240426.1 GI:11154350

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QY 1 GTCGAACGAAAGGCCTTTCGG 22
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;


```

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS 1 (bases 1 to 563)
TITLE Bonaldo,M.F., Lennon,G. and Soares,M.B.
NORMALIZATION and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
8889548
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
Tissue Procurement: Dr. Robin Davison
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 49-84, >AT-rich/low_complexity
Seq primer: M13 REVERSE.
FEATURES
source
Location/Qualifiers
1..563
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="C57BL/6"
/clones="UI-M-DJ2-bwb-b-23-0-UI"
/tissue_type="subfornical organ and postrema"
/dev_stage="Adult"
/lab_hosts="DH10B (Life Technologies) (T1 phage resistant)"
/clone_libs="NIH-BMAP_DJ2"
/notes="Organ: Brain; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-M-DJ2 is a subcloned cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is: GCTACATGAT, subfornical
organ and area postrema."
ORIGIN
Query Match 78.2%; Score 17.2; DB 3; Length 563;
Best Local Similarity 86.4%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GTCGAACGGAAGGCCTTTCCG 22
| | | | | | | | | | | | | | | | | |
Db 525 GTCAAGAGGAAGGCCTTTCCG 504

RESULT 20
AM154744/c
LOCUS AM154744 Oryzias latipes CAB gastrula Oryzias latipes cDNA clone
DEFINITION MCF0029J13-MGRbd1, mRNA sequence.
ACCESSION AM154744
VERSION AM154744.1 GI:81517022
KEYWORDS EST.
SOURCE Oryzias latipes (Japanese medaka)
ORGANISM Oryzias latipes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
1 (bases 1 to 618)
REFERENCE
AUTHORS Berger,A., Dohm,J.C., Hennig,S., Sasaki,T., Furutani-Seiki,M.,
Mitani,H., Shima,A., Lehrach,H., Wittbrodt,J., Kondoh,H.,
Shimizu,N. and Himmelbauer,H.
TITLE A UniGene cDNA set for the medaka Oryzias latipes obtained by
normalisation of embryonic and adult cDNA libraries
Unpublished (2005)
JOURNAL Contact: Himmelbauer H
COMMENT Department of Vertebrate Genomics
Max Planck Institute of Molecular Genetics
Innesstrasse 73, 14195 Berlin, GERMANY
Genome Center
Center: Max Planck Institute for Molecular Genetics Center code:
MPIMG Web site: http://www.molgen.mpg.de/
rodent
Genome Center
Center: Keio University, School of Medicine
Center code: Keio
Web site: http://www.dmb.med.keio.ac.jp/.
FEATURES
source
Location/Qualifiers
1..618
/organism="Oryzias latipes"
/mol_type="mRNA"
/db_xref="taxon:8090"
/clone="McF0029J13-MGRbd1"
/dev_stage="gastrula"
/clone_libs="Oryzias latipes CAB gastrula"
ORIGIN
Query Match 78.2%; Score 17.2; DB 1; Length 618;
Best Local Similarity 86.4%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GTCGAACGGAAGGCCTTTCCG 22
| | | | | | | | | | | | | | | | | |
Db 483 GTCAAGAGGACAGGCCTTTCCG 462

RESULT 21
AA754068
LOCUS AA754068 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
DEFINITION (indica cultivar-group) cDNA clone 97GS0781, mRNA sequence.
ACCESSION AA754068
VERSION AA754068.1 GI:2800774
KEYWORDS EST.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 620)
REFERENCE
AUTHORS Nahn,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R., Moon,E.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
TITLE Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
Unpublished (1998)
JOURNAL Contact: Eun M.Y.
COMMENT Department of Cyto Genetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyungido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahn, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
FEATURES
source
Location/Qualifiers
1..620

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/organisms="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/cultivar="Milyang 23"
/db_xref="taxon:39946"
/clone="97GS0781"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
/clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5' end with EcoRI and 3' end with Xho I site."

ORIGIN

Query Match 78.2%; Score 17.2; DB 1; Length 620;
Best Local Similarity 86.4%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCGCTTCGG 22
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Db 298 GTCGAACGGAAGGCGCTTCGG 319
|||||

RESULT 22
CR532627/c
LOCUS
DEFINITION
CR532627 Normalized Anopheles Head (NAH) Library Anopheles gambiae
cDNA clone AGAGL07R, mRNA sequence.
ACCESSION
CR532627.1 GI:49931744
VERSION
EST.
KEYWORDS
SOURCE
Anopheles gambiae (African malaria mosquito)
ORGANISM
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Anophelinae; Anopheles.
REFERENCE
1 (bases 1 to 646)
Lobo.N.L., Gardner.M., Romans.P. and Collins.F.H.
Anopheles gambiae EST, Center for Tropical Disease Research and
Training
Unpublished (2003)
JOURNAL
COMMENT
Contact: Frank H. Collins
Center for Tropical Disease Research and Training
University of Notre Dame
Notre Dame, IN 46556, USA
Tel: 574-631-9245
Fax: 574-631-3996
Email: frank.h.collins.75@nd.edu

FEATURES
source
1..646
/organism="Anopheles gambiae"
/mol_type="mRNA"
/db_xref="taxon:7165"
/clone="AGAGL07R"
/lab_host="E. coli DH10B"
/clone_lib="Normalized Anopheles Head (NAH) Library"
/note="Vector: p773D-PacI; Site_1: EcoRI (5' end); Site_2:
NotI (3' end); a directionally cloned and normalized, 4arr
oligo-T primed cDNA library constructed from strain 4arr
adult mosquito heads. Equal numbers of sugar fed males,
sugar fed females and 6, 24 and 48 hr post blood meal
females were used: Bonaldo, Lennon & Soares (1996):
Normalization and Subtraction: Two Approaches To
Facilitate Gene Discovery, Genome Research 6, 791-806.
ESTs sequenced from the M13 reverse priming site reading
from the 5' ends of the cDNAs are indicated by 'R' in the
clone name. ESTs sequenced from the M13 forward priming
site reading from the 3' ends of the cDNAs are indicated
by 'F' in the clone name."

site reading from the 3' ends of the cDNAs are indicated
by 'F' in the clone name."

ORIGIN

Query Match 78.2%; Score 17.2; DB 8; Length 646;
Best Local Similarity 86.4%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCGCTTCGG 22
|||||
Db 289 GTCGAACGGAAGGCGGATCGG 268
|||||

RESULT 23
BX618313/c
LOCUS
DEFINITION
BX618313 Normalized Anopheles Head (NAH) Library Anopheles gambiae
cDNA clone AGAE426TR, mRNA sequence.
ACCESSION
BX618313.1 GI:33536740
VERSION
EST.
KEYWORDS
SOURCE
Anopheles gambiae (African malaria mosquito)
ORGANISM
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Anophelinae; Anopheles.
REFERENCE
1 (bases 1 to 649)
Lobo.N.L., Gardner.M., Romans.P. and Collins.F.H.
Anopheles gambiae EST, Center for Tropical Disease Research and
Training
Unpublished (2003)
JOURNAL
COMMENT
Contact: Frank H. Collins
Center for Tropical Disease Research and Training
University of Notre Dame
Notre Dame, IN 46556, USA
Tel: 574-631-9245
Fax: 574-631-3996
Email: frank.h.collins.75@nd.edu

FEATURES
source
1..649
/organism="Anopheles gambiae"
/mol_type="mRNA"
/db_xref="taxon:7165"
/clone="AGAE426TR"
/lab_host="E. coli DH10B"
/clone_lib="Normalized Anopheles Head (NAH) Library"
/note="Vector: p773D-PacI; Site_1: EcoRI (5' end); Site_2:
NotI (3' end); a directionally cloned and normalized, 4arr
oligo-T primed cDNA library constructed from strain 4arr
adult mosquito heads. Equal numbers of sugar fed males,
sugar fed females and 6, 24 and 48 hr post blood meal
females were used: Bonaldo, Lennon & Soares (1996):
Normalization and Subtraction: Two Approaches To
Facilitate Gene Discovery, Genome Research 6, 791-806.
ESTs sequenced from the M13 reverse priming site reading
from the 5' ends of the cDNAs are indicated by 'R' in the
clone name. ESTs sequenced from the M13 forward priming
site reading from the 3' ends of the cDNAs are indicated
by 'F' in the clone name."

ORIGIN

Query Match 78.2%; Score 17.2; DB 4; Length 649;
Best Local Similarity 86.4%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCGCTTCGG 22
|||||
Db 211 GTCGAACGGAAGGCGGATCGG 190
|||||

RESULT 24
DU818647
LOCUS
DU818647 683 bp DNA linear GSS 13-DEC-2005

```

DEFINITION OG_ABA0092L10.r OG_ABA Oryza granulata genomic clone OG_ABA0092L10
3', genomic survey sequence.
ACCESSION DUB18647
VERSION DUB18647.1 GI:83614306
KEYWORDS GSS.
SOURCE Oryza granulata
ORGANISM Oryza granulata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 683)
AUTHORS SanMiguel,P., Westerman,R., Kim,H., Yu,Y., Wiersotski,M., Yost,D.,
Stum,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C.,
Hatfield,J., Soderlund,C., Wing,R. and Jackson,S.A.
WPAP (Oryza Map Alignment Project)- Purdue University
Unpublished (2004)
JOURNAL
COMMENT Contact: Scott A. Jackson
Jackson Laboratory
Purdue University
915 W. State St., West Lafayette, IN 47907, USA
Tel: 7654963621
Fax: 7654967255
Email: sjackson@purdue.edu
Basecalling by phred version 0.020425.c. This sequence was derived
from the raw sequence read by clipping with Lucy version 1.198.
Bases 111-793 of the raw sequence (length 1048) were retained after
clipping.
Plate: 0092 row: L column: 10
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
FEATURES             Location/Qualifiers
     source           1..683
                     /organism="Oryza granulata"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:110450"
                     /clone="OG_ABA0092L10"
                     /tissue_type="young leaves"
                     /lab_host="DH10B T1 phage resistant"
                     /clone_lib="OG_ABA"
                     /note="Vector: pGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match      78.2%; Score 17.2; DB 14; Length 683;
Best Local Similarity 86.4%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCGCTTTTCGG 22
Db 241 GTCGAGCGGTAGGCGCTTCGG 262

RESULT 25
DR370688
LOCUS DR370688 684 bp mRNA linear EST 29-JAN-2006
DEFINITION 103424 CERES-148 Arabidopsis thaliana cDNA clone 4267 3', mRNA
sequence.
ACCESSION DR370688
VERSION DR370688.1 GI:86074931
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 684)
AUTHORS Alexandrov,N.N., Troukhan,M.E., Brover,V.V., Tatarinova,T.,
Lu,Y.-P., Flavell,R.B. and Feldmann,K.A.
Features of Arabidopsis genes and genome discovered using
full-length cDNAs
Plant Mol. Biol. 60 (1), 71-87 (2006)
JOURNAL
COMMENT Contact: Alexandrov NN
Ceres, Inc
1535 Rancho Conejo Blvd., Thousand Oaks, CA 91320, USA

```

```

Tel: (805) 376-6539
Fax: (805) 498-1002
Email: nalexandrov@ceres-inc.com.
Location/Qualifiers
     source           1..684
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /strain="Mixed, WS and Landsberg erecta"
                     /db_xref="taxon:3702"
                     /clone="4267"
                     /tissue_type="Mixed floral buds, roots (9:1)"
                     /clone_lib="CERES-148"

ORIGIN
Query Match      78.2%; Score 17.2; DB 10; Length 684;
Best Local Similarity 86.4%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCGCTTTTCGG 22
Db 224 GTCGAGGTAAAGCGCTTTCGG 245

RESULT 26
BM622387/c
LOCUS BM622387 709 bp mRNA linear EST 26-FEB-2002
DEFINITION 17000687476225 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
19600449666435 5', mRNA sequence.
ACCESSION BM622387
VERSION BM622387.1 GI:18921898
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoides;
Culicidae; Anophelinae; Anopheles.
REFERENCE 1 (bases 1 to 709)
AUTHORS Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L.,
Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
Celera Anopheles gambiae EST project
Unpublished (2002)
JOURNAL
COMMENT Contact: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltRA@celera.com
Plate: NU01004HMD row: C column: 09
Seq primer: M13 Reverse.
Location/Qualifiers
     source           1..709
                     /organism="Anopheles gambiae"
                     /mol_type="mRNA"
                     /strain="RSP-ST (Reduced susc. to Permethrin - std.
chromosome)"
                     /db_xref="taxon:7165"
                     /clone="19600449666435"
                     /dev_stage="Adult"
                     /lab_host="DH10B"
                     /clone_lib="A.Gam.ad.cDNA1"
                     /note="Vector: pSport1; Site_1: SalI; Site_2: NotI; Whole
adult mosquitoes (mixed sex) frozen on liquid nitrogen.
cDNA inserts >500 bp cloned directionally into pSport 1.
Not a 1 site is 3'. Clones available through the Malaria
Research and Reference Reagent Resource Center
(www.malaria.mr4.org)."
```

ORIGIN

Query Match 78.2%; Score 17.2; DB 3; Length 709;
 Best Local Similarity 86.4%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCGCTTTTCGG 22


```

Db      290  GTCTACGAGGAGGCGCGATCGG 269
|||||
CC605085      724 bp      DNA      linear      GSS 18-JUN-2003
OCWFF25TH_ZM_0.7_1.5_KB_Zea_mays_genomic_clone_ZNMBMa0564F02,
genomic_survey_sequence.
CC605085      1      GI:31966506
GSS.
SOURCE
ORGANISM      Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 724)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Buddiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGWFF25TV
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: methylation filtered.
FEATURES      Location/Qualifiers
source
1. .724
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZNMBMa0564F02"
/clone_lib="ZM_0.7_1.5_KB"
/notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match      78.2%; Score 17.2; DB 12; Length 724;
Best Local Similarity 86.4%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  GTCTACGAGGAGGCGCTTTCGG 22
|||||
Db      692  GTCTACGAGGAGGCGCTTTCGG 713

RESULT 28
CR532626      727 bp      mRNA      linear      EST 07-JUL-2004
LOCUS
DEFINITION      CR532626 Normalized Anopheles Head (NAH) Library Anopheles gambiae
cDNA clone AGAGL07TF, mRNA sequence.
ACCESSION      CR532626
VERSION
KEYWORDS
SOURCE
ORGANISM      Anopheles gambiae (African malaria mosquito)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Anophelinae; Anopheles.
1 (bases 1 to 727)
Lobo,N.L., Gardner,M., Romans,P. and Collins,F.H.
Anopheles gambiae EST, Center for Tropical Disease Research and
Training
Unpublished (2003)
Contact: Frank H. Collins
Center for Tropical Disease Research and Training

FEATURES      Location/Qualifiers
source
1. .727
/organism="Anopheles gambiae"
/mol_type="mRNA"
/db_xref="taxon:7165"
/clone="AGAGL07TF"
/lab_host="E. coli DH10B"
/clone_lib="Normalized Anopheles Head (NAH) Library"
/notes="Vector: pT7T3D-PacI; Site 1: EcoRI (5'end); Site 2:
NotI (3'end); a directionally cloned and normalized, 4arr
oligo-T primed cDNA library constructed from strain 4arr
adult mosquito heads. Equal numbers of sugar fed males,
sugar fed females and 6, 24 and 48 hr post blood meal
females were used: Bonaldo, Lennon & Soares (1996):
Normalization and Subtraction: Two Approaches To
Facilitate Gene Discovery, Genome Research 6, 791-806.
ESTs sequenced from the M13 reverse priming site reading
from the 5' ends of the cDNAs are indicated by 'R' in the
clone name. ESTs sequenced from the M13 forward priming
site reading from the 3' ends of the cDNAs are indicated
by 'F' in the clone name."

ORIGIN
Query Match      78.2%; Score 17.2; DB 8; Length 727;
Best Local Similarity 86.4%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  GTCTACGAGGAGGCGCTTTCGG 22
|||||
Db      439  GTCTACGAGGAGGCGCGATCGG 460

RESULT 29
BU365226      803 bp      mRNA      linear      EST 28-NOV-2002
LOCUS
DEFINITION      BU365226 Gallus gallus cDNA clone CHEST523g12 5', mRNA
sequence.
ACCESSION      BU365226
VERSION
KEYWORDS
SOURCE
ORGANISM      Gallus gallus (chicken)
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 803)
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
12445392
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1. .803
/organism="Gallus gallus"

FEATURES      Location/Qualifiers
source
1. .803
/organism="Gallus gallus"

```

Db 290 GTCTACGAGGAGGCGCGATCGG 269

RESULT 27
CC605085 724 bp DNA linear GSS 18-JUN-2003
LOCUS
DEFINITION CC605085 Zea mays genomic clone ZNMBMa0564F02, genomic survey sequence.

ACCESSION CC605085
VERSION 1
KEYWORDS GI:31966506
SOURCE GSS.

ORGANISM Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 724)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Buddiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.

Consortium for Maize Genomics

Unpublished (2002)

Other GSSs: OGWFF25TV

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TR

Class: methylation filtered.

FEATURES Location/Qualifiers

source

1. .724

/organism="Zea mays"

/mol_type="genomic DNA"

/strain="B73"

/db_xref="taxon:4577"

/clone="ZNMBMa0564F02"

/clone_lib="ZM_0.7_1.5_KB"

/notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb

methylation filtered genomic DNA library"

ORIGIN

Query Match 78.2%; Score 17.2; DB 12; Length 724;

Best Local Similarity 86.4%; Pred. No. 1.3e+03;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTCTACGAGGAGGCGCTTTCGG 22

|||||

Db 692 GTCTACGAGGAGGCGCTTTCGG 713

RESULT 28

CR532626 727 bp mRNA linear EST 07-JUL-2004

LOCUS

DEFINITION CR532626 Normalized Anopheles Head (NAH) Library Anopheles gambiae

cDNA clone AGAGL07TF, mRNA sequence.

ACCESSION CR532626

VERSION

KEYWORDS

SOURCE

ORGANISM Anopheles gambiae (African malaria mosquito)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;

Culicidae; Anophelinae; Anopheles.

1 (bases 1 to 727)

Lobo,N.L., Gardner,M., Romans,P. and Collins,F.H.

Anopheles gambiae EST, Center for Tropical Disease Research and

Training

Unpublished (2003)

Contact: Frank H. Collins

Center for Tropical Disease Research and Training

FEATURES Location/Qualifiers

source

1. .727

/organism="Anopheles gambiae"

/mol_type="mRNA"

/db_xref="taxon:7165"

/clone="AGAGL07TF"

/lab_host="E. coli DH10B"

/clone_lib="Normalized Anopheles Head (NAH) Library"

/notes="Vector: pT7T3D-PacI; Site 1: EcoRI (5'end); Site 2:

NotI (3'end); a directionally cloned and normalized, 4arr

oligo-T primed cDNA library constructed from strain 4arr

adult mosquito heads. Equal numbers of sugar fed males,

sugar fed females and 6, 24 and 48 hr post blood meal

females were used: Bonaldo, Lennon & Soares (1996):

Normalization and Subtraction: Two Approaches To

Facilitate Gene Discovery, Genome Research 6, 791-806.

/mol_type="mRNA"
 /strain="Compton Line 151"
 /db_xref="taxon:9031"
 /clone="CHEST523g12"
 /sex="Female"
 /tissue_type="cerebrum"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="CSEQCHN72"
 /note="Organ: brain; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI. This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunt-ended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Query Match 78.2%; Score 17.2; DB 3; Length 803;
 Best Local Similarity 86.4%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAAGCCCTTTTCGG 22
 |||||
 DB 57 GTCCAAAGGAAAGCCCTTTCTG 78

RESULT 30

BE881910
 LOCUS BE881910 872 bp mRNA linear EST 20-OCT-2000
 DEFINITION 60150486F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906597 5', mRNA sequence.

ACCESSION BE881910 GI:10330686
 VERSION BE881910
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 872)

REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs@email.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: L1AM9715 row: 1 column: 22

High quality sequence start: 49

High quality sequence stop: 593.

Location/Qualifiers

1..872

FEATURES

source

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3906597"

/tissue_type="leiomyosarcoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_71"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2.1 kb. "

ORIGIN

Query Match 78.2%; Score 17.2; DB 7; Length 872;
 Best Local Similarity 86.4%; Pred. No. 1.4e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAAGCCCTTTTCGG 22
 |||||
 DB 758 GTCCAACTGAAGGCCCTTTTCGG 779

RESULT 31

CF885931/c
 LOCUS CF885931 945 bp mRNA linear EST 31-OCT-2003
 DEFINITION trico85xf21.b11 T.reesei mycelial culture, Version 6 October 2003
 Hypocrea jecorina cDNA clone trico85xf21, mRNA sequence.

ACCESSION CF885931

VERSION CF885931.1 GI:38140613

KEYWORDS EST.

SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)

ORGANISM

Hypocrea jecorina
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

REFERENCE

1 (bases 1 to 945)
 AUTHORS Diener, S.E., Dunn-Coleman, N., Foreman, P., Houfek, T.D.,
 Teunissen, P.J.M., van Solingen, P., Dankmeyer, L., Mitchell, T.K.,
 Ward, M. and Dean, R.A.

TITLE

Characterization of the protein processing and secretion pathways in a comprehensive set of expressed sequence tags from Trichoderma reesei

JOURNAL FEMS Microbiol. Lett. 230 (2), 275-282 (2004)

PUBMED

14757250

COMMENT

Contact: Ralph A. Dean
 Fungal Genomics Laboratory
 North Carolina State University
 Campus Box 7251, Raleigh, NC 27695, USA
 Tel: 919-513-0020
 Fax: 919-513-0024
 Email: ralph.dean@ncsu.edu

Seq primer: Lt-F1 primer.

Location/Qualifiers

source

1..945

/organism="Hypocrea jecorina"

/mol_type="mRNA"

/strain="QM6a"

/db_xref="taxon:51453"

/clone="trico85xf21"

/dev_stage="mycelia"

/clone_lib="T.reesei mycelial culture, Version 6 October 2003"

/note="Vector: pREP3Y; Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

Query Match 78.2%; Score 17.2; DB 5; Length 945;
 Best Local Similarity 86.4%; Pred. No. 1.4e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAAGCCCTTTTCGG 22
 |||||
 DB 375 GTCCAAAGTAAAGGCCCTTTTCGG 354

ORIGIN

Query Match 78.2%; Score 17.2; DB 5; Length 945;
 Best Local Similarity 86.4%; Pred. No. 1.4e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAAGCCCTTTTCGG 22
 |||||
 DB 375 GTCCAAAGTAAAGGCCCTTTTCGG 354

RESULT 32

CL065269/c
 LOCUS CL065269 952 bp DNA linear GSS 31-DEC-2003
 DEFINITION CH216-104C12_Sp6.1 CH216 Xenopus tropicalis genomic clone
 CH216-104C12, genomic survey sequence.

ACCESSION CL065269

VERSION CL065269.1 GI:40521182

```

KEYWORDS
SOURCE  Xenopus tropicalis (western clawed frog)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
REFERENCE
1 (bases 1 to 952)
AUTHORS  Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Mardis, E. and Wilson, R.
TITLE  A physical map of the xenopus tropicalis genome
JOURNAL  Unpublished (2003)
COMMENT  Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: SP6 ATTAGGTGACACTATAG
Class: BAC ends
High quality sequence start: 39
High quality sequence stop: 785.
FEATURES
source
1..952
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-104C12"
/sex="male"
/cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/notes="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
ORIGIN
Query Match 78.2%; Score 17.2; DB 12; Length 952;
Best Local Similarity 86.4%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTCGAACGGGAAGGCTTTTCGG 22
|||||
Db 501 GTCCAGGGAATGCTTTTCGG 480

RESULT 33
BG538412/c
LOCUS BG538412
DEFINITION 602567112F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4691739 5',
mRNA sequence.
ACCESSION BG538412
VERSION BG538412.1 GI:13530645
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 979)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC1511 row: g column: 04
High quality sequence stop: 658.
FEATURES
source
1..979
Location/Qualifiers

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4691739"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 77"
/notes="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggcgctcgcc); Site 2: SfiI (ggcattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTARGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
ORIGIN
Query Match 78.2%; Score 17.2; DB 2; Length 979;
Best Local Similarity 86.4%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTCGAACGGGAAGGCTTTTCGG 22
|||||
Db 745 GTCCGACGGAAACGTCTTTCGG 724

RESULT 34
CC939630/c
LOCUS CC939630
DEFINITION ZMMBBb0239D20.r ZMMBBb Zea mays genomic clone ZMMBBb0239D20 3',
genomic survey sequence.
ACCESSION CC939630
VERSION CC939630.1 GI:33625477
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 299)
AUTHORS Yu, Y., Kim, H.R., Hatfield, J., Soderlund, C., Bharti, A.K., Messing, J.
and Wing, R.
TITLE Sequencing of the maize genome
JOURNAL Unpublished (2003)
COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: T7
BACKWARD: M13r
Plate: 0239 row: D column: 20
Seq primer: M13r
Class: BAC ends.
FEATURES
source
1..299
Location/Qualifiers
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBBb0239D20"
/lab_host="DH10B"
/clone_lib="ZMMBBb"
/notes="Vector: pBelobAC11; Site 1: HindIII; Site 2:
HindIII; Zea mays L. ssp. mays"
ORIGIN
Query Match 76.4%; Score 16.8; DB 12; Length 299;

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CB378019	630 bp	mrna	linear	EST 16-MAY-2003
LOCUS				
DEFINITION	rq06all.y1 Heterodera glycines J3 Heterodera glycines cDNA 5' similar to WP:CE23823 H24K24.4 RNA-binding protein ;, mRNA sequence.			
ACCESSION	CB378019	GI:29127315		
VERSION				
KEYWORDS				
SOURCE	CB378019			
ORGANISM	Heterodera glycines			
REFERENCE	Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.			
AUTHORS	1 (bases 1 to 630)			
	McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hallier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Teagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.			
TITLE	The Washington Univ. Nematode EST Project, 1999			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: McCarter JP The Washington Univ. Nematode EST Project, 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This library was generated by cloning cDNAs directionally into Uni-ZAP(Stratagene) (T3 primer/Scori are at the 5'-end and T7/XhoI are at the 3'-end). The library was excised [now in pBluescript SK(+)] and normalized (Bonaldo et al 1996 Genome Research 6:791-806). Library constructed by Thomas Baum (tbaum@iastate.edu), Iowa State University, Plant Pathology Department and Jeff McDermott (jpmcd@mstate.edu). Seq primer: T3 from Gibco.			
FEATURES	<p>Location/Qualifiers</p> <p>1..630</p> <p>/organism="Heterodera glycines"</p> <p>/mol_type="mrna"</p> <p>/db_xref="taxon:51029"</p> <p>/sex="mixed"</p> <p>/tissue_type="whole organism"</p> <p>/dev_stage="3rd stage juvenile"</p> <p>/lab_host="DH108"</p> <p>/clone_lib="Heterodera glycines J3"</p> <p>/note=vector: pBluescript SK+ (Stratagene); Site_1: XhoI; Site_2: EcoRI; This library was generated by cloning cDNAs directionally into Uni-ZAP(Stratagene) (T3 primer/Scori are at the 5'-end and T7/XhoI are at the 3'-end). The library was excised [now in pBluescript SK(+)] and normalized (now in pBluescript SK(+)) and normalized (Bonaldo et al 1996 Genome Research 6:791-806). Library constructed by Thomas Baum (tbaum@iastate.edu), Iowa State University, Plant Pathology Department and Jeff McDermott (jpmcd@mstate.edu)."</p>			
ORIGIN	<p>Query Match 76.4%; Score 16.8; DB 4; Length 630;</p> <p>Best Local Similarity 90.0%; Pred. No. 2.1e+03;</p> <p>Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;</p>			
QY	2	TCGAACGGAAGGCTTTTCG	21	
DB	512	TCGAACGGAAGGCTTTTGG	531	
RESULT 41				
DT727398				
LOCUS	DT727398	680 bp	mrna	linear EST 13-SEP-2005
DEFINITION	EST1161248 Aquilegia cDNA library Aquilegia formosa x Aquilegia pubescens cDNA clone COLSP66, mRNA sequence.			
ACCESSION	DT727398			

```

REFERENCE
AUTHORS      1 (bases 1 to 777)
              Kim,H., Collura,K., Missotski,M., Byrne,M., Stum,D., Smart,D.,
              Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
              Wing,R.
TITLE        OWAP (Oryza Map Alignment Project) - Arizona Genomics Institute
JOURNAL      Unpublished (2005)
COMMENT      Contact: Rod A. Wing
              Arizona Genomics Institute
              University of Arizona
              Forbes Building Room 303, Tucson, AZ 85721-0036, USA
              Tel: 520 626 9595
              Fax: 520 621 1259
              Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0099 row: F column: 04
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

FEATURES
source      Location/Qualifiers
            1..777
              /organism="Oryza officinalis"
              /mol_type="genomic DNA"
              /db_xref="taxon:4535"
              /clone="OO_Ba0099F04"
              /tissue_type="leaves"
              /lab_host="DH108"
              /clone_lib="OO_Ba"
              /notes="Vector: pGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match      76.4%; Score 16.8; DB 14; Length 777;
Best Local Similarity 90.0%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3 CGAACGGAAAGGCGCTTCGG 22
        |||||
Db      273 CGAACGGAAAGGCGCTTCGG 254

RESULT 43
CF700782/c
LOCUS      CF700782
DEFINITION CF700782TR C.neoformans strain JEC21 mRNA linear EST 16-AUG-2004
            neoformans cDNA clone CCAGU31, mRNA sequence.
ACCESSION  CF700782
VERSION     CF700782.1 GI:41554941
SOURCE      Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
            var. neoformans)
ORGANISM    Cryptococcus neoformans var. neoformans
            Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
            Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
            Filobasidiella.
REFERENCE   1 (bases 1 to 802)
AUTHORS     Loftus,B.
TITLE       End sequencing of clones from a Full length enriched, normalized
            JEC21 cDNA library
JOURNAL     Unpublished (2003)
COMMENT     Other_ESTs: CCAGU31TF
            Contact: Brendan Loftus
            The Institute for Genomic Research (TIGR; www.tigr.org)
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-3543
            Fax: 301-838-0208
            Email: bjoftus@tigr.org
            Seq primer: TR.
            Location/Qualifiers
            1..802
              /organism="Cryptococcus neoformans var. neoformans"
              /mol_type="mRNA"
              /strain="JEC21"
              /db_xref="taxon:40410"

```

```

/clone="CCAGU31"
/clone_lib="C.neoformans strain JEC21"
/notes="Vector: pCMVSPORT6; Site_1: NotI_EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

ORIGIN
Query Match      76.4%; Score 16.8; DB 5; Length 802;
Best Local Similarity 90.0%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 TCGAACGGAAAGGCGCTTCG 21
        |||||
Db      350 TCCTAACGGAAAGGCGCTTCG 331

RESULT 44
DY361640
LOCUS      DY361640
DEFINITION DY361640.1 Ed Zingiber officinale cDNA clone ZO_Ed0007M16
            3', mRNA sequence.
ACCESSION  DY361640
VERSION     DY361640.1 GI:87094856
KEYWORDS    EST.
SOURCE      Zingiber officinale
            Zingiber officinale
            Zingiber officinale
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales;
            Zingiberaceae; Zingiber.
REFERENCE   1 (bases 1 to 824)
AUTHORS     Ma,X.O., Koo,H.J., Haller,K.P., Soderlund,C.A. and Gang,D.R.
TITLE       Comparative Analysis of Expressed Sequence Tags from Different
            Organs of Ginger and Turmeric. Insights into Specialized Metabolism
            in Traditional Medicinal Plants
JOURNAL     Unpublished (2006)
COMMENT     Contact: David R. Gang
            Department of Plant Sciences
            The University of Arizona
            Forbes Building Room 303, Tucson, AZ 85721-0036, USA
            Tel: 520 621 7154
            Fax: 520 621 7186
            Email: gang@ag.arizona.edu
            Plate: 0007 row: M column: 16.
            Location/Qualifiers
            1..824
              /organism="zingiber officinale"
              /mol_type="mRNA"
              /cultivar="Yellow Ginger"
              /db_xref="taxon:94328"
              /clone="ZO_Ed0007M16"
              /tissue_type="rhizome"
              /lab_host="TUC 121"
              /clone_lib="ZO_Ed"
              /notes="Vector: pBluescriptIISK-; Site_1: EcoRI; Site_2:
              XhoI; Greenhouse, soil grown"

ORIGIN
Query Match      76.4%; Score 16.8; DB 10; Length 824;
Best Local Similarity 90.0%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GTCGAACGGAAAGGCGCTTTC 20
        |||||
Db      338 GACGAACGGAAAGGCGTTC 357

RESULT 45
CF722314/c
LOCUS      CF722314
DEFINITION CF722314 C.neoformans strain JEC21 Cryptococcus neoformans var.
            neoformans cDNA clone CCAGS66, mRNA sequence.
ACCESSION  CF722314

```



```

RESULT 48
CZ520644/c
LOCUS
DEFINITION
ACCESSION
VERSION
CZ520644.1 GI:63246065
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 930)
Nunberg,A., Bedell,J.A., Citek,R.W., Robbins,D., McMenamy,J.,
Peterson,S., Jones,J., Fries,J., Budiman,M.A., Nguyen,H.,
Clifton,S.W. and Stacey,G.
BAC end sequences from Glycine max Williams 82 cultivar genome
Unpublished (2005)
Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Class: BAC ends.
FEATURES             source
Location/Qualifiers
1..930
/mol_type="Glycine max"
/mol_type="genomic DNA"
/db_xref="taxon:3847"
/clone_lib="GMW2"
/notes="Glycine max BAC library"

ORIGIN
Query Match          76.4%;   Score 16.8;   DB 13;   Length 930;
Best Local Similarity 90.0%;   Pred. No. 2.2e+03;
Matches 18;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

QY 1  GTCTACGCGAAGGCGCTTC 20
Db 549 GTCTACGCGAAGGCGCTTC 530

RESULT 49
DT803768
LOCUS
DEFINITION
127434557 Tl1 Tribolium castaneum cDNA clone 104E3 5', mRNA
sequence.
ACCESSION
DT803768
VERSION
DT803768.1 GI:75735768
KEYWORDS
SOURCE
Tribolium castaneum (red flour beetle)
Tribolium castaneum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Tenebrionidae; Tribolium.
1 (bases 1 to 946)
Alkins,J., Beeman,R., Brown,S., Park,Y., Richards,S., Weinstock,G.
and Gibbs,R.
An analysis of Tribolium castaneum expressed sequence tags
Unpublished (2005)
Contact: Stephen Richards
Human Genome Sequencing Center
Baylor College of Medicine
One Baylor Plaza, Houston, TX 77030, USA
Tel: 713-798-6667
Email: stephen@bcm.tmc.edu
NCBI Trace Archive:
Insert Length: 1750 Std Error: 0.25
Plate: 104 row: E column: 3.
FEATURES             source
Location/Qualifiers
1..946
/mol_type="genomic DNA"
/db_xref="taxon:4934"

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/organism="Tribolium castaneum"
/mol_type="mRNA"
/db_xref="GA2"
/clone="taxon:7070"
/tissue_type="Whole larvae"
/dev_stage="larvae"
/clone_lib="TL1"
/notes="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: MluI;
Library constructed by Yoonseong Park"

ORIGIN
Query Match          76.4%;   Score 16.8;   DB 10;   Length 946;
Best Local Similarity 90.0%;   Pred. No. 2.2e+03;
Matches 18;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

QY 3  CGAACGGAAGGCGCTTTCGG 22
Db 534 CGAACGGAAGGCGCTTTCGG 553

RESULT 50
CNS06NF5/c
LOCUS
DEFINITION
T3 end of clone AU0AA011F11 of library AU0AA from strain CBS 3082
of Saccharomyces kluyveri, genomic survey sequence.
ACCESSION
AL406695
VERSION
AL406695.1 GI:12171027
KEYWORDS
Saccharomyces kluyveri
SOURCE
Saccharomyces kluyveri
ORGANISM
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
1 (bases 1 to 958)
Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Lorente,B.,
Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekai,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
11152876

REFERENCE
2 (bases 1 to 958)
Neuveglise,C., Bon,E., Lepingle,A., Wincker,P., Artiguenave,F.,
Gaillardin,C. and Casaregola,S.
Genomic exploration of the hemiascomycetous yeasts: 9.
Saccharomyces kluyveri
FEBS Lett. 487 (1), 56-60 (2000)
11152884

REFERENCE
3 (bases 1 to 958)
Genoscope.
Direct Submission
Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
1..958
Location/Qualifiers
/organism="Saccharomyces kluyveri"
/mol_type="genomic DNA"
/db_xref="CBS 3082"

FEATURES             source
Location/Qualifiers
1..958
/organism="Saccharomyces kluyveri"
/mol_type="genomic DNA"
/db_xref="CBS 3082"

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/misc_feature
/clone="AU00A011F11"
/clone_lib="AU00A"
/note="end : T3"
<1..>54
/inference="non-experimental evidence, no additional
details recorded"
/note="similar to Saccharomyces cerevisiae ORF YDL074c [
weak similarity to spindle pole body protein NUF1 ]"
<798..>956
/inference="non-experimental evidence, no additional
details recorded"
/note="similar to Saccharomyces cerevisiae ORF YLR405w [
similarity to A.brasiliense nifR3 protein ]"

ORIGIN
Query Match 76.4%; Score 16.8; DB 14; Length 958;
Best Local Similarity 90.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCTTCG 21
|||||
Db 483 TCGAACGGAAGGCTGCCG 464

RESULT 51
CNS04EXR/c
LOCUS
DEFINITION CNS04EXR 1003 bp DNA linear GSS 01-SEP-2000
Tetraodon nigroviridis genome survey sequence PUC-ORI end of clone
105024 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL287640
VERSION AL287640.1 GI:8026141
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontoidea; Tetraodontidae; Tetraodon.
REFERENCE 1
AUTHORS Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fzanes,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
10835645
REFERENCE 2
AUTHORS Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)
10899143
REFERENCE 3 (bases 1 to 1003)
Genoscope.
Direct Submission
Genoscope.
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/tetraodon.
Location/Qualifiers
1..1003
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="105024"
/clone_lib="G"
/note="Genoscope sequence ID : CORG105BH12SP1"

FEATURES
source
1..1003
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBBb0027F02"
/lab_host="E. coli DH10B"
/clone_lib="ZMMBBb (HindIII)"
/note="Vector: pCUGI; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match 76.4%; Score 16.8; DB 13; Length 1007;
Best Local Similarity 90.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTC 20
|||||
Db 68 GTCGAACGGAAGGCTTC 49

RESULT 53
LOCUS
DEFINITION APKG3109.b2 HF4000_12-21-03 uncultured marine microorganism
HF4000_12-21-03 genomic clone HF4000_13841008109, genomic survey
sequence.
ACCESSION DU772735
VERSION DU772735.1 GI:85786920
KEYWORDS GSS.
SOURCE uncultured marine microorganism HF4000_12-21-03
uncultured marine microorganism HF4000_12-21-03

```

```

ORIGIN
end : PUC-ORI"

Query Match 76.4%; Score 16.8; DB 14; Length 1003;
Best Local Similarity 90.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTC 20
|||||
Db 782 GTCGAACGGAAGGCTTC 763

RESULT 52
LOCUS
DEFINITION ZMMBBb0027F02f ZMMBBb (HindIII) Zea mays genomic clone
ZMMBBb0027F02 5', genomic survey sequence.
ACCESSION CL295780
VERSION CL295780.1 GI:42574876
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1007)
AUTHORS Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
Sequencing of the maize genome at PCR (2003c)
Unpublished (2003)
JOURNAL Contact: Bharti,A.K.
COMMENT Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
130 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: T7
Class: BAC ends
High quality sequence start: 111.
Location/Qualifiers
1..1007
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBBb0027F02"
/lab_host="E. coli DH10B"
/clone_lib="ZMMBBb (HindIII)"
/note="Vector: pCUGI; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match 76.4%; Score 16.8; DB 13; Length 1007;
Best Local Similarity 90.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTC 20
|||||
Db 68 GTCGAACGGAAGGCTTC 49

RESULT 53
LOCUS
DEFINITION APKG3109.b2 HF4000_12-21-03 uncultured marine microorganism
HF4000_12-21-03 genomic clone HF4000_13841008109, genomic survey
sequence.
ACCESSION DU772735
VERSION DU772735.1 GI:85786920
KEYWORDS GSS.
SOURCE uncultured marine microorganism HF4000_12-21-03
uncultured marine microorganism HF4000_12-21-03

```

unclassified sequences; environmental samples.

REFERENCE AUTHORS

1 (bases 1 to 1019)
DeLong, E.F., Preston, C.M., Mincer, T., Rich, V., Hallam, S.J.,
Frigaard, N.U., Martinez, A., Sullivan, M., Edwards, R., Chisholm, S.W.
and Karl, D.M.

TITLE

Comparative genomics reveals ecological trends in stratified
microbial communities in the ocean's interior

JOURNAL

Science (2006) In press

COMMENT

Contact: Susan Lucas, Alex Copeland, Sam Pitluck, Alla Lapidus,
Kerrie Barry, Tijana Glavinadelrio, David Bruce, Paul Richardson
and Edward DeLong

US DOE Joint Genome Institute

US DOE Joint Genome Institute

2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA

Tel: 617-253-5271

Fax: 617-253-2679

Email: PMRichardson@lbl.gov; delong@mit.edu

North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid
DNA library prepared from marine picoplankton in the less than 1.6
um, greater than 0.22 um fraction. Sample Date: 12/21/2003

Coordinates: 22.45 N, 158 W Depth 4000 m Temperature: 1.46 C

Salinity: 34.69 Oxygen: 147.8 umol/kg

Class: fosmid ends.

FEATURES

source

Location/Qualifiers

1. .1019

/organism="uncultured marine microorganism

HF4000_12-21-03"

/mol_type="genomic DNA"

/db_xref="taxon:361148"

/clone="HF4000_13841008109"

/cell_type="marine picoplankton, less than 1.8 um, greater

than 0.22 um fraction"

/clone_lib="HF4000_12-21-03"

/notes="Vector: pCCIFOS; North Pacific Subtropical Gyre

(Hawaii) picoplankton genomic fosmid DNA library prepared
from marine picoplankton in the less than 1.6 um, greater
than 0.22 um fraction. Picoplankton collected at 4000 m

depth on 10/7/2002. Coordinates: 22.45 N, 158 W. Sample
Date: 12/21/2003 Coordinates: 22.45 N, 158 W Depth 4000 m

Temperature: 1.46 C Salinity: 34.69 Oxygen: 147.8 umol/kg"

ORIGIN

Query Match

Best Local Similarity 76.4%; Score 16.8; DB 14; Length 1019;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy

1 GTCGACGGAAAGCCTTTC 20

|||||

Db

303 GTCGACGGAAAGCCTATGC 322

RESULT 54

DU760208

LOCUS

DEFINITION ASNG3054.b2 HF200_10-06-02 uncultured marine microorganism

HF200_10-06-02 genomic clone HF0200_090F10, genomic survey

sequence.

DU760208

DU760208.1 GI:85770044

GSS.

uncultured marine microorganism HF200_10-06-02

uncultured marine microorganism HF200_10-06-02

unclassified sequences; environmental samples.

1 (bases 1 to 1043)

REFERENCE

AUTHORS

DeLong, E.F., Preston, C.M., Mincer, T., Rich, V., Hallam, S.J.,

Frigaard, N.U., Martinez, A., Sullivan, M., Edwards, R., Chisholm, S.W.

and Karl, D.M.

Comparative genomics reveals ecological trends in stratified

microbial communities in the ocean's interior

JOURNAL

COMMENT

Contact: Susan Lucas, Alex Copeland, Sam Pitluck, Alla Lapidus,

Kerrie Barry, Tijana Glavinadelrio, David Bruce, Paul Richardson

and Edward DeLong

US DOE Joint Genome Institute

US DOE Joint Genome Institute

2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA

Tel: 617-253-5271

Fax: 617-253-2679

Email: PMRichardson@lbl.gov; delong@mit.edu

North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid
DNA library prepared from marine picoplankton in the less than 1.6

um, greater than 0.22 um fraction. Sample Date: 10/6/2002

Coordinates: 22.45 N, 158 W Depth 200 m Temperature: 18.53 C

Salinity: 35.04 psu Oxygen: 198.8 umol/kg

Class: fosmid ends.

Location/Qualifiers

1. .1043

/organism="uncultured marine microorganism HF200_10-06-02"

/mol_type="genomic DNA"

/db_xref="taxon:361147"

/clone="HF0200_090F10"

/cell_type="marine picoplankton, less than 1.8 um, greater

than 0.22 um fraction"

/clone_lib="HF200_10-06-02"

/notes="Vector: pCCIFOS; North Pacific Subtropical Gyre
(Hawaii) picoplankton genomic fosmid DNA library prepared

from marine picoplankton in the less than 1.6 um, greater
than 0.22 um fraction. Picoplankton collected at 200 m

depth on 10/6/2002. Coordinates: 22.45 N, 158 W. Sample
Date: 10/6/2002 Coordinates: 22.45 N, 158 W Depth 200 m

Temperature: 18.53 C Salinity: 35.04 psu Oxygen: 198.8

umol/kg"

ORIGIN

Query Match

Best Local Similarity 76.4%; Score 16.8; DB 14; Length 1043;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy

1 GTCGACGGAAAGCCTTTCG 22

|||||

Db

83 GTCGACGGAAAGCCTTTCG 104

RESULT 55

CO684942

LOCUS

DEFINITION DG11-193n18 DG11-kidney Canis familiaris cDNA 3', mRNA sequence.

CO684942

ACCESSION

CO684942.1 GI:50633608

ESL.

Canis familiaris (dog)

Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;

Canis.

1 (bases 1 to 305)

Schlueter, T., Hermanns, J., Weindel, M., Schuette, D., Kranz, H.,

Henrich, J., and Loebbert, R.

Dog arrayTAG cDNA clone collection

Unpublished (2004)

Contact: Thomas Schlueter

LION Bioscience AG

Walhoferstrasse 98, D-69123 Heidelberg, Germany

Tel: +49 6221 4038 150

Fax: +49 6221 4038 290

Email: Thomas.Schlueter@lionbioscience.com.

FEATURES

source

Location/Qualifiers

1. .305

/organism="Canis familiaris"

/mol_type="mRNA"

/strain="Beagle"

/db_xref="taxon:9615"

/tissue_type="kidney"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="DG11-kidney"

```

ORIGIN
Query Match          74.5%; Score 16.4; DB 8; Length 305;
Best Local Similarity 94.4%; Pred. No. 3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AACCGAAGGCGCTTCG 22
    ||| ||||| ||||| |||
Db 135 AACGAAAGGCGCTTCG 152

RESULT 56
BF623830
LOCUS
DEFINITION BP663510 RAFL21 Arabidopsis thaliana cDNA clone RAFL21-66-P16 5',
            mRNA sequence.
ACCESSION BP663510
VERSION BP663510.1 GI:59924483
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (bases 1 to 412)
AUTHORS Seki,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Akiyama,K.,
        Iida,K., Enju,A., Sakurai,T., Arakawa,T., Carninci,P., Fukuda,S.,
        Iida,J., Kawai,J., Sasaki,D., Shiraki,T., Hayashizaki,Y. and
        Shinozaki,K.
TITLE Large-Scale Analysis of RIKEN Arabidopsis Full-length cDNAs
JOURNAL Unpublished (2005)
COMMENT Contact: Motoaki Seki
        Plant Functional Genomics Research Group
        RIKEN Genomic Sciences Center
        3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
        Tel: 81-298-36-4359
        Fax: 81-298-36-9060
        Email: mseki@rtc.riken.go.jp
        An Arabidopsis full-length cDNA library was constructed essentially
        as reported previously (Seki et al., 1998, 2002). This clone is in a
        modified pBluescript vector.
        Please visit our web site (http://pfweb.gsc.riken.jp and
        http://arge.gsc.riken.jp) for further details.
FEATURES
            source
                1..412
                /organism="Arabidopsis thaliana"
                /mol_type="mRNA"
                /db_xref="taxon:3702"
                /clone="RAFL21-66-P16"
                /lab_host="DH10B"
                /clone_lib="RAFL21"
                /note="Site 1: BamHI; Site 2: SalI; Subtraction Library.
                The sequence was obtained from samples subjected to
                various stress and plant hormones-treated"
ORIGIN
Query Match          74.5%; Score 16.4; DB 3; Length 412;
Best Local Similarity 94.4%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAACGGAAGCGCTTCG 21
    ||| ||||| ||||| |||
Db 197 GAACGGAAGGCGCTTCG 214

RESULT 57
BF623830
LOCUS
DEFINITION BF623830 HVSMEa0007D03f Hordeum vulgare seedling shoot EST library
            HVCdNA0001 (Cold stress) Hordeum vulgare subsp. vulgare cDNA clone
            HVSMEa0007D03f, mRNA sequence.
ACCESSION BF623830

```

```

VERSION BF623830.2 GI:13082086
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 492)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D.,
        Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Oates,R.,
        Choi,D.W., Fenton,R.D. and Main,D.
TITLE Development of a genetically and physically anchored EST resource
        for barley genomics: Morex cold-stressed seedling shoot cDNA
        library
JOURNAL Unpublished (2001)
COMMENT On Dec 18, 2000 this sequence version replaced gi:11887564.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 241
Seq primer: AATTACCCCTCACTAAGGG
High quality sequence stop: 491.
FEATURES
            source
                1..492
                /organism="Hordeum vulgare subsp. vulgare"
                /mol_type="mRNA"
                /cultivar="Morex"
                /sub_species="vulgare"
                /db_xref="taxon:112509"
                /clone="HVSMEa0007D03f"
                /tissue_type="Seedling shoot"
                /lab_host="TJC121"
                /clone_lib="Hordeum vulgare seedling shoot EST library
                HVCdNA0001 (Cold stress)"
                /note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;
                Seeds were surface sterilized then germinated under axenic
                conditions in the dark at room temperature on filter paper
                with water, nystatin and cefotaxime in covered
                crystallization dishes. Five-day old seedlings were
                incubated at 50C for 2 days. Shoots were then harvested,
                total RNA was prepared, poly(A) RNA was purified, one
                primary unamplified cDNA library was made, and 600000 pfu
                were in vivo excised to give pBluescript SK(-) cDNA
                phagemids. These steps were performed in the TJ Close
                laboratory at the University of California, Riverside
                (Choi, Close, Fenton). Phagemids were plated and picked at
                the Clemson University Genomics Institute (CUGI) (Begum,
                Palmer, Frisch, Atkins and Wing). Plasmid DNA
                preparations, DNA sequencing and sequence analysis were
                performed at CUGI (Wing, Yu, Frisch, Henry, Simmons,
                Oates, Rambo, Main). The sequence has been trimmed to
                remove vector sequence and contains a minimum of 100 bases
                of phred value 20 or above. For more details on library
                preparation and sequence analysis see
                http://www.genome.clemson.edu/projects/barley. To order
                this clone see http://www.genome.clemson.edu/orders Also
                see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                Genetically and physically anchored EST resources for
                barley genomics. Barley Genetics Newsletter 31:29-30.
                (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
ORIGIN
Query Match          74.5%; Score 16.4; DB 7; Length 492;
Best Local Similarity 94.4%; Pred. No. 3.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTT 18
    ||| ||||| ||||| |||
Db 472 GTCGAACGGAAGGCGGT 489

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RESULT 58
BF257478

LOCUS
DEFINITION

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE

JOURNAL
COMMENT

BF257478
HVSMEF0013A10f

493 bp
mrna

linear

EST 22-OCT-2001

(Etiolated and unstressed) Hordeum vulgare subsp. vulgare cDNA

clone HVSMEF0013A10f, mRNA sequence.

BF257478
BF257478.2

GI:13118835

EST.

Hordeum vulgare subsp. vulgare

Hordeum vulgare subsp. vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Poideae; Triticeae; Hordeum.

1 (bases 1 to 493)

Wing, R., Close, T. J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D. W., Fenton, R. D., Oates, R. and Main, D.

Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling root cDNA library Unpublished (2001)

On Nov 16, 2000 this sequence version replaced gi:1186591.

Contact: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Total hg bases = 431

Seq primer: AATTAACCTCACTAAAGG

High quality sequence stop: 491.

Location/Qualifiers

1. .493

/organism="Hordeum vulgare subsp. vulgare"

/mol_type="mRNA"

/cultivar="Morex"

/sub_species="vulgare"

/db_xref="taxon:112509"

/clone="HVSMEF0013A10f"

/tissue_type="Seedling root"

/lab_host="TJCL121"

/clone_lib="Hordeum vulgare seedling root EST library HVCDA0007 (Etiolated and unstressed)"

/notes="vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedling roots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/g99pages/bgn/31/cover.html>)

Query Match
Best Local Similarity 74.5%; Score 16.4; DB 7; Length 493;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTT 18
|||||

Db 456 GTCGAACGGAAGGCCTT 473
|||||

RESULT 59
BF253911

LOCUS
DEFINITION

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE

JOURNAL
COMMENT

BF253911
HVSMEF0002H13f

544 bp
mrna

linear

EST 22-OCT-2001

(Etiolated and unstressed) Hordeum vulgare subsp. vulgare cDNA

clone HVSMEF0002H13f, mRNA sequence.

BF253911
BF253911.2

GI:13116801

EST.

Hordeum vulgare subsp. vulgare

Hordeum vulgare subsp. vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Poideae; Triticeae; Hordeum.

1 (bases 1 to 544)

Wing, R., Close, T. J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D. W., Fenton, R. D., Oates, R. and Main, D.

Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling root cDNA library Unpublished (2001)

On Nov 16, 2000 this sequence version replaced gi:1183016.

Contact: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Total hg bases = 327

Seq primer: AATTAACCTCACTAAAGG

High quality sequence stop: 463.

Location/Qualifiers

1. .544

/organism="Hordeum vulgare subsp. vulgare"

/mol_type="mRNA"

/cultivar="Morex"

/sub_species="vulgare"

/db_xref="taxon:112509"

/clone="HVSMEF0002H13f"

/tissue_type="Seedling root"

/lab_host="TJCL121"

/clone_lib="Hordeum vulgare seedling root EST library HVCDA0007 (Etiolated and unstressed)"

/notes="vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedling roots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order

this clone see <http://www.genome.clemson.edu/orders> Also see clone TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)"

ORIGIN

Query Match 74.5%; Score 16.4; DB 7; Length 544;
Best Local Similarity 94.4%; Pred. No. 3.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCGCTT 18
|||||

Db 141 GTCGACGGAAGGCGGTT 158
|||||

RESULT 60
BE571264 585 bp mRNA linear EST 15-AUG-2000
DEFINITION 601330701F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:3708169 5',
mRNA sequence.
BE571264
ACCESSION BE571264.1 GI:9814984
VERSION EST.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 585)
NTH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LUAM8927 row: a column: 02
High quality sequence start: 4
High quality sequence stop: 583.
Location/Qualifiers

FEATURES

source 1..585

/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3708169"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP Mam6"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally, primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

Location/Qualifiers

FEATURES

source 1..585

/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3708169"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP Mam6"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally, primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

ORIGIN

Query Match 74.5%; Score 16.4; DB 7; Length 585;
Best Local Similarity 94.4%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCGCTTTC 20
|||||

Db 256 CGAACGGAAGGCGCTTTC 273
|||||

RESULT 61

BU398878

LOCUS

DEFINITION

603533950F1 CSEQCHN58 Gallus gallus cDNA clone CHEST492d14 5', mRNA

sequence.

ACCESSION BU398878

VERSION BU398878.1

KEYWORDS GI:25767934

SOURCE EST.

ORGANISM Gallus gallus (chicken)

Gallus gallus

Archozoaria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 603)

AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,

Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)

PUBMED 12445392

COMMENT Contact: Simon Hubbard

Department of Biomolecular Sciences

University of Manchester Institute of Science and Technology

(UMIST)

PO Box 88, Manchester, M60 1QD, UK

Tel: 01612008930

Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

Location/Qualifiers

source 1..603

/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="CHEST492d14"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQCHN58"
/note="Organ: small intestine; Vector: pBluescript II
KS(+); Site 1: EcoRI; Site 2: NotI; This normalized
library was constructed from 1 million independent clones.
cDNA synthesis was initiated using an oligo(dT) primer.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN

Query Match 74.5%; Score 16.4; DB 3; Length 603;

Best Local Similarity 94.4%; Pred. No. 3.3e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAACGGAAGGCGCTTTCG 21
|||||

Db 273 GAAAGGAAGGCGCTTTCG 290
|||||

RESULT 62

BU306528

LOCUS

DEFINITION

603739007F1 CSEQCHN56 Gallus gallus cDNA clone CHEST633n2 5', mRNA

sequence.

ACCESSION BU306528

VERSION BU306528.1

KEYWORDS GI:25756262

SOURCE EST.

ORGANISM Gallus gallus (chicken)

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
 AUTHORS Boardman,P.E., Sanz-Eguerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
 TITLE A Comprehensive Collection of Chicken cDNAs
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
 PUBMED 1245392
 COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.

1. .625
 Location/Qualifiers

/organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Compton Line 151"
 /db_xref="taxon:9031"
 /clone="CHEST633n2"
 /sex="Female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="CSEQCHN56"
 /note="Organ: small intestine; Vector: pBluescript II
 KS(+); Site 1: EcoRI; Site 2: NotI; This normalized
 library was constructed from 1 million independent clones.
 cDNA synthesis was initiated using an oligo(dT) primer,
 using methylated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA
 was blunt-ended, ligated to NotI adapters, digested with
 EcoRI, size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pBluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."

FEATURES

source

1. .625
 Location/Qualifiers

/organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Compton Line 151"
 /db_xref="taxon:9031"
 /clone="CHEST633n2"
 /sex="Female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="CSEQCHN56"
 /note="Organ: small intestine; Vector: pBluescript II
 KS(+); Site 1: EcoRI; Site 2: NotI; This normalized
 library was constructed from 1 million independent clones.
 cDNA synthesis was initiated using an oligo(dT) primer,
 using methylated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA
 was blunt-ended, ligated to NotI adapters, digested with
 EcoRI, size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pBluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."

ORIGIN

Query Match 74.5%; Score 16.4; DB 3; Length 625;
 Best Local Similarity 94.4%; Pred. No. 3.3e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAACGGAAAGCGCTTCG 21

|||||

Db 290 GAAAGGAAGCGCTTCG 307

RESULT 63

BF625550

LOCUS

DEFINITION

BF625550 639 bp mRNA linear EST 17-OCT-2001
 HVSMEa0011E08f Hordeum vulgare seedling shoot EST library
 HVCdNA0001 (Cold stress) Hordeum vulgare subsp. vulgare cDNA clone
 HVSMEa0011E08f, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Hordeum vulgare subsp. vulgare

Hordeum vulgare subsp. vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Pooideae; Triticeae; Hordeum.

1 (bases 1 to 639)

Wing,R., Close,T.J., Kleinohs,A., Wise,R., Begum,D., Frisch,D.,
 Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Oates,R.,
 Choi,D.W., Fenton,R.D. and Main,D.

Development of a genetically and physically anchored EST resource
 for barley genomics: Morex cold-stressed seedling shoot cDNA
 library

REFERENCE

AUTHORS

TITLE

Library

JOURNAL

COMMENT

Unpublished (2001)
 On Dec 18, 2000 this sequence version replaced gi:11889284.
 Contact: Wing RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: twing@clemson.edu
 Total hq bases = 490
 Seq primer: AATTAACCTCTACTAAAGG
 High quality sequence stop: 598.

FEATURES

source

1. .639

/organism="Hordeum vulgare subsp. vulgare"

/mol_type="mRNA"

/cultivar="Morex"

/sub_species="vulgare"

/db_xref="taxon:112509"

/clone="HVSMEa0011E08f"

/tissue_type="Seedling shoot"

/lab_host="TJCl21"

/clone_lib="Hordeum vulgare seedling shoot EST library
 HVCdNA0001 (Cold stress)"

/note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;
 Seeds were surface sterilized then germinated under axenic
 conditions in the dark at room temperature on filter paper
 with water, nystatin and cefotaxime in covered
 crystallization dishes. Five-day old seedlings were
 incubated at 50C for 2 days. Shoots were then harvested,
 total RNA was prepared, poly(A) RNA was purified, one
 primary unamplified cDNA library was made, and 600000 pfu
 were in vivo excised to give pBluescript SK(-) cDNA
 phagemids. These steps were performed in the TJ Close
 laboratory at the University of California, Riverside
 (Choi, Close, Fenton). Phagemids were plated and picked at
 the Clemson University Genomics Institute (CUGI) (Begum,
 Palmer, Frisch, Atkins and Wing). Plasmid DNA
 preparations, DNA sequencing and sequence analysis were
 performed at CUGI (Wing, Yu, Frisch, Henry, Simmons,
 Oates, Rambo, Main). The sequence has been trimmed to
 remove vector sequence and contains a minimum of 100 bases
 of phred value 20 or above. For more details on library
 preparation and sequence analysis see
 http://www.genome.clemson.edu/projects/barley. To order
 this clone see http://www.genome.clemson.edu/orders Also
 see Close TJ, Wing R, Kleinohs A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
 (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

ORIGIN

Query Match 74.5%; Score 16.4; DB 7; Length 639;
 Best Local Similarity 94.4%; Pred. No. 3.3e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGCGCTT 18

|||||

Db 474 GTCGAACGGAAGCGCTT 491

RESULT 64

BU283959

LOCUS

DEFINITION

BU283959 643 bp mRNA linear EST 27-NOV-2002
 603600041F1 CSEQCHN54 Gallus gallus cDNA clone CHEST573a12 5', mRNA
 sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Gallus gallus (chicken)

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

REFERENCE
AUTHORS Phasianinae; Gallus.
1 (bases 1 to 643)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES
source
1..643
Location/Qualifiers
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clones="CHEST573a12"
/sex="Female"
/tissue_type="not cerebrum or cerebellum"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQCHN54"
/note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site_2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN

Query Match 74.5%; Score 16.4; DB 3; Length 643;
Best Local Similarity 94.4%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 4 GAACGGAAAGCCCTTTCG 21
||| ||||| ||||| |||||
Db 10 GAAAGGAAGGCGCTTTCG 27

RESULT 65
BH794488
LOCUS 660 bp DNA linear GSS 02-APR-2002
DEFINITION ME MBA0002P13f Manihot esculenta Manihot esculenta genomic clone
ME MBA0002P13f, genomic survey sequence.
ACCESSION BH794488
VERSION BH794488.1 GI:19892621
KEYWORDS GSS.
SOURCE Manihot esculenta (cassava)
ORGANISM Manihot esculenta
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;
Manihoteae; Manihot.
1 (bases 1 to 660)
Tomkins, J., Fregene, M., Main, D., Kim, H., Wing, R. and Tohme, J.
Bacterial artificial chromosome (BAC) library resource for
positional cloning of pest and disease resistance genes in cassava
(Manihot esculenta Crantz)
JOURNAL Plant Mol. Biol. 56 (4), 555-561 (2004)
PUBMED 15630619

COMMENT Contact: Tomkins J
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634, USA
Tel: 864 656 6419
Fax: 864 656 4293
Email: jtmkns@clemson.edu
Total High Quality bases = 281
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence stop: 658.

FEATURES
source

1..660
Location/Qualifiers
/organism="Manihot esculenta"
/mol_type="genomic DNA"
/strain="MECW72"
/db_xref="taxon:3983"
/clone="ME_MBA0002P13f"
/tissue_type="Leaf"
/lab_host="E. coli"
/clone_lib="Manihot esculenta"
/note="Vector: pCUGIBAC-1; Site_1: HindIII; Site_2: NotI;
For more details on library preparation and sequence
analysis see
http://www.genome.clemson.edu/projects/etc/cassava/ME_MBA
To order clones from this library see
http://www.genome.clemson.edu/orders "

ORIGIN

Query Match 74.5%; Score 16.4; DB 11; Length 660;
Best Local Similarity 94.4%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 4 GAACGGAAAGCCCTTTCG 21
||| ||||| ||||| |||||
Db 225 GAAAGGAAGGCGCTTTCG 242

RESULT 66
BF622265
LOCUS 698 bp mRNA linear EST 17-OCT-2001
DEFINITION HVSMEa0002G13f Hordeum vulgare seedling shoot EST library
HVSMEa0002G13f, mRNA sequence.
ACCESSION BF622265
VERSION BF622265.2 GI:13080041
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Poaceae; Triticeae; Hordeum.

REFERENCE
AUTHORS 1 (bases 1 to 698)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D.,
Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Oates, R.,
Choi, D.W., Fenton, R.D. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex cold-stressed seedling shoot cDNA
library
Unpublished (2001)
On Dec 18, 2000 this sequence version replaced gi:11885999.
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 356
Seq primer: AATTAAACCTCACTAAAGGG
High quality sequence stop: 589.
FEATURES
source
1..698
Location/Qualifiers

/organism="Hordeum vulgare subsp. vulgare"

/mol_type="mRNA"
/cultivar="Morex"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="HVSMEa002G13f"
/tissue_type="Seedling shoot"
/lab_host="TJC121"
/clone_lib="Hordeum vulgare seedling shoot EST library
HVCDA0001 (Cold stress)"
/notes="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;
Seeds were surface sterilized then germinated under axenic
conditions in the dark at room temperature on filter paper
with water, nystatin and cefotaxime in covered
crystallization dishes. Five-day old seedlings were
incubated at 50C for 2 days. Shoots were then harvested,
total RNA was prepared, poly(A) RNA was purified, one
primary unamplified cDNA library was made, and 60000 pfu
were in vivo excised to give pBluescript SK(-) cDNA
phagemids. These steps were performed in the TJ Close
laboratory at the University of California, Riverside
(Choi, Close, Fenton). Phagemids were plated and picked at
the Clemson University Genomics Institute (CUGI) (Begum,
Palmer, Frisch, Atkins and Wing). Plasmid DNA
preparations, DNA sequencing and sequence analysis were
performed at CUGI (Wing, Yu, Frisch, Henry, Simmons,
Oates, Rambo, Main). The sequence has been trimmed to
remove vector sequence and contains a minimum of 100 bases
of phred value 20 or above. For more details on library
preparation and sequence analysis see
<http://www.genome.clemson.edu/projects/barley>. To order
this clone see <http://www.genome.clemson.edu/orders> Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)"

ORIGIN

Query Match 74.5%; Score 16.4; DB 7; Length 698;
Best Local Similarity 94.4%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTT 18
|||||
Db 461 GTCGAACGGAAGGCCTT 478

RESULT 67

BU412995
LOCUS 603154843F1 CSEQRBL05 Gallus gallus cDNA clone CHEST167e12 5', mRNA
DEFINITION sequence.

ACCESSION BU412995
VERSION BU412995.1 GI:25905666
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 709)
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Pong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)

COMMENT 12445392
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)

PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409

FEATURES

source

Email: Simon.Hubbard@umist.ac.uk.

Location/Qualifiers
1..709
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer"
/db_xref="taxon:9031"
/clone="CHEST167e12"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQRBL05"
/notes="Organ: ovary; Vector: pBluescript II KS(+); Site 1:
EcoRI; Site 2: NotI; Modification of pBluescript II KS(+)
[Stratagene] vector to accommodate cDNA produced with the
cloned cDNA libraries from messenger RNA for improved 3'
end DNA sequencing by Glenn Fu, et al. U.S. Patent #
6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
Ligate in double stranded adaptor containing BsgI and
BamHI sites [5'ggcgctgagcccgatccgaaaaaaag]
[5'aattcttttttcggatccggggtgcacgc]"

ORIGIN

Query Match 74.5%; Score 16.4; DB 3; Length 709;
Best Local Similarity 94.4%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAACGGAAGGCCTTCG 21
|||||
Db 354 GAAAGGAAGGCCTTCG 371

RESULT 68

EX855983/c

LOCUS 740 bp mRNA linear EST 20-MAY-2004
DEFINITION tcay Oncorhynchus mykiss cDNA clone tcay0040b.g.16 5prim,
mRNA sequence.

ACCESSION EX855983
VERSION EX855983.2 GI:42752904
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

REFERENCE

AUTHORS Govoroun,M., Guiguen,Y. and Le Gac,F.
TITLE Construction and primary characterization of normalized cDNA
libraries in rainbow trout, Oncorhynchus mykiss
JOURNAL Unpublished (2003)
COMMENT On Dec 16, 2003 this sequence version replaced gi:39952993.
Contact: Guiguen Y

INRA - SCRIBE
Campus de Beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20

Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.

Plate: 0040 row: g column: 16

Seq primer: M13R.

FEATURES

source

Location/Qualifiers
1..740
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="tcay0040b.g.16"
/tissue_type="adipose tissue, blood, brain,
differentiating gonads, gills, interrenal, intestine,
kidney, liver, muscle, ovary, pituitary, testis"
/dev_stage="from embryos to adults"

ORIGIN

Query Match 74.5%; Score 16.4; DB 4; Length 740;
 Best Local Similarity 94.4%; Pred. No. 3.4e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GTCCGAACGGAAGGCGCTT 18
 |||||GTCCGAACGGAAGGCGCTT 532

Db 549 GTCCGAACGGAAGGCGCTT 532

/lab host="DH10B"
 /clone lib="tcay"
 /notes=Vector: pT73D-PacI; Rainbow trout multi-tissues -
 normalized + 1 subtraction (tcay) : Clone distribution :
 AGENAE Resource centre. Francois PIUMI, radiobiologie et
 Francois.PIUMI@jouy.inra.fr, INRA, CEA radiobiologie et
 Etude du genome (LREG), Domaine de Vilvert, 78352,
 Jouy-en-Josas cedex, France, +33 (0) 1.34.65.28.02, +33
 (0) 1.34.65.22.73"

ORIGIN

Query Match 74.5%; Score 16.4; DB 4; Length 740;
 Best Local Similarity 94.4%; Pred. No. 3.4e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GTCCGAACGGAAGGCGCTT 18
 |||||GTCCGAACGGAAGGCGCTT 532

Db 549 GTCCGAACGGAAGGCGCTT 532

RESULT 69
 BF982698 747 bp mRNA linear EST 23-JAN-2001
 LOCUS 602305084F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4396461 5',
 DEFINITION mRNA sequence.

ACCESSION BF982698
 VERSION BF982698.1 GI:12385510
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE

1 (bases 1 to 747)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

AUTHORS

CONTACT: Robert Strausberg, Ph.D.

EMAIL: cgapbs-r@mail.nih.gov

TISSUE Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LHAM10095 row: 9 column: 22

High quality sequence stop: 659.

FEATURES

source

1..747
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4396461"
 /tissue_type="duodenal adenocarcinoma, cell line"
 /lab host="DH10B (phage-resistant)"
 /clone lib="NIH_MGC 88"
 /note="Organ: small intestine; Vector: pCMV-SPORTS;
 Site1: NotI; Site2: SalI; Cloned unidirectionally;
 oligo-dr primed. Average insert size 1.767 kb. Library
 enriched for full-length clones and constructed by Life
 Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 74.5%; Score 16.4; DB 2; Length 747;
 Best Local Similarity 94.4%; Pred. No. 3.4e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GTCCGAACGGAAGGCGCTT 18
 |||||GTCCGAACGGAAGGCGCTT 681

Db 664 GTCCGAACGGAAGGCGCTT 681

RESULT 70

BE195630

LOCUS

DEFINITION HVSMEH0089P24f Hordeum vulgare 5-45 DAP spike EST library
 HVCDA0009 (5 to 45 DAP) Hordeum vulgare subsp. vulgare cDNA clone
 BE195630

ACCESSION

VERSION BE195630

KEYWORDS

SOURCE EST.

ORGANISM

Hordeum vulgare subsp. vulgare
 Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Poideae; Triticeae; Hordeum.

REFERENCE

AUTHORS

1 (bases 1 to 799)

Wing, R., Close, T.J., Kleinohs, A., Wise, R., Begum, D., Frisch, D.,
 Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmonds, J., Choi, D.W.,
 Fenton, R.D., Close, S.J., Oates, R., and Main, D.

Development of a genetically and physically anchored EST resource

for barley genomics: Morex 5-45 DAP spike cDNA library

Unpublished (2001)

On Jun 26, 2000 this sequence version replaced gi:1188307.

Contact: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Total hq bases = 293

Seq primer: AATTACCCCTCACTAAAGG

High quality sequence stop: 769.

FEATURES

source

1..799
 /organism="Hordeum vulgare subsp. vulgare"

/mol_type="mRNA"

/cultivar="Morex"

/sub_species="vulgare"

/db_xref="taxon:112509"

/clone="HVSMEH0089P24f"

/tissue_type="5-45 DAP Spike"

/lab_host="SOLR"

/clone lib="Hordeum vulgare 5-45 DAP spike EST library

HVCDA0009 (5 to 45 DAP)"

/notes=Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;

plants were grown in the greenhouse at the University of

California, Riverside (Fenton, SJ Close, TJ Close). Whole

spikes with awns trimmed were collected at 5, 10, 15, 20,

30 and 45 DAP (Fenton). Total RNA was prepared from each

pool, equal quantities of all six RNA pools were combined,

poly(A) RNA was purified from the mixture, one primary

unamplified cDNA library was made, and 1 million pfu were

in vivo excised to give plasmids SK(-) cDNA phagemids

(Choi) in the TJ Close lab at the University of California,

Riverside. Phagemids were plated and picked at the Clemson

University Genomics Institute (CUGI) (Begum, Palmer,

Frisch, Atkins and Wing). Plasmid DNA preparations, DNA

sequencing and sequence analysis were performed at CUGI

(Wing, Yu, Frisch, Henry, Simmonds, Oates, Rambo, Main).

The sequence has been trimmed to remove vector sequence

and contains a minimum of 100 bases of phred value 20 or

above. For more details on library preparation and

sequence analysis see

<http://www.genome.clemson.edu/projects/barley>. To order

this clone see <http://www.genome.clemson.edu/orders> Also

see Close TJ, Wing R, Kleinohs A, Wise R (2001)

Genetically and physically anchored EST resources for

barley genomics. Barley Genetics Newsletter 31:29-30.

(<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)"

ORIGIN

Query Match 74.5%; Score 16.4; DB 7; Length 799;
 Best Local Similarity 94.4%; Pred. No. 3.4e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTT 18
 |||||
 Db 471 GTCGAACGGAAGGCCTT 488
 |||||

RESULT 71
 BU409605

LOCUS
 DEFINITION 60315733F1 CSEORBL03 Gallus gallus cdna clone CHEST174b10 5', mRNA
 EST 29-NOV-2002

ACCESSION
 VERSION BU409605
 KEYWORDS
 SOURCE EST.
 ORGANISM Gallus gallus (chicken)

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 1 (bases 1 to 847)

TITLE Boardman,P.B., Sanz-Esquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
 A Comprehensive Collection of Chicken cDNAs
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
 PUBLISHED 12445392

COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.
 Location/Qualifiers
 1. 847
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Layer and broiler"
 /db_xref="taxon:9031"
 /clone="CHEST174b10"
 /sex="Male and female"
 /tissue_type="Chondrocytes isolated from growth plate
 cartilage"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="CSEORBL03"
 /notes="vector: pBluescript II KS(+); Site_1: EcoRI;
 Site_2: NotI; Modification of pBluescript II KS(+)
 [Stratagene] vector to accommodate cDNA produced with the
 T-trimmed protocol (Construction of uni-directionally
 cloned cDNA libraries from messenger RNA for improved 3'
 end DNA sequencing by Glenn Fu, et al. U.S. Patent #
 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
 Ligate in double stranded adaptor containing BsgI and
 BamHI sites [5'ggcgcgtgcagcccgatcgcaaaaaag]
 [5'aattcttttttggatccgggtgcacgc]"

ORIGIN
 Query Match 74.5%; Score 16.4; DB 3; Length 847;
 Best Local Similarity 94.4%; Pred. No. 3.4e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAACGGAAGGCCTTTCG 21
 |||||
 Db 278 GAAAGGAAGGCCTTTCG 295
 |||||

RESULT 72
 CNS02922/c

LOCUS
 DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
 245N04 of library G from Tetraodon nigroviridis, genomic survey

sequence.
 AL186707

ACCESSION
 VERSION AL186707.1 GI:7824811
 KEYWORDS GSS; genome survey sequence.
 SOURCE Tetraodon nigroviridis
 ORGANISM Tetraodon nigroviridis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 Tetraodontidae; Tetraodontidae; Tetraodon.
 1
 Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
 Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
 Saurin,W. and Weissenbach,J
 Estimate of human gene number provided by genome-wide analysis
 using Tetraodon nigroviridis DNA sequence
 Nat. Genet. 25 (2), 235-238 (2000)
 10835645

REFERENCE
 2
 Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
 Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
 Saurin,W., Bernot,A. and Weissenbach,J.
 Characterization and repeat analysis of the compact genome of the
 freshwater pufferfish Tetraodon nigroviridis
 Genome Res. 10 (7), 939-949 (2000)
 10899143

REFERENCE
 3 (bases 1 to 883)
 Genoscope.
 Direct Submission
 Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
 - Web : www.genoscope.cns.fr)
 This sequence is a single read and was generated as part of a large
 scale clone-end sequencing project of the Tetraodon nigroviridis
 genome. For more information, please take a look at
 http://www.genoscope.cns.fr/Tetraodon.
 Location/Qualifiers
 1. 883
 /organism="Tetraodon nigroviridis"
 /mol_type="genomic DNA"
 /db_xref="taxon:99883"
 /clone="245N04"
 /clone_lib="G"
 /notes="Genoscope sequence ID : COAG245DG02SP1
 end : PUC-Ori"

ORIGIN
 Query Match 74.5%; Score 16.4; DB 14; Length 883;
 Best Local Similarity 94.4%; Pred. No. 3.5e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCCTTT 19
 |||||
 Db 368 TTGAACGGAAGGCCTTT 351
 |||||

RESULT 73
 COS83238/c

LOCUS
 DEFINITION ILLUMIGEN_MQ_44583 Katze MMLV Macaca mulatta cdna clone
 IB1UM:16736 5' similar to Bases 1 to 944 highly similar to human
 ITIH3 (Hs.76716), mRNA sequence.

ACCESSION
 VERSION COS83238.1 GI:50415893
 KEYWORDS
 SOURCE EST.
 ORGANISM Macaca mulatta (rhesus monkey)
 Macaca mulatta
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Cercopithecoidea; Cercopithecinae; Macaca.
 1 (bases 1 to 944)
 Magness,C.L., Fellin,P.C., Thomas,M.J., Korth,M.J., Agy,M.B.,
 Prolli,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and

TITLE
JOURNAL
PUBLISHED
COMMENT

Idonato,S.P.
 Analysis of the Macaca mulatta transcriptome and the sequence divergence between Macaca and human
 Genome Biol. 6 (7), R60 (2005)
 15998449
 Contact: C. Magness
 Illumigen Biosciences Inc.
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
 Tel: 2063780400
 Fax: 2063780408
 Email: cmagness@illumigen.com
 Sequenced on 2004.06.18. 633 Q20 bases. Library Preparation: Prof. Michael Katze Lab at University of Washington DNA Sequencing: Illumigen Biosciences Inc. For further information, see <http://www.macaque.org>
 PCR Primers
 FORWARD: CCCTCACTAAGGGAACAAAA
 BACKWARD: CACTATAGGCGGATTTGGTA
 Insert Length: 944 Std Error: 0.00
 Plate: CL000392 row: H column: 04
 Seq primer: CCCTCACTAAGGGAACAAAA
 POLYA=No.

FEATURES
 source

1. .944
 /location="Qualifiers
 /organism="Macaca mulatta"
 /mol_type="mRNA"
 /strain="Indian"
 /db_xref="taxon:9544"
 /clone="IBIUM:16736"
 /sex="female"
 /dev_stage="adult"
 /lab_host="Electromax DH10B"
 /clone_lib="Katze MMLV"
 /note="Organ: liver; Vector: pDONR 222; Site 1: BarG I; Site 2: BarG I; Created from CloneMiner cDNA_Library Construction kit (catalog #18249-029)"

ORIGIN

Query Match 74.5%; Score 16.4; DB 8; Length 944;
 Best Local Similarity 94.4%; Pred. No. 3.5e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AACGGAAGGCTTTTCGG 22
 |||||
 Db 837 AACGGAAGGCTTTTCGG 820

RESULT 74
 CC213477/c
LOCUS
 DEFINITION
 CC213477 genomic survey sequence.
ACCESSION
 CC213477
VERSION
 CC213477.1 GI:30532145
KEYWORDS
 GSS.
SOURCE
 ORGANISM
 Gallus gallus (chicken)
 Gallus gallus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 1 (bases 1 to 1124)
 Warren,W., Graves,T., Higginsbotham,J., Wylie,K., Carter,J., McPherson,J., Kremitzki,C., Higginsbotham,J., Mardis,E. and Wilson,R.
 Gallus gallus BAC End Reads
 Unpublished (2003)
 Contact: Richard K. Wilson
 Genome Sequencing Center
 Washington University School of Medicine
 Email: submissions@watson.wustl.edu
 Insert Length: 182000 Std Error: 0.00
 Seq primer: Sp6 ATTAGTGACACTATAG
 Class: BAC ends
 High quality sequence start: 103

FEATURES
 source

1. .1124
 /organism="Gallus gallus"
 /mol_type="genomic DNA"
 /strain="Red Jungle Fowl"
 /db_xref="taxon:9031"
 /clone="CH261-65024"
 /sex="female"
 /cell_line="UCD001, inbred 256"
 /clone_lib="CH261"
 /note="Vector: pIARAC2.1; Site 1: EcoRI; Site 2: EcoRI; CH261 Female Chicken library - For library and clone ordering information: <http://www.chori.org/bacpac>"

ORIGIN

Query Match 74.5%; Score 16.4; DB 12; Length 1124;
 Best Local Similarity 94.4%; Pred. No. 3.6e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTT 18
 |||||
 Db 34 GTCGACAGAAAGGCCTT 17

RESULT 75
 DR139870/c
LOCUS
 DEFINITION
 49349140 Drosophila pseudoobscura embryonic cDNA library Drosophila pseudoobscura cDNA clone A7 3', mRNA sequence.
ACCESSION
 DR139870
VERSION
 DR139870.1 GI:67884960
KEYWORDS
 EST.
SOURCE
 ORGANISM
 Drosophila pseudoobscura
 Drosophila pseudoobscura
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 1173)
 Richards,S., Liu,Y., Bettencourt,B.R., Hradecky,P., Letovsky,S., Nielsen,R., Thornton,K., Hubisz,M.J., Chen,R., Meisl,R.P., Couronne,O., Hua,S., Smith,M.A., Zhang,P., Liu,J., Bussemaker,H.J., van Batenburg,M.F., Howells,S.L., Scherer,S.E., Sodergren,E., Matthews,B.B., Crosby,M.A., Schroeder,A.J., Ortiz-Barrientos,D., Rives,C.M., Metzker,M.L., Muzny,D.M., Scott,G., Steffen,D., Wheeler,D.A., Worley,K.C., Havlak,P., Durbin,K.J., Egan,A., Gill,R., Hume,J., Morgan,M.B., Miner,G., Hamilton,C., Huang,Y., Waldron,L., Verdusco,D., Clerc-Blankenburg,K.P., Dubchak,I., Noor,M.A., Anderson,W., White,K.P., Clark,A.G., Schaeffer,S.W., Gelbart,W., Weinstock,G.M. and Gibbs,R.A.
 Comparative genome sequencing of Drosophila pseudoobscura: chromosomal, gene, and cis-element evolution
 Genome Res. 15 (1), 1-18 (2005)
 15632085
 Contact: Stephen Richards
 Human Genome Sequencing Center
 Baylor College of Medicine
 One Baylor Plaza, Houston, TX 77030, USA
 Tel: 713-798-6667
 Email: stephen@bcm.tmc.edu
 NCHI Trace Archive: 226722030
 Insert Length: 1750 Std Error: 0.25.
 Location/Qualifiers

FEATURES
 source

1. .1173
 /organism="Drosophila pseudoobscura"
 /mol_type="mRNA"
 /db_xref="taxon:7237"
 /clone="A7"
 /dev_stage="0-18h embryos"
 /clone_lib="Drosophila pseudoobscura embryonic cDNA library"
 /note="Vector: pOTB7; Site 1: EcoRI; Site 2: XhoI; oligo dt priming from poly A+ RNA, directionally cloned"

ORIGIN

Query Match 74.5%; Score 16.4; DB 9; Length 1173;
 Best Local Similarity 89.5%; Pred. No. 3.6e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19
 ||||| ||||| |||||
 Db 54 GTCGAACGGAAGGCCTTT 36

RESULT 76
 BZ548902/c
 LOCUS
 DEFINITION BZ548902 1330 bp DNA linear GSS 17-DEC-2002
 pacsl-60_1548.s1 pacsl-60 Pseudomonas aeruginosa genomic clone
 pacsl-60_1548, genomic survey sequence.
 ACCESSION BZ548902
 VERSION BZ548902.1 GI:27152483
 KEYWORDS GSS.
 SOURCE Pseudomonas aeruginosa
 ORGANISM Pseudomonas aeruginosa
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 Pseudomonadaceae; Pseudomonas.
 REFERENCE 1 (bases 1 to 1330)
 AUTHORS Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
 Burns,J.L., Kaul,R. and Olsen,M.V.
 TITLE Whole-Genome-Sequence variation among multiple isolates of
 Pseudomonas aeruginosa library
 JOURNAL J. Bacteriol. (2002) In press
 COMMENT Contact: Chris K. Raymond
 Genome Center
 University of Washington
 Box 352145, Seattle, WA 98105-2145, USA
 Tel: 2062216954
 Fax: 2066857244
 Email: craymond@u.washington.edu
 Class: shotgun.

FEATURES
 source
 1..1330
 /organism="Pseudomonas aeruginosa"
 /mol_type="genomic DNA"
 /strain="1-60"
 /db_xref="taxon:287"
 /clone="pacsl-60_1548"
 /clone_lib="pacsl-60"
 /note="clinical isolate 1-60 Whole genomic shotgun
 library."

ORIGIN

Query Match 74.5%; Score 16.4; DB 11; Length 1330;
 Best Local Similarity 94.4%; Pred. No. 3.7e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AACGGAAGCCTTCGG 22
 ||||| ||||| |||||
 Db 1240 AAGCGAAGCCTTCGG 1223

RESULT 77
 DT975169
 LOCUS
 DEFINITION DT975169 1370 bp mRNA linear EST 22-SEP-2005
 CLJ157-C04.yld-s SHGC-CLJ Gasterosteus aculeatus cDNA clone
 CLJ157-C04 5', mRNA sequence.
 ACCESSION DT975169
 VERSION DT975169.1 GI:76098976
 KEYWORDS EST.
 SOURCE Gasterosteus aculeatus (three spined stickleback)
 ORGANISM Gasterosteus aculeatus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
 Gasterosteidae; Gasterosteus.
 REFERENCE 1 (bases 1 to 1370)

AUTHORS Kingsley,D.M., Peichel,C., Balabhadra,S., Grimwood,J., Dickson,M.,
 Schmutz,J. and Myers,R.M.
 TITLE Expressed sequence tags from Gasterosteus aculeatus
 JOURNAL Unpublished (2003)
 COMMENT Contact: Grimwood, Jane
 Stanford Human Genome Center
 Stanford University School of Medicine
 975 S California Ave, Palo Alto, CA 94304, USA
 Tel: 650 320 5917
 Fax: 650 320 5801
 Email: jane@shgc.stanford.edu
 Plate: 157
 High quality sequence stop: 822.

FEATURES
 source
 1..1370
 /organism="Gasterosteus aculeatus"
 /mol_type="mRNA"
 /strain="Bitruufjordur marine sticklebacks, Iceland"
 /db_xref="taxon:69293"
 /clone="CLJ157-C04"
 /sex="mixed male and female"
 /tissue_type="whole larva"
 /dev_stages="21 day old larvae collected at Swarup Stage 30
 (J. Embryol. Exp. Morphol 6: 373-383.1958)"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="SHGC-CLJ"
 /note="Vector: Express 1; Total and poly A+ RNA was
 isolated from the indicated stickleback tissue, and a cDNA
 library was constructed in the Express 1 plasmid vector by
 Open Biosystems. First strand cDNA synthesis was primed
 with an 54 bp linker primer containing an oligodT sequence
 preceded by a synthetic NotI site (first strand primer:
 5'-GACTAGTTCTAGATCGAGCGCGCC(T)25-3'). Following
 second strand synthesis, cDNAs were made blunt at the end
 corresponding to the original 5 prime end of mRNA, and
 cloned directionally into the NotI and EcoRV sites of
 Express 1. Note that the EcoRV site is typically destroyed
 in the blunt end cloning, leaving a junction of the form
 'xxATC'(where is ATC is the second half of the EcoRV
 site, and xxx is derived from the cDNA sequence). A map of
 the Express 1 vector is available at:
 http://www.openbiosystems.com/cdna_library_construction.fa
 q.php#18 The primary library was transformed and amplified
 in DH10B (T1 phage resistant) bacteria. Clones available
 from Open Biosystems:
 http://www.openbiosystems.com/stickleback"

ORIGIN

Query Match 74.5%; Score 16.4; DB 10; Length 1370;
 Best Local Similarity 94.4%; Pred. No. 3.7e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCCTTT 19
 ||||| ||||| |||||
 Db 982 TCTAACGGAAGGCCTTT 999

RESULT 78
 DN730360
 LOCUS
 DEFINITION DN730360 1462 bp mRNA linear EST 31-MAR-2005
 CNB52-E02.x1d-t SHGC-CNB Gasterosteus aculeatus cDNA clone
 CNB52-E02 3', mRNA sequence.
 ACCESSION DN730360
 VERSION DN730360.1 GI:62106596
 KEYWORDS EST.
 SOURCE Gasterosteus aculeatus (three spined stickleback)
 ORGANISM Gasterosteus aculeatus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
 Gasterosteidae; Gasterosteus.
 REFERENCE 1 (bases 1 to 1462)
 AUTHORS Kingsley,D.M., Peichel,C., Balabhadra,S., Grimwood,J., Dickson,M.,

TITLE
JOURNAL
COMMENT
Schmutz, J. and Myers, R.M.
Expressed sequence tags from *Gasterosteus aculeatus*
Unpublished (2003)
Contact: Grimwood, Jane
Stanford Human Genome Center
Stanford University School of Medicine
975 S California Ave, Palo Alto, CA 94304, USA
Tel: 650 320 5917
Fax: 650 320 5801
Email: jane@shgc.stanford.edu
Plate: 52
High quality sequence start: 8
High quality sequence stop: 771.

FEATURES

source

Location/Qualifiers
1. 1462
/organism="Gasterosteus aculeatus"
/mol_type="mRNA"
/strain="Conner Creek sticklebacks, WA USA"
/db_xref="taxon:69293"
/clone="CNB52-E02"
/sex="mixed male and female"
/tissue_type="brain"
/dev_stage="adult"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="SHGC-CNB"
/note="Vector: Express 1; Total and poly A+ RNA was isolated from the indicated stickleback tissue, and a cDNA library was constructed in the Express 1 plasmid vector by Open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligo(dT) sequence preceded by a synthetic NotI site (first strand primer: 5'-GACATGTCATGATCGAGCGGCCCTTC-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5 prime end of mRNA, and cloned directionally into the NotI and EcoRV sites of Express 1. Note that the EcoRV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxxATC' (where is ATC is the second half of the EcoRV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at:
http://www.openbiosystems.com/cdna_library_construction_fa_q.php#8 The primary library was transformed and amplified in DH10B (T1 phage resistant) bacteria. Clones available from Open Biosystems:
<http://www.openbiosystems.com/stickleback>"

ORIGIN

Query Match 74.5%; Score 16.4; DB 9; Length 1462;
Best Local Similarity 94.4%; Pred. No. 3.7e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CGAAGCGGAAGGCCCTTTC 20
|||||
Db 899 CGAAGCGGAAGGCCCTTTC 916

RESULT 79

B1527919/c

LOCUS B1527919 182 bp mRNA linear EST 29-AUG-2001
DEFINITION 1024085G10.x1 C. reinhardtii CC-1690, normalized, Lambda Zap II
Chlamydomonas reinhardtii cDNA, mRNA sequence.

B1527919

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Chlamydomonas reinhardtii

Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;

Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas.

1 (bases 1 to 182)

Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C.,

Lefebvre, P., McDermott, J. P., Shrager, J., Silflow, C. and Stern, D.

Analyses of the Chlamydomonas reinhardtii Genome: A Model,

Unicellular System for Analyzing Gene Function and Regulation in

JOURNAL

COMMENT

Vascular Plants. Project: 1024b
Unpublished (2001)
Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.

FEATURES

source

Location/Qualifiers
1. 182
/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap II"
/note="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2: XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into Lambda Zap II (Stratagene) in the EcoRI (5') and XhoI (3') sites. pBluescript II SK- plasmids were excised from the lambda Zap clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."

ORIGIN

Query Match 73.6%; Score 16.2; DB 2; Length 182;
Best Local Similarity 85.7%; Pred. No. 3.4e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGACGCGGAAGGCCCTTTCG 21

|||

Db 179 GTGACGCGGAAGGCCCTTTCG 159

RESULT 80

CF045077

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 267)

Genoplante.

Genoplante, a major partnership french program in plant genomics

Unpublished (2003)

Contact: Genoplante

Genoplante

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'Genoplante' (<http://www.genoplante.com>and <http://genoplante-info.infobiogen.fr>).

Location/Qualifiers

1. 267

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="F2"

/db_xref="taxon:4577"

/clone="QCJ8all"

/tissue_type="cell lignification part of the 6th leaf"

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ORIGIN
/clone_lib="QCJ"

Query Match      73.6%; Score 16.2; DB 5; Length 267;
Best Local Similarity 85.7%; Pred. No. 3.7e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TCGAACGGAAGGCGCTTTCGG 22
    ||||| ||||| ||||| ||||| |||||
Db 186 TCGAACGGAAGGCGCTTTCGG 206

RESULT 81
CF044432      288 bp mRNA linear EST 17-JUL-2003
LOCUS
DEFINITION QJ2907.yg QCJ Zea mays cDNA clone QJ2907, mRNA sequence.
ACCESSION CF044432
VERSION CF044432.1 GI:32939613
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 288)
Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
JOURNAL
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).

FEATURES
source
1..288
/mol_type="mRNA"
/db_xref="taxon:4577"
/clone="QJ2907"
/tissue_type="cell lignification part of the 6th leaf"
/clone_lib="QCJ"

ORIGIN

Query Match      73.6%; Score 16.2; DB 5; Length 289;
Best Local Similarity 85.7%; Pred. No. 3.7e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TCGAACGGAAGGCGCTTTCGG 22
    ||||| ||||| ||||| ||||| |||||
Db 207 TCGAACGGAAGGCGCTTTCGG 227

RESULT 82
BW531407      294 bp mRNA linear EST 12-SEP-2005
LOCUS
DEFINITION BW531407 Yutaka Satou unpublished cDNA library (cslv) Ciona
savigny cDNA clone cslv017o20 5', mRNA sequence.
ACCESSION BW531407
VERSION BW531407.1 GI:51693105
KEYWORDS EST.
SOURCE Ciona savigny
ORGANISM Ciona savigny
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 294)
Vinson,J.P., Jaffe,D.B., O'Neill,K., Karlsson,E.K.,
Strange-Thomann,N., Anderson,S., Mesirov,J.P., Satoh,N., Satou,Y.,
Nusbaum,C., Birren,B., Galagan,J.E. and Lander,E.S.
Assembly of polymorphic genomes: Algorithms and application to

ORIGIN

Ciona savigny
Genome Res. 15 (8), 1127-1135 (2005)
16077012
Contact: Yutaka Satou
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4095
Fax: 81-75-705-1113
Email: yutaka@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
1..294
/organism="Ciona savigny"
/mol_type="mRNA"
/db_xref="taxon:51511"
/clone="cslv017o20"
/dev_stage="larva"
/clone_lib="Yutaka Satou unpublished cDNA library (cslv)"

FEATURES
source
1..294
/organism="Lactuca serriola"
/mol_type="mRNA"
/db_xref="taxon:75943"
/clone="QGE11022"
/lab_host="E.coli"
/clone_lib="QG EFGHJ lettuce serriola"
/note="vector: pBRCDNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,

ORIGIN

Query Match      73.6%; Score 16.2; DB 4; Length 294;
Best Local Similarity 85.7%; Pred. No. 3.7e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TCGAACGGAAGGCGCTTTCGG 22
    ||||| ||||| ||||| ||||| |||||
Db 271 TCGCCGGGATGCGCTTTCGG 291

RESULT 83
BQ980749      298 bp mRNA linear EST 03-OCT-2005
LOCUS
DEFINITION QGE11022.yg.abl QG EFGHJ lettuce serriola Lactuca serriola cDNA
clone QGE11022, mRNA sequence.
ACCESSION BQ980749
VERSION BQ980749.1 GI:22398272
KEYWORDS EST.
SOURCE Lactuca serriola
ORGANISM Lactuca serriola
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
1 (bases 1 to 298)
Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,
Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
Lai,Z., Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozika@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
singleton, see http://cgdb.ucdavis.edu/ for details.
Plate: QGE11 row: 0 column: 22.
Location/Qualifiers
1..298
/organism="Lactuca serriola"
/mol_type="mRNA"
/db_xref="taxon:75943"
/clone="QGE11022"
/lab_host="E.coli"
/clone_lib="QG EFGHJ lettuce serriola"
/note="vector: pBRCDNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,

```


REFERENCE AUTHORS	1 (bases 1 to 346) McCulloch,A., Wilson,T., Molenaar,A., Grigor,M., Davis,S., Glenn,M., Havukkala,I., Watson,J., Crawford,A., Wheeler,T., Hagemann,L., Lee,R., Hein,W., Johnstone,P., Maqbool,N., McMahon,C., McCracken,J., Stelwagen,K., Farr,V., Singh,K., Whitley,J., Nicholas,K., Savin,K., Mather,A., McPartlan,H., Whitley,J., Wells,M., Bowman,P., Goddard,M., Langford,C., McEwan,J. and Atkinson,P.
TITLE	AgResearch, Genesis and Primary Industry Victoria Bovine BSE Project
JOURNAL COMMENT	Unpublished (2006) Contact: Maqbool N AgResearch Ltd. Invermay Agricultural Centre, Puddle Alley, Private Bag 50034, Mosgiel, New Zealand Email: nauman.maqbool@agresearch.co.nz.
FEATURES source	Location/Qualifiers 1. .346 /organism="Bos taurus" /mol_type="mRNA" /db_xref="taxon:9913" /tissue_type="Posterior brain" /clone_lib="BPBA" /note="Vector: pBK-CMV; Bovine posterior brain stem cDNA library derived from tissue harvested from an unknown breed calf by Allan Crawford on 28/09/99"
ORIGIN	
Query Match	73.6%; Score 16.2; DB 10; Length 346;
Best Local Similarity	85.7%; Pred. No. 3.8e+03;
Matches	18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	2 TCGAACGGAAGGCGCTTCGG 22
Db	96 TCAAGGAAGGCGATTCGG 116
RESULT 87	
CZ003780/c	
LOCUS	CZ003780 370 bp DNA linear GSS 04-JAN-2005
DEFINITION	OA_BBa0052008.r OA_BBa Oryza alta genomic clone OA_BBa0052008 3', genomic survey sequence.
ACCESSION	CZ003780
VERSION	CZ003780.1 GI:57034984
KEYWORDS	GSS.
SOURCE	Oryza alta
ORGANISM	Oryza alta Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE AUTHORS	1 (bases 1 to 370) SanMiguel,P., Westerman,R., Kim,H., Yu,Y., Wissotski,M., Yost,D., Scum,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C., Wing,R. and Jackson,S.A. OMAP (Oryza Map Alignment Project) - Purdue University Unpublished (2004) Contact: Scott A. Jackson Jackson Laboratory Purdue University 915 W. State St., West Lafayette, IN 47907, USA Tel: 7654963621 Fax: 7654967255 Email: sjackson@purdue.edu
TITLE	Basecalling by phred version 0.020425.c. This sequence was derived from the raw sequence read by clipping with Lucy version 1.19c.
JOURNAL COMMENT	Bases 180-549 of the raw sequence (length 978) were retained after clipping. Plate: 0052 row: 0 column: 08 Seq primer: CAC TCA TTA GGC ACC CCA Class: BAC ends.
FEATURES source	Location/Qualifiers 1. .370 /organism="Oryza alta"
ORIGIN	
Query Match	73.6%; Score 16.2; DB 13; Length 370;
Best Local Similarity	85.7%; Pred. No. 3.8e+03;
Matches	18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	2 TCGAACGGAAGGCGCTTCGG 22
Db	47 TCGAACGGAAGGCGCTCCCG 27
RESULT 88	
AA652906	
LOCUS	AA652906 379 bp mRNA linear EST 25-NOV-1997
DEFINITION	ms68a07.s1 NCI_CGAP Pr-2 Homo sapiens cDNA clone IMAGE:1188756 similar to gb:U01124 40S RIBOSOMAL PROTEIN S13 (HUMAN);, mRNA sequence.
ACCESSION	AA652906
VERSION	AA652906.1 GI:2584558
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE AUTHORS	1 (bases 1 to 379) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap . National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgaps-r@mail.nih.gov
JOURNAL COMMENT	Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
FEATURES source	Trace considered overall poor quality Insert Length: 705 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1. Location/Qualifiers 1. .379 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:1188756" /sex="Male" /dev_stage="45 years old" /lab_host="DH10B" /clone_lib="NCI_CGAP Pr-2" /note="Vector: pAMP10; Site 1: NotI; Site 2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNase-treated, total cellular RNA obtained from 5,000-10,000 microdissected preneoplastic cells histologically-determined to be prostatic intraepithelial neoplasia 2 (PIN2) cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was

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ORIGIN
Query Match      73.6%; Score 16.2; DB 1; Length 379;
Best Local Similarity 85.7%; Pred. No. 3.8e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTTCGG 22
    ||||| ||||| ||||| ||||| |||||
Db 352 TCGAAAGGAAGGCGCTTTTCGG 372

RESULT 89
CK291892
LOCUS
DEFINITION
EST754606 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NEMC541 3'
end, mRNA sequence.
CK291892
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE
1 (bases 1 to 390)
AUTHORS
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H. and Baker, B.
TITLE
Generation of EST sequences from Nicotiana benthamiana
JOURNAL
Unpublished (2003)
COMMENT
Other ESTs: EST754605
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: GTA ATA CGA CTC ACT ATA GGG C.

FEATURES
Location/Qualifiers
1..390
/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NBMC541"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN
Query Match      73.6%; Score 16.2; DB 5; Length 390;
Best Local Similarity 85.7%; Pred. No. 3.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTTCGG 22
    ||||| ||||| ||||| ||||| |||||
Db 241 TCGAAAGGGAAGGCGCTTTTCGG 261

RESULT 90

```

```

AW400594
LOCUS
DEFINITION
LamdiSest091est L.digitata sporophyte Lambda ZapII Laminaria
digitata cDNA, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Laminaria digitata
Laminaria digitata
Eukaryota; stramenopiles; Phaeophyceae; Laminariales;
Laminariaceae; Laminaria.
1 (bases 1 to 399)
REFERENCE
AUTHORS
Crepineau, F., Roscoe, T., Kaas, R., Kloareg, B. and Boyen, C.
TITLE
Characterisation of complementary DNAs from the expressed sequence
tag analysis of life cycle stages of Laminaria digitata
(Phaeophyceae)
JOURNAL
Plant Mol. Biol. 43 (4), 503-513 (2000)
PUBMED
11052202
COMMENT
Contact: Boyen C
Centre d'Etudes Oceanologique et de Biologie Marine
CNRS-LPR9042, Université P. & M. Curie
BP74, F-29682 Roscoff cedex, France
Tel: 33 2 98 29 23 32
Fax: 33 2 98 29 23 24
Email: est@sb-roscoff.fr.
Location/Qualifiers
1..399
/organism="Laminaria digitata"
/mol_type="mRNA"
/db_xref="taxon:80365"
/dev_stage="sporophyte"
/lab_host="SOLR"
/clone_lib="L.digitata sporophyte Lambda ZapII"
/notes="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
XhoI; The Laminaria sporophyte library, constructed by T
Roscoe and F Crepineau, was oligo-(dT) primed and
directionally cloned into a Uni-ZAPTM XR vector
(Stratagene, la Jolla, CA, USA) using total mRNA from
sporophytes harvested at l'ile de Sieck (F)."

ORIGIN
Query Match      73.6%; Score 16.2; DB 7; Length 399;
Best Local Similarity 85.7%; Pred. No. 3.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTTCGG 22
    ||||| ||||| ||||| ||||| |||||
Db 199 TCGAACGTAAGACCTGTCGG 219

RESULT 91
CG857155/c
LOCUS
DEFINITION
ZMMB5C0465N21r ZMMB5C (EcoRI) Zea mays genomic clone ZMMB5C0465N21
3', genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 431)
REFERENCE
AUTHORS
Bharti, A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C.,
Zohovetz, V., Fuks, G., Yu, Y., Wing, R. and Messing, J.
TITLE
Sequencing of the maize genome at PGIR (2003c)
JOURNAL
Unpublished (2003)
COMMENT
Contact: Bharti, A.K.
Dr. Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA

```

```

Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksmann.rutgers.edu
Seq primer: SP6
Class: BAC ends
High quality sequence start: 105.

FEATURES
    source
        1..431
            /organism="Zea mays"
            /mol_type="genomic DNA"
            /cultivar="B73"
            /db_xref="taxon:4577"
            /clone="ZMMBBC0265N21"
            /lab_host="E. coli DH10B"
            /clone_lib="ZMMBBC (ECORI)"
            /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"

ORIGIN
Query Match      73.6%; Score 16.2; DB 12; Length 431;
Best Local Similarity 85.7%; Pred. No. 3.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  1  GTCGACGGAAAGCGCTTTCG 21
      ||||| ||||| ||||| |||||
Db   78  GTCGAGCGTCAAGGCGCTTTCG 58

RESULT 92
BW530083 LOCUS
DEFINITION
    BW530083 Yutaka Satou unpublished cDNA library (cslv) Ciona
    savignyi cDNA clone cslv013h24 5', mRNA sequence.
ACCESSION
    BW530083
VERSION
    BW530083.1 GI:51691781
KEYWORDS
    EST.
SOURCE
    Ciona savignyi
    ORGANISM
        Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
        Phlebobranchia; Clonidae; Ciona.
REFERENCE
    1 (bases 1 to 490)
    Vinson,J.P., Jaffe,D.B., O'Neill,K., Karlsson,B.K.,
    Stange-Thomann,N., Anderson,S., Mesirov,J.P., Satoh,N., Satou,Y.,
    Nusbbaum,C., Birren,B., Galagan,J.E. and Lander,E.S.
    Assembly of polymorphic genomes: Algorithms and application to
    Ciona savignyi
    Genome Res. 15 (8), 1127-1135 (2005)
JOURNAL
    16077012
PUBMED
Contact: Yutaka Satou
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4095
Fax: 81-75-703-1113
Email: yutaka@ascidian.zool.kyoto-u.ac.jp.

FEATURES
    source
        1..490
            /organism="Ciona savignyi"
            /mol_type="mRNA"
            /db_xref="taxon:51511"
            /clone="cslv013h24"
            /dev_stage="larva"
            /clone_lib="Yutaka Satou unpublished cDNA library (cslv)"

ORIGIN
Query Match      73.6%; Score 16.2; DB 4; Length 490;
Best Local Similarity 85.7%; Pred. No. 4e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2  TCGAACGGAAAGCGCTTTCG 22
      ||| ||||| ||||| |||||
Db   257  TCGGCCGAATGCCTTTCG 277

Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksmann.rutgers.edu
Seq primer: SP6
Class: BAC ends
High quality sequence start: 105.

FEATURES
    source
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            /organism="Zea mays"
            /mol_type="genomic DNA"
            /cultivar="B73"
            /db_xref="taxon:4577"
            /clone="ZMMBBC0265N21"
            /lab_host="E. coli DH10B"
            /clone_lib="ZMMBBC (ECORI)"
            /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"

ORIGIN
Query Match      73.6%; Score 16.2; DB 12; Length 431;
Best Local Similarity 85.7%; Pred. No. 3.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  1  GTCGACGGAAAGCGCTTTCG 21
      ||||| ||||| ||||| |||||
Db   78  GTCGAGCGTCAAGGCGCTTTCG 58

RESULT 92
BW530083 LOCUS
DEFINITION
    BW530083 Yutaka Satou unpublished cDNA library (cslv) Ciona
    savignyi cDNA clone cslv013h24 5', mRNA sequence.
ACCESSION
    BW530083
VERSION
    BW530083.1 GI:51691781
KEYWORDS
    EST.
SOURCE
    Ciona savignyi
    ORGANISM
        Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
        Phlebobranchia; Clonidae; Ciona.
REFERENCE
    1 (bases 1 to 490)
    Vinson,J.P., Jaffe,D.B., O'Neill,K., Karlsson,B.K.,
    Stange-Thomann,N., Anderson,S., Mesirov,J.P., Satoh,N., Satou,Y.,
    Nusbbaum,C., Birren,B., Galagan,J.E. and Lander,E.S.
    Assembly of polymorphic genomes: Algorithms and application to
    Ciona savignyi
    Genome Res. 15 (8), 1127-1135 (2005)
JOURNAL
    16077012
PUBMED
Contact: Yutaka Satou
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4095
Fax: 81-75-703-1113
Email: yutaka@ascidian.zool.kyoto-u.ac.jp.

FEATURES
    source
        1..490
            /organism="Ciona savignyi"
            /mol_type="mRNA"
            /db_xref="taxon:51511"
            /clone="cslv013h24"
            /dev_stage="larva"
            /clone_lib="Yutaka Satou unpublished cDNA library (cslv)"

ORIGIN
Query Match      73.6%; Score 16.2; DB 4; Length 490;
Best Local Similarity 85.7%; Pred. No. 4e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2  TCGAACGGAAAGCGCTTTCG 22
      ||| ||||| ||||| |||||
Db   257  TCGGCCGAATGCCTTTCG 277

```


Best Local Similarity 85.7%; Pred. No. 4e+03; Mismatches 3; Indels 0; Gaps 0;
Matches 18; Conservative 0;

QY 2 TCGAACGGAAGGCTTTTCG 22
|||||
Db 83 TCGAACGGAATGCTGCGG 103
|||||

RESULT 97
LOCUS CX608591/c
DEFINITION ANR1_39_B09_g1_A002 mRNA linear EST 14-JAN-2005
ANR1_39_B09_A002 5', mRNA sequence.

ACCESSION CX608591
VERSION CX608591.1 GI:57807311
KEYWORDS EST.
SOURCE Sorghum bicolor (sorghum)

ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE 1 (Bases 1 to 537)
AUTHORS Cordonnier-Pratt,M.-M., Suzuki,Y., Sugano,S., Klein,R., Lim,S.,
Liang,C., Sun,F. and Pratt,L.H.

TITLE A Sorghum EST database: anaerobic roots
JOURNAL Unpublished (2005)
COMMENT Other_ESTs: ANR1_39_B09.bi_A002

Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University;
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.

Seq primer: Sug5 (CTTCTGCTCTAAAGCTCG).

FEATURES

source
Location/Qualifiers
1..537
/organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="BTx623"
/db_xref="taxon:4558"
/clones="ANR1_39_B09_A002"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Anaerobic roots"
/note="Organ: Root; Vector: pME18S-FL3; Site 1: XhoI;
Site 2: XhoI; The library was prepared from polyA+ RNA
isolated from seedlings of sorghum BTx623 grown in
hydroponic culture. At 8 days of age, medium was purged
with nitrogen gas for 3 hr prior to stopping aeration.
Roots were harvested after 3, 27, and 72 hr. Material from
all time points was combined prior to RNA isolation.
Double-stranded cDNA was cloned unidirectionally into
different DraIII sites of the pME18S-FL3 vector (5-prime
DraIII site is CACTGTGTG, 3-prime DraIII site is
CACCATTGTG). XhoI excises the cDNA insert."

ORIGIN

Query Match 73.6%; Score 16.2; DB 9; Length 537;
Best Local Similarity 85.7%; Pred. No. 4.1e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TCGAACGGAAGGCTTTTCG 22
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Db 21 TCGAACTGAAGGCTTTTGGG 1
|||||

RESULT 98

LOCUS CB826166/c
DEFINITION

ACCESSION CB826166.1 GI:29963900
VERSION
KEYWORDS EST.
SOURCE Heterodera glycines

ORGANISM Heterodera glycines
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.

REFERENCE

AUTHORS

1 (Bases 1 to 548)

McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,

Wyllie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,

Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,

Tsagarishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,

Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,

Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,

McCann,R., Waterston,R. and Wilson,R.

The Washington Univ. Nematode EST Project, 1999

Unpublished (1999)

Contact: McCarter JP

The Washington Univ. Nematode EST Project, 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This library was generated by cloning cDNAs directionally into

Uni-ZAP(Stratagene) (T3 primer/EcoRI are at the 5'-end and T7/XhoI

are at the 3'-end). The library was excised [now in pBluescript

SK(+)] and normalized (Bonaldo et al 1996 Genome Research

6:791-806). Library constructed by Thomas Baum (tbaum@iastate.edu),

Iowa State University, Plant Pathology Department and Jeff

McDermott (jpmcderm@iastate.edu).

Seq primer: -40RP from Gibco

High quality sequence stop: 466.

Location/Qualifiers

1..548

/organism="Heterodera glycines"

/mol_type="mRNA"

/db_xref="taxon:51029"

/sex="female"

/tissue_type="whole organism"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="Heterodera glycines virgin female"

/note="Vector: pBluescript SK+ (Stratagene); Site 1: XhoI;

Site 2: EcoRI; This library was generated by cloning cDNAs

directionally into Uni-ZAP(Stratagene) (T3 primer/EcoRI

are at the 5'-end and T7/XhoI are at the 3'-end). The

library was excised [now in pBluescript SK(+)] and

normalized (Bonaldo et al 1996 Genome Research 6:791-806).

Library constructed by Thomas Baum (tbaum@iastate.edu),

Iowa State University, Plant Pathology Department and Jeff

McDermott (jpmcderm@iastate.edu)."

ORIGIN

Query Match 73.6%; Score 16.2; DB 4; Length 548;
Best Local Similarity 85.7%; Pred. No. 4.1e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCTTTTCG 21

|||||

Db 94 GCCAACGGAATGCTTTTCG 74

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RESULT 99

LOCUS AV822903

AV822903

565 bp mRNA linear EST 01-APR-2002

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DEFINITION AV822903 RAFL5 Arabidopsis thaliana cDNA clone RAFL05-13-A02 5',
mRNA sequence.
ACCESSION AV822903
VERSION AV822903.1 GI:19864955
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (bases 1 to 565)
AUTHORS Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
and Shinozaki,K.
TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)
JOURNAL Unpublished (2002)
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msekicr@riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). This clone is in a
modified pBluescript vector as a SstI/XhoI insert. Please visit our
web site (http://www.gsc.riken.go.jp/e/plant/index\_e.html) for
further details.

FEATURES             source
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        1..565
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            /mol_type="mRNA"
            /db_xref="taxon:3702"
            /clone="RAFL05-13-A02"
            /dev_stage="rosette plants"
            /lab_host="SOLR"
            /clone_lib="RAFL5"
            /note="Site 1: SstI; Site 2: XhoI; subjected to
dehydration-treated(1,2,5,10,24 hr)"

ORIGIN
Query Match      73.6%; Score 16.2; DB 7; Length 565;
Best Local Similarity 81.8%; Pred. No. 4.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTCGACGCGAAGGCGCTTTCGG 22
    ||||| ||||| ||||| ||||| |||||
Db 446 GTCGAAAGGAANGGACTTTCTG 467

RESULT 100
CW966724/C
LOCUS CW966724 569 bp DNA linear GSS 21-DEC-2004
DEFINITION ATAA-aab25f11.g1 Ancylostoma caninum whole genome shotgun library
(AIAGSS 001) Ancylostoma caninum genomic, genomic survey sequence.
ACCESSION CW966724
VERSION CW966724.1 GI:56767451
KEYWORDS GSS.
SOURCE Ancylostoma caninum (dog hookworm)
ORGANISM Ancylostoma caninum
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Ancylostomatoidae; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
REFERENCE 1 (bases 1 to 569)
AUTHORS Mitreva,M., McCarter,J.P., Pape,D., Ritter,E., Tsagareishvili,R.,
Ronko,I., Martin,J., Wylie,T., Dante,M., Meyer,R., Messina,D.,
Waterston,R.H., Clifton,S.W. and Wilson,R.
TITLE Genome Survey sequences from the parasitic nematode Ancylostoma
caninum
JOURNAL Unpublished (2004)
COMMENT Contact: Mitreva M
Washington University in St. Louis
Washington University School of Medicine

```

```

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: nematode@watson.wustl.edu
Genomic DNA provided by John Hawdon (mtmjnh@gwumc.edu) DNA
sequenced by Washington University Genome Sequencing Center
Class: Shotgun.
FEATURES             source
    source
        1..569
            /organism="Ancylostoma caninum"
            /mol_type="genomic DNA"
            /strain="Baltimore"
            /db_xref="taxon:29170"
            /dev_stage="Adult"
            /lab_host="GS10"
            /clone_lib="Ancylostoma caninum whole genome shotgun
library (AIAGSS 001)"
            /note="Vector: POTW13; Site 1: BstXI; Site 2: BstXI;
Ancylostoma caninum genomic DNA was randomly sheared,
end-repaired and size fractionated to enrich for 2-4 kb
fragments. Genomic DNA was provided by John Hawdon
(mtmjnh@gwumc.edu) at George Washington University.
Sequencing by Washington University Genome Sequencing
Center, St. Louis, MO."

ORIGIN
Query Match      73.6%; Score 16.2; DB 13; Length 569;
Best Local Similarity 85.7%; Pred. No. 4.1e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTCGG 22
    ||||| ||||| ||||| ||||| |||||
Db 510 TCGAACTGAAATGCTTTAGG 490

Search completed: May 19, 2006, 07:06:01
Job time : 1491.35 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 18, 2006, 23:59:38 ; Search time 67.3253 Seconds

(without alignments)
611.425 Million cell updates/sec

Title: US-10-665-708-23

Perfect score: 22

Sequence: 1 gtcgaacggaaggcttcgg 22

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 1403666 seqs, 93554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 300 summaries

Database : Issued Patents_NA.*

- 1: /EMC Celerra_SIDS3/ptodata/2/ina/1_COMB.seq.*
- 2: /EMC Celerra_SIDS3/ptodata/2/ina/5_COMB.seq.*
- 3: /EMC Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq.*
- 4: /EMC Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq.*
- 5: /EMC Celerra_SIDS3/ptodata/2/ina/7_COMB.seq.*
- 6: /EMC Celerra_SIDS3/ptodata/2/ina/H_COMB.seq.*
- 7: /EMC Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq.*
- 8: /EMC Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq.*
- 9: /EMC Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq.*
- 10: /EMC Celerra_SIDS3/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	3	US-09-738-274-23
2	21	95.5	24	3	US-09-738-274-22
3	21	95.5	25	3	US-09-738-274-21
4	19	86.4	19	3	US-09-738-274-24
5	18.8	85.5	1584	3	US-09-949-230A-1
6	17.4	79.1	25	2	US-08-485-602-61
7	17.4	79.1	25	2	US-08-757-180-60
8	17.4	79.1	25	2	US-08-745-638-61
9	17.4	79.1	32	3	US-09-738-972-7
10	17.4	79.1	32	3	US-09-738-972-14
11	17.2	78.2	1437	3	US-10-085-871C-1
12	17.2	78.2	1471	3	US-10-085-871C-2
13	17.2	78.2	1488	5	US-10-756-683B-1
14	17	77.3	1475	3	US-08-641-291A-92
15	16.4	74.5	23	2	US-08-485-602-56
16	16.4	74.5	23	2	US-08-757-180-55
17	16.4	74.5	23	2	US-08-745-638-56
18	16	72.7	23	3	US-09-738-274-27
19	16	72.7	26	3	US-09-738-274-28
20	16	72.7	1460	3	US-09-463-618A-1
21	16	72.7	1460	3	US-10-062-777-1
22	15.8	71.8	32	3	US-09-738-274-14
23	15.8	71.8	375	3	US-09-489-039A-1391

24	15.8	71.8	573	2	US-08-008-216-7	Sequence 7, Appli
25	15.8	71.8	573	2	US-08-459-569-7	Sequence 7, Appli
26	15.8	71.8	573	2	US-08-458-831-7	Sequence 7, Appli
27	15.8	71.8	1074	2	US-08-008-216-6	Sequence 6, Appli
28	15.8	71.8	1074	2	US-08-459-569-6	Sequence 6, Appli
29	15.8	71.8	1074	2	US-08-458-831-6	Sequence 6, Appli
30	15.8	71.8	1464	2	US-08-938-858-1	Sequence 1, Appli
31	15.8	71.8	1464	3	US-09-726-774-7	Sequence 7, Appli
32	15.8	71.8	21126	2	US-08-008-216-19	Sequence 19, Appli
33	15.8	71.8	21126	2	US-08-459-569-19	Sequence 19, Appli
34	15.8	71.8	21126	2	US-08-458-831-19	Sequence 19, Appli
35	15.8	71.8	36241	3	US-08-311-731A-134	Sequence 134, App
36	15.8	71.8	36470	3	US-08-311-731A-123	Sequence 123, App
37	15.8	71.8	4403765	3	US-09-103-840A-2	Sequence 2, Appli
38	15.8	71.8	4411529	3	US-09-103-840A-1	Sequence 1, Appli
39	15.6	70.9	439	3	US-09-585-173B-27	Sequence 27, Appli
40	15.6	70.9	601	3	US-09-949-016-175492	Sequence 175492,
41	15.6	70.9	601	3	US-09-949-016-175493	Sequence 175493,
42	15.6	70.9	1662	3	US-09-489-039A-3119	Sequence 3119, Ap
43	15.6	70.9	2444	3	US-09-640-211A-190	Sequence 190, App
44	15.6	70.9	3111	3	US-09-489-039A-3095	Sequence 3095, Ap
45	15.6	70.9	3257	3	US-09-585-173B-39	Sequence 39, Appli
46	15.6	70.9	157822	3	US-09-949-016-16723	Sequence 16723, A
47	15.4	70.0	27	2	US-08-485-602-53	Sequence 53, Appli
48	15.4	70.0	27	2	US-08-757-180-52	Sequence 52, Appli
49	15.4	70.0	27	2	US-08-745-638-53	Sequence 53, Appli
50	15.4	70.0	28	3	US-09-738-972-8	Sequence 8, Appli
51	15.4	70.0	28	3	US-09-738-972-15	Sequence 15, Appli
52	15.4	70.0	455	3	US-09-640-211A-60	Sequence 60, Appli
53	15.4	70.0	455	3	US-09-640-211A-1958	Sequence 1958, Ap
54	15.4	70.0	466	3	US-09-270-767-6474	Sequence 6474, Ap
55	15.4	70.0	466	3	US-09-270-767-21756	Sequence 21756, A
56	15.4	70.0	861	3	US-09-902-540-4420	Sequence 4420, Ap
57	15.4	70.0	23677	3	US-09-902-540-1218	Sequence 1218, Ap
58	15.2	69.1	409	3	US-09-533-559-1639	Sequence 1639, Ap
59	15.2	69.1	601	3	US-09-949-016-125882	Sequence 125882,
60	15.2	69.1	601	3	US-09-221-017B-580	Sequence 580, App
61	15.2	69.1	622	3	US-09-657-289A-21	Sequence 21, Appli
62	15.2	69.1	1392	3	US-09-257-584-1	Sequence 1, Appli
63	15.2	69.1	1542	3	US-09-134-000C-2261	Sequence 2261, Ap
64	15.2	69.1	138282	3	US-09-949-016-15307	Sequence 15307, A
65	15.2	69.1	166698	3	US-09-949-016-16038	Sequence 16038, A
66	15.2	69.1	611587	4	US-09-531-120-209	Sequence 209, App
67	15	68.2	1429	3	US-09-023-655-689	Sequence 689, App
68	14.8	67.3	87	2	US-08-433-126A-221	Sequence 221, App
69	14.8	67.3	87	2	US-08-433-126A-221	Sequence 221, App
70	14.8	67.3	87	3	US-08-976-413A-221	Sequence 221, App
71	14.8	67.3	87	3	PCT-US96-06059-221	Sequence 408, App
72	14.8	67.3	107	3	US-09-016-434-408	Sequence 408, App
73	14.8	67.3	362	3	US-09-513-999C-2742	Sequence 2742, Ap
74	14.8	67.3	532	3	US-09-270-767-29724	Sequence 29724, A
75	14.8	67.3	543	3	US-09-252-991A-5578	Sequence 5578, Ap
76	14.8	67.3	600	3	US-09-252-991A-5650	Sequence 5650, Ap
77	14.8	67.3	601	3	US-09-949-016-82725	Sequence 82725, A
78	14.8	67.3	601	3	US-09-949-016-82726	Sequence 82726, A
79	14.8	67.3	601	3	US-09-949-016-82727	Sequence 82727, A
80	14.8	67.3	601	3	US-09-949-016-148702	Sequence 148702,
81	14.8	67.3	637	3	US-09-533-559-7113	Sequence 7113, Ap
82	14.8	67.3	645	3	US-09-248-796A-4578	Sequence 4578, Ap
83	14.8	67.3	795	3	US-09-328-352-3521	Sequence 3521, Ap
84	14.8	67.3	1160	3	US-09-270-767-13705	Sequence 13705, A
85	14.8	67.3	1429	3	US-09-949-016-2374	Sequence 2374, Ap
86	14.8	67.3	4029	3	US-09-270-767-163	Sequence 163, App
87	14.8	67.3	4029	3	US-09-270-767-15445	Sequence 15445, A
88	14.8	67.3	11050	3	US-09-949-016-14116	Sequence 14116, A
89	14.8	67.3	35916	3	US-09-949-016-15957	Sequence 15957, A
90	14.8	67.3	36855	3	US-09-949-016-17095	Sequence 17095, A
91	14.8	67.3	83462	3	US-09-949-016-15116	Sequence 15116, A
92	14.8	67.3	93894	3	US-09-949-016-13629	Sequence 13629, A
93	14.8	67.3	124480	3	US-09-949-016-15921	Sequence 15921, A
94	14.8	67.3	152132	3	US-09-949-016-13845	Sequence 13845, A
95	14.8	67.3	152145	3	US-09-949-016-12371	Sequence 12371, A
96	14.8	67.3	152582	3	US-09-949-016-12086	Sequence 12086, A

C 97	14.8	67.3	152583	3	US-09-949-016-17390	Sequence 17390, A	170	14.4	65.5	126	3	US-09-270-767-7911	Sequence 7911, Ap
C 98	14.8	67.3	152583	3	US-09-949-016-17391	Sequence 17391, A	171	14.4	65.5	126	3	US-09-270-767-23193	Sequence 23193, A
C 99	14.8	67.3	213456	3	US-09-820-007-3	Sequence 1, Appli	172	14.4	65.5	372	3	US-09-252-991A-13315	Sequence 13315, A
100	14.8	67.3	332820	3	US-09-949-016-14139	Sequence 14139, A	C 173	14.4	65.5	601	3	US-09-949-016-200123	Sequence 200123, A
101	14.6	66.4	87	2	US-08-433-126A-221	Sequence 221, App	C 174	14.4	65.5	625	3	US-09-533-559-263	Sequence 263, App
102	14.6	66.4	87	2	US-08-433-124A-221	Sequence 221, App	C 175	14.4	65.5	732	3	US-09-502-540-5323	Sequence 5323, Ap
103	14.6	66.4	87	3	US-08-976-013A-221	Sequence 221, App	C 176	14.4	65.5	1446	3	US-08-787-091-1	Sequence 1, Appli
104	14.6	66.4	87	7	PCT-US96-06059-221	Sequence 221, App	C 177	14.4	65.5	1446	3	US-09-949-016-12049	Sequence 12049, A
105	14.6	66.4	108	3	US-09-270-767-6972	Sequence 6972, Ap	C 178	14.4	65.5	5484	3	US-09-949-016-15589	Sequence 15589, A
106	14.6	66.4	108	3	US-09-270-767-22554	Sequence 22554, A	C 179	14.4	65.5	25190	3	US-09-949-016-15906	Sequence 15906, A
107	14.6	66.4	269	3	US-09-513-990C-24178	Sequence 24178, A	C 180	14.4	65.5	35614	3	US-09-902-540-1259	Sequence 1259, Ap
C 108	14.6	66.4	417	3	US-09-252-991A-3429	Sequence 3429, Ap	181	14.4	65.5	37068	3	US-09-949-016-12543	Sequence 12543, A
C 109	14.6	66.4	513	3	US-09-270-767-6571	Sequence 6571, Ap	182	14.4	65.5	37068	3	US-09-949-016-17376	Sequence 17376, A
110	14.6	66.4	513	3	US-09-270-767-1853	Sequence 1853, A	183	14.4	65.5	194889	3	US-09-949-016-15654	Sequence 15654, A
C 111	14.6	66.4	552	3	US-09-252-991A-6201	Sequence 6201, Ap	184	14.4	65.5	1830121	3	US-09-557-884-1	Sequence 1, Appli
C 112	14.6	66.4	864	3	US-09-252-991A-3395	Sequence 3395, Ap	185	14.4	65.5	1830121	3	US-09-643-990A-1	Sequence 1, Appli
C 113	14.6	66.4	924	3	US-09-489-039A-1891	Sequence 1891, Ap	186	14.4	65.5	1830121	3	US-10-158-865-1	Sequence 1, Appli
C 114	14.6	66.4	963	3	US-09-902-540-3236	Sequence 3236, Ap	C 187	14.2	64.5	206	3	US-09-621-976-10737	Sequence 10737, A
C 115	14.6	66.4	1090	3	US-09-270-767-1952	Sequence 1952, Ap	188	14.2	64.5	301	3	US-09-439-313-247	Sequence 247, App
C 116	14.6	66.4	1090	3	US-09-270-767-17234	Sequence 17234, Ap	189	14.2	64.5	301	3	US-09-352-616A-247	Sequence 247, App
C 117	14.6	66.4	1095	3	US-09-252-991A-3352	Sequence 3352, Ap	190	14.2	64.5	301	3	US-09-232-149A-247	Sequence 247, App
C 118	14.6	66.4	1119	5	US-09-974-300-514	Sequence 514, App	191	14.2	64.5	301	3	US-09-159-812-247	Sequence 247, App
119	14.6	66.4	1269	3	US-09-311-170-1	Sequence 1, Appli	192	14.2	64.5	301	3	US-09-636-215-247	Sequence 247, App
C 120	14.6	66.4	1355	3	US-09-599-360B-64	Sequence 64, Appl	193	14.2	64.5	301	3	US-09-685-166A-247	Sequence 247, App
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C 125	14.6	66.4	2352	3	US-09-600-823-2	Sequence 2, Appli	198	14.2	64.5	301	3	US-09-657-279-247	Sequence 247, App
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127	14.6	66.4	2499	2	US-08-485-618-96	Sequence 96, Appl	200	14.2	64.5	387	3	US-10-144-678A-247	Sequence 247, App
128	14.6	66.4	2499	2	US-08-605-672-96	Sequence 96, Appl	201	14.2	64.5	387	3	US-09-902-540-4070	Sequence 4070, Ap
129	14.6	66.4	2499	2	US-08-482-293A-96	Sequence 96, Appl	202	14.2	64.5	436	3	US-09-513-998C-2012	Sequence 2012, Ap
130	14.6	66.4	2499	2	US-08-943-363-96	Sequence 96, Appl	203	14.2	64.5	511	3	US-09-533-559-963	Sequence 963, App
131	14.6	66.4	2499	3	US-09-193-043-96	Sequence 96, Appl	204	14.2	64.5	570	5	US-09-974-300-1034	Sequence 1034, Ap
132	14.6	66.4	2499	3	US-09-688-307A-96	Sequence 96, Appl	205	14.2	64.5	600	3	US-09-370-838-264	Sequence 264, App
133	14.6	66.4	2499	3	US-09-350-259-96	Sequence 96, Appl	206	14.2	64.5	600	3	US-09-854-133-264	Sequence 264, App
134	14.6	66.4	3297	3	US-09-476-202A-1	Sequence 1, Appli	207	14.2	64.5	601	3	US-09-949-016-19628	Sequence 19628, A
135	14.6	66.4	3726	2	US-08-173-497-1	Sequence 1, Appli	208	14.2	64.5	601	3	US-09-949-016-40881	Sequence 40881, A
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142	14.6	66.4	3726	3	US-09-193-043-1	Sequence 1, Appli	215	14.2	64.5	601	3	US-09-949-016-79652	Sequence 79652, A
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144	14.6	66.4	3726	3	US-09-350-259-1	Sequence 1, Appli	C 217	14.2	64.5	601	3	US-09-949-016-119403	Sequence 119403, A
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147	14.6	66.4	3785	2	US-08-605-672-98	Sequence 98, Appl	C 220	14.2	64.5	601	3	US-09-949-016-152398	Sequence 152398, A
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150	14.6	66.4	3785	3	US-09-193-043-98	Sequence 98, Appl	C 223	14.2	64.5	601	3	US-09-949-016-203130	Sequence 203130, A
151	14.6	66.4	3785	3	US-09-688-307A-98	Sequence 98, Appl	C 224	14.2	64.5	601	3	US-09-949-016-203170	Sequence 203170, A
152	14.6	66.4	3785	3	US-09-350-259-98	Sequence 98, Appl	C 225	14.2	64.5	601	3	US-09-949-016-203171	Sequence 203171, A
153	14.6	66.4	3956	2	US-08-485-618-97	Sequence 97, Appl	C 226	14.2	64.5	601	3	US-09-949-016-203172	Sequence 203172, A
154	14.6	66.4	3956	2	US-08-605-672-97	Sequence 97, Appl	C 227	14.2	64.5	658	3	US-09-533-559-337	Sequence 337, App
155	14.6	66.4	3956	2	US-08-482-293A-97	Sequence 97, Appl	C 228	14.2	64.5	672	5	US-09-974-300-7755	Sequence 7755, Ap
156	14.6	66.4	3956	2	US-08-943-363-97	Sequence 97, Appl	229	14.2	64.5	834	3	US-09-134-001C-1552	Sequence 1552, Ap
157	14.6	66.4	3956	2	US-09-193-043-97	Sequence 97, Appl	230	14.2	64.5	898	3	US-09-484-970B-79	Sequence 79, Appl
158	14.6	66.4	3956	3	US-09-688-307A-97	Sequence 97, Appl	231	14.2	64.5	1005	2	US-08-287-442-8	Sequence 8, Appli
159	14.6	66.4	3956	3	US-09-350-259-97	Sequence 97, Appl	232	14.2	64.5	1005	2	US-08-459-701-8	Sequence 8, Appli
160	14.6	66.4	14431	3	US-09-302-540-1149	Sequence 1149, Ap	233	14.2	64.5	1005	2	US-08-460-298-8	Sequence 8, Appli
161	14.6	66.4	21777	3	US-09-476-202A-3	Sequence 3, Appli	234	14.2	64.5	1005	2	US-08-459-174-8	Sequence 8, Appli
162	14.6	66.4	31769	3	US-09-949-002-734	Sequence 734, App	235	14.2	64.5	1095	3	US-10-029-180-61	Sequence 61, Appl
C 163	14.6	66.4	34855	3	US-09-949-016-13004	Sequence 13004, A	236	14.2	64.5	1131	3	US-09-420-211-1	Sequence 1, Appli
C 164	14.6	66.4	56302	3	US-09-949-016-11892	Sequence 11892, A	237	14.2	64.5	1431	3	US-09-949-016-4277	Sequence 4277, Ap
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C 166	14.6	66.4	91232	3	US-09-949-002-607	Sequence 607, App	C 239	14.2	64.5	1498	3	US-09-608-285A-45	Sequence 45, Appl
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C 168	14.6	66.4	187595	3	US-09-949-016-15546	Sequence 15546, A	241	14.2	64.5	1568	3	US-09-043-937A-1	Sequence 1, Appli
C 169	14.6	66.4	228851	3	US-09-949-016-13781	Sequence 13781, A	242	14.2	64.5	1575	3	US-09-489-039A-4426	Sequence 4426, Ap

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SEQUENCE 54, Appl
SEQUENCE 22, Appl

; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-23

Query Match 100.0%; Score 22; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTCGAACGGAAGGCGCTTCGG 22

RESULT 2
US-09-738-274-22
; Sequence 22, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-22

Query Match 95.5%; Score 21; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTCG 21
Db 4 GTCGAACGGAAGGCGCTTCG 24

RESULT 3
US-09-738-274-21
; Sequence 21, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
```

ALIGNMENTS

```

: APPLICANT: RODRIGUE, Marc
:
: TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
:
: TITLE OF INVENTION: MYCOBACTERIUM SPECIES
:
: FILE REFERENCE: GP107-02.UT
:
: CURRENT APPLICATION NUMBER: US/09/738,274
:
: CURRENT FILING DATE: 2000-12-15
:
: PRIOR APPLICATION NUMBER: 60/172,190
:
: PRIOR FILING DATE: 1999-12-17
:
: NUMBER OF SEQ ID NOS: 42
:
: SOFTWARE: PatentIn Ver. 2.0
:
: SEQ ID NO 21
:
: LENGTH: 25
:
: TYPE: DNA
:
: ORGANISM: Artificial Sequence
:
: FEATURE:
:
: OTHER INFORMATION: Description of Artificial Sequence: primer
:
: OTHER INFORMATION: oligonucleotide
:
: US-09-738-274-21

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Query Match	95.5%;	Score 21;	DB 3;	Length 25;
Best Local Similarity	100.0%;	Pred. No. 0.19;		
Matches 21; Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
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Dd	5	GTCAACGGAAAGCCTTTCG	25	

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RESULT 4
US-09-738-274-24
; Sequence 24, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GFI07-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-24

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Best Local Similarity 100.0%; Pred. No. 1.9;
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RESULT 5
US-09-949-230A-1
; Sequence 1, Application US/09949230A
; Patent No. 6551591
; GENERAL INFORMATION:
; APPLICANT: Essential Therapeutics, Inc.
; TITLE OF INVENTION: New Antibiotics for Microbispora
; FILE REFERENCE: 262/0095

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; CURRENT APPLICATION NUMBER: US/09/949,230A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1584
; TYPE: DNA
; ORGANISM: Microbispora corallina
; FEATURE:
; NAME/KEY: n
; LOCATION: (1350)..(1584)
; OTHER INFORMATION: Unsure
; NAME/KEY: misc_feature
; LOCATION: (1350)..(1584)
; OTHER INFORMATION: Unsure
; US-09-949-230A-1

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Query Match      85.5%; Score 18.8; DB 3; Length 1584;
Best Local Similarity 90.9%; Pred. NO. 5.7;
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Db 128 GTCAGCGGAAAGCCCTTCGG 149

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RESULT 6
US-08-485-602-61
; Sequence 61, Application US/08485602
; Patent No. 5712095
; GENERAL INFORMATION:
; APPLICANT: Britschgi, Theresa B.
; APPLICANT: Cangelosi, Gerard A.
; TITLE OF INVENTION: Rapid and Se
; TITLE OF INVENTION: Antibiotic-R
; TITLE OF INVENTION: Probes Speci
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townse
; STREET: One Market Plaza, Steu
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 11652
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: rRNA
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium habana
; US-08-485-602-61

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Query Match 79.1%; Score 17.4; DB 2; Length 25;
 Best Local Similarity 80.0%; Pred. No. 14;
 Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCCTTCGG 22
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RESULT 7

US-08-757-180-60
 ; Sequence 60, Application US/08757180
 ; Patent No. 5726021
 ; GENERAL INFORMATION:
 ; APPLICANT: Britschgi, Theresa B
 ; APPLICANT: Cangelosi, Gerard A
 ; TITLE OF INVENTION: RAPID LYSIS METHODS FOR RELEASING INTACT
 ; TITLE OF INVENTION: RIBOSOMAL RNA PRECURSORS FROM MYCOBACTERIUM
 ; NUMBER OF SEQUENCES: 98
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Neave
 ; STREET: 1251 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: United States of America
 ; ZIP: 10020
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/757,180
 ; FILING DATE: 27-NOV-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/261,068
 ; FILING DATE: 16-JUN-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hsi, Petrina S
 ; REGISTRATION NUMBER: 38,496
 ; REFERENCE/DOCKET NUMBER: BD3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-596-9000
 ; TELEFAX: 212-596-9090
 ; INFORMATION FOR SEQ ID NO: 60:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 25 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: rRNA
 ; ORIGINAL SOURCE:
 ; ORGANISM: Mycobacterium simiae
 US-08-757-180-60

Query Match 79.1%; Score 17.4; DB 2; Length 25;
 Best Local Similarity 80.0%; Pred. No. 14;
 Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCCTTCGG 22
 |||||
 Db 1 CGAACGGAAGNCCCUCCG 20

RESULT 8

US-08-745-638-61
 ; Sequence 61, Application US/08745638
 ; Patent No. 5770373
 ; GENERAL INFORMATION:
 ; APPLICANT: Britschgi, Theresa B.
 ; APPLICANT: Cangelosi, Gerard A.

; TITLE OF INVENTION: Rapid and Sensitive Detection of
 ; TITLE OF INVENTION: Antibiotic-Resistant Mycobacteria Using Oligonucleotide
 ; TITLE OF INVENTION: Probes Specific for Ribosomal RNA Precursors
 ; NUMBER OF SEQUENCES: 89
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew
 ; STREET: One Market Plaza, Steuart Street Tower
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94105-1492

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/745,638
 ; FILING DATE: 08-NOV-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/485,602
 ; FILING DATE: 07-JUN-1995
 ; APPLICATION NUMBER: US 08/261,068
 ; FILING DATE: 16-JUN-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Weber, Kenneth A.
 ; REGISTRATION NUMBER: 31,677
 ; REFERENCE/DOCKET NUMBER: 11652-79-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 543-9600
 ; TELEFAX: (415) 543-5043
 ; INFORMATION FOR SEQ ID NO: 61:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 25 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: rRNA
 ; ORIGINAL SOURCE:
 ; ORGANISM: Mycobacterium habana
 US-08-745-638-61

Query Match 79.1%; Score 17.4; DB 2; Length 25;
 Best Local Similarity 80.0%; Pred. No. 14;
 Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCCTTCGG 22
 |||||
 Db 1 CGAACGGAAGNCCCUCCG 20

RESULT 9

US-09-738-972-7
 ; Sequence 7, Application US/09738972
 ; Patent No. 6747141
 ; GENERAL INFORMATION:
 ; APPLICANT: BRENTANO, Steven T.
 ; APPLICANT: LANKFORD, Roger L.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
 ; TITLE OF INVENTION: AVIUM COMPLEX SPECIES
 ; FILE REFERENCE: GP119-02.UT
 ; CURRENT APPLICATION NUMBER: US/09/738,972
 ; CURRENT FILING DATE: 2000-12-15
 ; PRIOR APPLICATION NUMBER: 60/171,202
 ; PRIOR FILING DATE: 1999-12-15
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 32
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: primer
US-09-738-972-7

Query Match 79.1%; Score 17.4; DB 3; Length 32;
Best Local Similarity 94.7%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19
Db 5 GTCGAACGGAAGGCCTCT 23

RESULT 10

US-09-738-972-14/C
; Sequence 14, Application US/09738972
; Patent No. 6747141
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GPl19-02.UT
; CURRENT APPLICATION NUMBER: US/09/738.972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-738-972-14

Query Match 79.1%; Score 17.4; DB 3; Length 32;
Best Local Similarity 94.7%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19
Db 28 GTCGAACGGAAGGCCTCT 10

RESULT 11

US-10-085-871C-1
; Sequence 1, Application US/10085871C
; Patent No. 6716615
; GENERAL INFORMATION:
; APPLICANT: Lee, Fang-Yu
; APPLICANT: Lee, Ming-Liang
; APPLICANT: Anderson, Hong C.
; APPLICANT: Chiu, Chung-Ching
; TITLE OF INVENTION: New Strains of Saccharothrix, Process for Producing Pravastatin U
; FILE REFERENCE: 004135.P005
; CURRENT APPLICATION NUMBER: US/10/085.871C
; CURRENT FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1437
; TYPE: DNA
; ORGANISM: Saccharothrix 44442
US-10-085-871C-1

Query Match 78.2%; Score 17.2; DB 3; Length 1437;
Best Local Similarity 86.4%; Pred. No. 38;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTTCCG 22
Db 34 GTCGAGCGGTAAGGCCCTTCGG 55

RESULT 12

US-10-085-871C-2
; Sequence 2, Application US/10085871C
; Patent No. 6716615
; GENERAL INFORMATION:
; APPLICANT: Lee, Fang-Yu
; APPLICANT: Lee, Ming-Liang
; APPLICANT: Anderson, Hong C.
; APPLICANT: Chiu, Chung-Ching
; TITLE OF INVENTION: New Strains of Saccharothrix, Process for Producing Pravastatin U
; FILE REFERENCE: 004135.P005
; CURRENT APPLICATION NUMBER: US/10/085.871C
; CURRENT FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1471
; TYPE: DNA
; ORGANISM: Saccharothrix 45494
US-10-085-871C-2

Query Match 78.2%; Score 17.2; DB 3; Length 1471;
Best Local Similarity 86.4%; Pred. No. 38;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTTCCG 22
Db 34 GTCGAGCGGTAAGGCCCTTCGG 55

RESULT 13

US-10-756-683B-1
; Sequence 1, Application US/10756683B
; Patent No. 7022875
; GENERAL INFORMATION:
; APPLICANT: Hwang, Byung Kook
; APPLICANT: Lee, Jung Yeop
; TITLE OF INVENTION: THIOTUTACIN AND ANTIFUNGAL AND ANTIOOMYCETE COMPOSITION FOR
; TITLE OF INVENTION: CONTROLLING PLANT DISEASES USING THE SAME
; FILE REFERENCE: 4228-102
; CURRENT APPLICATION NUMBER: US/10/756.683B
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: KR 10-2003-0015628
; PRIOR FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: KR 10-2003-0015629
; PRIOR FILING DATE: 2003-03-13
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1488
; TYPE: DNA
; ORGANISM: Lechevalieria aerocolonigenes
US-10-756-683B-1

Query Match 78.2%; Score 17.2; DB 5; Length 1488;
Best Local Similarity 86.4%; Pred. No. 38;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTTCCG 22
Db 46 GTCGAGCGGTAAGGCCCTTCGG 67

RESULT 14

US-08-641-291A-92
; Sequence 92, Application US/08641291A
; Patent No. 6037122

```
; GENERAL INFORMATION:
; APPLICANT: MABILAT Claude
; TITLE OF INVENTION: NUCLEOTIDE FRAGMENT OF THE 16S RIBOSOMAL RNA OF CORYNEBACTERI
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release # 1.0, version # 1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/641,291A
; FILING DATE: 30-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 38273
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1475 base pairs
; TYPE: nucleotide
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: rRNA
; US-08-641-291A-92

Query Match 77.3%; Score 17; DB 3; Length 1475;
Best Local Similarity 88.2%; Pred. No. 48;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCCT 17
   |:|||||:
Db 28 GUCGAACGGAAGGCCU 44

RESULT 15
US-08-485-602-56
; Sequence 56, Application US/08485602
; Patent No. 5712095
; GENERAL INFORMATION:
; APPLICANT: Britschgi, Theresa B.
; APPLICANT: Cangelosi, Gerard A.
; TITLE OF INVENTION: Rapid and Sensitive Detection of
; TITLE OF INVENTION: Antibiotic-Resistant Mycobacteria Using Oligonucleotide
; TITLE OF INVENTION: Probes Specific for Ribosomal RNA Precursors
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,602
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
```

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,068
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 11652-79-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: rRNA
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium intracellulare
; US-08-485-602-56

Query Match 74.5%; Score 16.4; DB 2; Length 23;
Best Local Similarity 78.9%; Pred. No. 44;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAACGGAAGCCTTCGG 22
   |||||:|:|
Db 1 GAACGGAAGNCCUCGG 19

RESULT 16
US-08-757-180-55
; Sequence 55, Application US/08757180
; Patent No. 5726021
; GENERAL INFORMATION:
; APPLICANT: Britschgi, Theresa B
; APPLICANT: Cangelosi, Gerard A
; TITLE OF INVENTION: RAPID LYSIS METHODS FOR RELEASING INTACT
; TITLE OF INVENTION: RIBOSOMAL RNA PRECURSORS FROM MYCOBACTERIUM
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,180
; FILING DATE: 27-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,068
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hsi, Petrina S
; REGISTRATION NUMBER: 38,496
; REFERENCE/DOCKET NUMBER: BD3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: rRNA
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; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium intracellulare
US-08-757-180-55

Query Match      74.5%; Score 16.4; DB 2; Length 23;
Best Local Similarity 78.9%; Pred. No. 44;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAACGGAAGCCCTTCGG 22
Db 1 GAACGGAAGNCCCUCCG 19

RESULT 17
US-08-745-638-56
; Sequence 56, Application US/08745638
; Patent No. 5770373
; GENERAL INFORMATION:
; APPLICANT: Britschgi, Theresa B.
; APPLICANT: Cangelosi, Gerard A.
; TITLE OF INVENTION: Rapid and Sensitive Detection of
; TITLE OF INVENTION: Antibiotic-Resistant Mycobacteria Using Oligonucleotide
; TITLE OF INVENTION: Probes Specific for Ribosomal RNA Precursors
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/745,638
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,602
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/261,068
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 11652-79-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: tRNA
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium intracellulare
US-08-745-638-56
```

```
Query Match      74.5%; Score 16.4; DB 2; Length 23;
Best Local Similarity 78.9%; Pred. No. 44;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAACGGAAGCCCTTCGG 22
Db 1 GAACGGAAGNCCCUCCG 19
```

, RESULT 18

```
US-09-738-274-27
; Sequence 27, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-27

Query Match      72.7%; Score 16; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16
Db 4 GTCGAACGGAAGGCC 19

RESULT 19
US-09-738-274-28
; Sequence 28, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-28

Query Match      72.7%; Score 16; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16
Db 1 GTCGAACGGAAGGCC 16
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```
RESULT 20
US-09-463-618A-1
; Sequence 1, Application US/09463618A
; Patent No. 6368835
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: A PROCESS FOR PRODUCING A BRAN PICKLES FLAVORING SOLUTION
; FILE REFERENCE: 11142WO
; CURRENT APPLICATION NUMBER: US/09/463,618A
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: H10-166226
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Corynebacterium sp.NK-1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (166)
; OTHER INFORMATION: n is "a" or "g" or "c" or "t".
US-09-463-618A-1

Query Match          72.7%; Score 16; DB 3; Length 1460;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16
Db 42 GTCGAACGGAAGGCC 57

RESULT 21
US-10-062-777-1
; Sequence 1, Application US/10062777
; Patent No. 6589774
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: A PROCESS FOR PRODUCING A BRAN PICKLES FLAVORING SOLUTION
; FILE REFERENCE: 11142WO
; CURRENT APPLICATION NUMBER: US/10/062,777
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/463,618
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Corynebacterium sp.NK-1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (166)
; OTHER INFORMATION: n is "a" or "g" or "c" or "t".
US-10-062-777-1

Query Match          72.7%; Score 16; DB 3; Length 1460;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16
Db 42 GTCGAACGGAAGGCC 57

RESULT 22
US-09-738-274-14
; Sequence 14, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
```

```
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GPl07-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-14

Query Match          71.8%; Score 15.8; DB 3; Length 32;
Best Local Similarity 89.5%; Pred. No. 95;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTT 19
Db 5 GTCGAACGGAAGGCTCT 23

RESULT 23
US-09-489-039A-1391
; Sequence 1391, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 1391
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-1391

Query Match          71.8%; Score 15.8; DB 3; Length 375;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCCCTTCG 21
Db 332 CGAACGGAAGGCCCTTCG 350

RESULT 24
US-08-008-216-7
; Sequence 7, Application US/08008216
; Patent No. 5366887
; GENERAL INFORMATION:
; APPLICANT: Slightom, Jerry L.
; APPLICANT: Tepfer, David A.
; TITLE OF INVENTION: R1 T-DNA Promoters
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY, CARY, AMES & FRYE
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
```



```
;
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/008,216
; FILING DATE: 25-JAN-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhorst, Marnie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: P1020US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 573 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Agrobacterium rhizogenes
; STRAIN: Strain A4
; IMMEDIATE SOURCE:
; LIBRARY: Convolvulus arvensis plant cells
; CLONE: Clone 7
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (1..573)
; OTHER INFORMATION: /label= ORF7
; OTHER INFORMATION: through 5643 of Seq. ID No. 5366887 19. It is read 5' to
; OTHER INFORMATION: 3' from the complementary strand."
; US-08-008-216-7

Query Match 71.8%; Score 15.8; DB 2; Length 573;
Best Local Similarity 89.5%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGACGCGAAAGGCCTTT 19
|||||
Db 507 GTCGACGCGACAGGCCTTT 525

RESULT 25
US-08-459-569-7
; Sequence 7, Application US/08459569
; Patent No. 5543501
; GENERAL INFORMATION:
; APPLICANT: Slightom, Jerry L.
; APPLICANT: Tepfer, David A.
; TITLE OF INVENTION: Ri T-DNA Promoters
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY, CARY, AMES & FRYE
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
```

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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,569
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,216
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhorst, Marnie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: P1020US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 573 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Agrobacterium rhizogenes
; STRAIN: Strain A4
; IMMEDIATE SOURCE:
; LIBRARY: Convolvulus arvensis plant cells
; CLONE: Clone 7
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (1..573)
; OTHER INFORMATION: /label= ORF7
; OTHER INFORMATION: through 5643 of Seq. ID No. 5543501
; OTHER INFORMATION: 3' from the complementary strand."
; US-08-459-569-7

Query Match 71.8%; Score 15.8; DB 2; Length 573;
Best Local Similarity 89.5%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGACGCGAAAGGCCTTT 19
|||||
Db 507 GTCGACGCGACAGGCCTTT 525

RESULT 26
US-08-458-831-7
; Sequence 7, Application US/08458831
; Patent No. 5824866
; GENERAL INFORMATION:
; APPLICANT: Slightom, Jerry L.
; APPLICANT: Tepfer, David A.
; TITLE OF INVENTION: Ri T-DNA Promoters
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY, CARY, AMES & FRYE
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/458,831
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
```

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,216
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhorst, Marnie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: P1020US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 573 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Agrobacterium rhizogenes
; STRAIN: Strain A4
; IMMEDIATE SOURCE:
; LIBRARY: Convolvulus arvensis plant cells
; CLONE: Clone 7
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (1..573)
; OTHER INFORMATION: /label= ORF7
; OTHER INFORMATION: /note= "Sequence ORF7 corresponds to bases 5071
; Patent No. 5824866
; OTHER INFORMATION: through 5643 of Seq. ID No. 5824866 19. It is read 5' to
; OTHER INFORMATION: 3' from the complementary strand."
; US-08-458-831-7

Query Match 71.8%; Score 15.8; DB 2; Length 573;
Best Local Similarity 89.5%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCGCTTT 19
Db 507 GTCGAACGACAGGCGCTTT 525

RESULT 27
US-08-008-216-6
; Sequence 6, Application US/08008216
; Patent No. 5366887
; GENERAL INFORMATION:
; APPLICANT: Slightom, Jerry L.
; APPLICANT: Tepfer, David A.
; TITLE OF INVENTION: Ri T-DNA Promoters
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY, CARY, AMES & FRYE
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/008,216
; FILING DATE: 25-JAN-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; ATTORNEY/AGENT INFORMATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,216
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhorst, Marnie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: P1020US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048

; NAME: Barnhorst, Marnie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: P1020US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1074 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Agrobacterium rhizogenes
; STRAIN: Strain A4
; IMMEDIATE SOURCE:
; LIBRARY: Convolvulus arvensis plant cells
; CLONE: Clone 7
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..1074
; OTHER INFORMATION: /label= ORF6
; OTHER INFORMATION: /note= "Sequence ORF6 corresponds to bases 5143
; OTHER INFORMATION: through 6216 of Seq. ID No. 5366887 19."
; US-08-008-216-6

Query Match 71.8%; Score 15.8; DB 2; Length 1074;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCGCTTT 19
Db 435 GTCGAACGACAGGCGCTTT 453

RESULT 28
US-08-459-569-6
; Sequence 6, Application US/08459569
; Patent No. 5543501
; GENERAL INFORMATION:
; APPLICANT: Slightom, Jerry L.
; APPLICANT: Tepfer, David A.
; TITLE OF INVENTION: Ri T-DNA Promoters
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY, CARY, AMES & FRYE
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,569
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,216
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhorst, Marnie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: P1020US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048
```

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; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1074 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Agrobacterium rhizogenes
; STRAIN: Strain A4
; IMMEDIATE SOURCE:
; LIBRARY: Convolvulus arvensis plant cells
; CLONE: Clone 7
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..1074
; OTHER INFORMATION: /label= ORF6
; OTHER INFORMATION: /note= "Sequence ORF6 corresponds to bases 5143
; Patent No. 5843501
; OTHER INFORMATION: through 6216 of Seq. ID No. 5543501 19."
US-08-459-569-6

Query Match 71.8%; Score 15.8; DB 2; Length 1074;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCCTTT 19
Db 435 GTCGACGACAAAGGCCTTT 453

RESULT 29
US-08-458-831-6
; Sequence 6, Application US/08458831
; Patent No. 5824866
; GENERAL INFORMATION:
; APPLICANT: Slightom, Jerry L.
; APPLICANT: Tepfer, David A.
; TITLE OF INVENTION: Ri T-DNA Promoters
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY, CARY, AMES & FRYE
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,831
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,216
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhorst, Marnie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: P1020US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1074 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
US-08-938-858-1

Query Match 71.8%; Score 15.8; DB 2; Length 1464;
Best Local Similarity 89.5%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCCTTT 19
Db 435 GTCGACGACAAAGGCCTTT 453

RESULT 30
US-08-938-858-1
; Sequence 1, Application US/08938858
; Patent No. 5985569
; GENERAL INFORMATION:
; APPLICANT: Foxall, Paul A.
; APPLICANT: Kumar, Harish
; TITLE OF INVENTION: Primers for Amplification of a Genus
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Becton Dickinson and Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07417-6800
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,858
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fugit, Donna R.
; REGISTRATION NUMBER: 32,135
; REFERENCE/DOCKET NUMBER: P-3490/5510-12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-847-7166
; TELEFAX: 201-848-9228
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1464 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
US-08-938-858-1
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```
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GTCGAACGGAAGGCCTTT 19
      |||||
Db 24 GTCGAACGGAAGGTCTCT 42
      |||||

RESULT 31
US-09-726-774-7
; Sequence 7, Application US/09726774
; Patent No. 6677153
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; FILE OF INVENTION: Composition
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/09/726,774
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-726-774-7

Query Match 71.8%; Score 15.8; DB 3; Length 1464;
Best Local Similarity 89.5%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GTCGAACGGAAGGCCTTT 19
      |||||
Db 24 GTCGAACGGAAGGTCTCT 42
      |||||

RESULT 32
US-08-008-216-19
; Sequence 19, Application US/08008216
; Patent No. 5366887
; GENERAL INFORMATION:
; APPLICANT: Slightom, Jerry L.
; APPLICANT: Tepfer, David A.
; TITLE OF INVENTION: Ri T-DNA Promoters
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY, CARY, AMES & FRYE
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/008,216
; FILING DATE: 25-JAN-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhorst, Marnie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: P1020US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 19:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21126 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Agrobacterium rhizogenes
; STRAIN: STRAIN A4
; IMMEDIATE SOURCE:
; LIBRARY: CONVULVULUS ARVENSIS PLANT CELLS
; CLONE: CLONE 7
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (937..2262)
; OTHER INFORMATION: /label= ORF1SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (2649..3458)
; OTHER INFORMATION: /label= ORF2SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 3726..4799
; OTHER INFORMATION: /label= ORF3SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (4041..4400)
; OTHER INFORMATION: /label= ORF4SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (4607..4918)
; OTHER INFORMATION: /label= ORF5SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 5143..6216
; OTHER INFORMATION: /label= ORF6SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (5071..5643)
; OTHER INFORMATION: /label= ORF7SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 6609..8888
; OTHER INFORMATION: /label= ORF8SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (6576..6830)
; OTHER INFORMATION: /label= ORF9SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 9748..10044
; OTHER INFORMATION: /label= ORF10SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (10509..11282)
; OTHER INFORMATION: /label= ORF11SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 12466..13002
; OTHER INFORMATION: /label= ORF12SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 13723..14319
; OTHER INFORMATION: /label= ORF13SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 15659..16210
; OTHER INFORMATION: /label= ORF14SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (16517..17545)
; OTHER INFORMATION: /label= ORF15SUBSEQUENCE
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;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (17737..18189)
; OTHER INFORMATION: /label= ORF16SUBSEQUENCE
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (18177..18743)
; OTHER INFORMATION: /label= ORF17SUBSEQUENCE
;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (19031..19390)
; OTHER INFORMATION: /label= ORF18SUBSEQUENCE
;
US-08-008-216-19

Query Match 71.8%; Score 15.8; DB
Best Local Similarity 89.5%; Pred. No. 3.3e+0
Matches 17; Conservative 0; Mismatches

Qy 1 GTCGAACGGAAGGCCTTT 19
||||| |||||||
Db 5577 GTCGAACGACAAAGGCCTTT 5595

RESULT 33
US-08-459-569-19
; Sequence 19, Application US/08459569
; Patent No. 5543501
; GENERAL INFORMATION:
; APPLICANT: Slightom, Jerry L.
; APPLICANT: Tefter, David A.
; TITLE OF INVENTION: R1 T-DNA Promoters
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY, CARY, AMES & FRYE
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,569
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,216
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhorst, Marnie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: PI020US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21126 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Agrobacterium rhizogenes
; STRAIN: STRAIN A4
; IMMEDIATE SOURCE:
; LIBRARY: CONVOLVULUS ARVENSIS PLANT CELLS

```

US-08-459-569-19

Query Match 71.8%; Score 15.8; DB 2; Length 21126;
Best Local Similarity 89.5%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTT 19
||||| |||||||
Db 5577 GTCGAACGACAAAGGCCTTT 5595

RESULT 34

US-08-458-831-19
; Sequence 19, Application US/08458831
; Patent No. 5824866
; GENERAL INFORMATION:
; APPLICANT: Slightcom, Jerry L.
; APPLICANT: Tepfer, David A.
; TITLE OF INVENTION: R1 T-DNA Promoters
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY, CARY, AMES & FRYE
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,831
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,216
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhorst, Marnie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: P1020U51
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21126 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Agrobacterium rhizogenes
; STRAIN: STRAIN A4
; IMMEDIATE SOURCE:
; LIBRARY: CONVOLVULUS ARVENSIS PLANT CELLS
; CLONE: CLONE 7
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (937..2262)
; OTHER INFORMATION: /label= ORF1SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (2649..3458)
; OTHER INFORMATION: /label= ORF2SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 3726..4799

; OTHER INFORMATION: /label= ORF3SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (4041..4400)
; OTHER INFORMATION: /label= ORF4SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (4607..4918)
; OTHER INFORMATION: /label= ORF5SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 5143..6216
; OTHER INFORMATION: /label= ORF6SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (5071..5643)
; OTHER INFORMATION: /label= ORF7SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 6609..8888
; OTHER INFORMATION: /label= ORF8SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (6576..6830)
; OTHER INFORMATION: /label= ORF9SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 9748..10044
; OTHER INFORMATION: /label= ORF10SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (10509..11282)
; OTHER INFORMATION: /label= ORF11SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 12466..13002
; OTHER INFORMATION: /label= ORF12SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 13723..14319
; OTHER INFORMATION: /label= ORF13SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 15659..16210
; OTHER INFORMATION: /label= ORF14SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (16517..17545)
; OTHER INFORMATION: /label= ORF15SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (17737..18189)
; OTHER INFORMATION: /label= ORF16SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (18177..18743)
; OTHER INFORMATION: /label= ORF17SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (19031..19390)
; OTHER INFORMATION: /label= ORF18SUBSEQUENCE
US-08-458-831-19

Query Match 71.8%; Score 15.8; DB 2; Length 21126;
Best Local Similarity 89.5%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTT 19
||||| |||||||
Db 5577 GTCGAACGACAAAGGCCTTT 5595

RESULT 35

US-08-311-731A-134/c
; Sequence 134, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36241 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium leprae
US-08-311-731A-134
Query Match 71.8%; Score 15.8; DB 3; Length 36241;
Best Local Similarity 89.5%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GTCGAACGGAAGGCGCTTT 19
Db 3937 GTCGAACGGAAGGCTCT 3919
RESULT 36
US-08-311-731A-123/c
; Sequence 123, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36470 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: MYCOBACTERIUM LEPRAE
US-08-311-731A-123
Query Match 71.8%; Score 15.8; DB 3; Length 36470;
Best Local Similarity 89.5%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GTCGAACGGAAGGCGCTTT 19
Db 36184 GTCGAACGGAAGGCTCT 36166
RESULT 37
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
Query Match 71.8%; Score 15.8; DB 3; Length 4403765;
Best Local Similarity 89.5%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GTCGAACGGAAGGCGCTTT 19
Db 1471431 GTCGAACGGAAGGCTCT 1471449

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RESULT 38
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007,00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37RV
US-09-103-840A-1

Query Match          71.8%; Score 15.8; DB 3; Length 4411529;
Best Local Similarity 89.5%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTT 19
Db 1471907 GTCGAACGGAAGGCTCT 1471925

RESULT 39
US-09-585-173B-27/c
; Sequence 27, Application US/09585173B
; Patent No. 6570063
; GENERAL INFORMATION:
; APPLICANT: Butler, Karlene
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Gutteridge, Steven
; APPLICANT: Maxwell, Carl
; TITLE OF INVENTION: Magnesium Chelataase
; FILE REFERENCE: BB1370 US NA
; CURRENT APPLICATION NUMBER: US/09/585,173B
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/137,461
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 27
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Zea mays
US-09-585-173B-27

Query Match          70.9%; Score 15.6; DB 3; Length 439;
Best Local Similarity 81.8%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTT 22
Db 182 GTCGAACGGAAGGACTTCGG 161

RESULT 40
US-09-949-016-175492
; Sequence 175492, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
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; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175492
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-175492

Query Match          70.9%; Score 15.6; DB 3; Length 601;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTT 22
Db 209 GTAGAAGGTACAGGCTTCGG 230

RESULT 41
US-09-949-016-175493
; Sequence 175493, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175493
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-175493

Query Match          70.9%; Score 15.6; DB 3; Length 601;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTT 22
Db 43 GTAGAAGGTACAGGCTTCGG 64

RESULT 42
US-09-489-039A-3119/c
; Sequence 3119, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
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; SEQ ID NO 3119
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-3119

Query Match 70.9%; Score 15.6; DB 3; Length 1662;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTTCGG 22
||||| ||||| ||||| ||||| |||||
Db 1527 GTCGAAGCGAAAGCCCTGCG 1506

RESULT 43

US-09-640-211A-190/c
; Sequence 190, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:

; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 190
; LENGTH: 2444
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-190

Query Match 70.9%; Score 15.6; DB 3; Length 2444;
Best Local Similarity 81.8%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTTCGG 22
||||| ||||| ||||| ||||| |||||
Db 1935 GTCGAAGTGAATGCTCTCGG 1914

RESULT 44

US-09-489-039A-3095
; Sequence 3095, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 3095
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-3095

Query Match 70.9%; Score 15.6; DB 3; Length 3111;
Best Local Similarity 81.8%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTTCGG 22
||||| ||||| ||||| ||||| |||||
Db 970 GTCGAAGCGAAAGCCCTGCG 991

RESULT 45

US-09-585-173B-39/c
; Sequence 39, Application US/09585173B
; Patent No. 6570063
; GENERAL INFORMATION:
; APPLICANT: Butler, Karlene
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Gutteridge, Steven
; APPLICANT: Maxwell, Carl
; TITLE OF INVENTION: Magnesium Chelataase
; FILE REFERENCE: BB1370 US NA
; CURRENT APPLICATION NUMBER: US/09/585,173B
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/137,461
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 39
; LENGTH: 3257
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-585-173B-39

Query Match 70.9%; Score 15.6; DB 3; Length 3257;
Best Local Similarity 81.8%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTTCGG 22
||||| ||||| ||||| ||||| |||||
Db 2498 GTCGAACGCAAAAGACTTGCG 2477

RESULT 46

US-09-949-016-16723
; Sequence 16723, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16723
; LENGTH: 157822
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16723

Query Match 70.9%; Score 15.6; DB 3; Length 157822;
Best Local Similarity 81.8%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTTCGG 22
||||| ||||| ||||| ||||| |||||
Db 145332 GTAGAAGGTACAGGCTTTTCGG 145353

RESULT 47

US-08-485-602-53
; Sequence 53, Application US/08485602
; Patent No. 5712095
; GENERAL INFORMATION:

```

; APPLICANT: Britschgi, Theresa B.
; APPLICANT: Cangelosi, Gerard A.
; TITLE OF INVENTION: Rapid and Sensitive Detection of
; TITLE OF INVENTION: Antibiotic-Resistant Mycobacteria Using Oligonucleotide
; TITLE OF INVENTION: Probes Specific for Ribosomal RNA Precursors
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,602
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,068
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 11652-79-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: rRNA
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium avium
;
US-08-485-602-53

Query Match 70.0%; Score 15.4; DB 2; Length 27;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 CGAACGGAAGGCTTT 19
Db 1 CGAACGGAAGGCTTT 17

RESULT 49
US-08-757-180-52
; Sequence 52, Application US/08757180
; Patent No. 5726021
; GENERAL INFORMATION:
; APPLICANT: Britschgi, Theresa B.
; APPLICANT: Cangelosi, Gerard A.
; TITLE OF INVENTION: RAPID LYSIS METHODS FOR RELEASING INTACT
; TITLE OF INVENTION: RIBOSOMAL RNA PRECURSORS FROM MYCOBACTERIUM
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible

```

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,180
; FILING DATE: 27-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,068
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hsi, Petrina S.
; REGISTRATION NUMBER: 38,496
; REFERENCE/DOCKET NUMBER: BD3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: rRNA
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium avium
;
US-08-757-180-52

Query Match 70.0%; Score 15.4; DB 2; Length 27;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 CGAACGGAAGGCTTT 19
Db 1 CGAACGGAAGGCTTT 17

RESULT 49
US-08-745-638-53
; Sequence 53, Application US/08745638
; Patent No. 5770373
; GENERAL INFORMATION:
; APPLICANT: Britschgi, Theresa B.
; APPLICANT: Cangelosi, Gerard A.
; TITLE OF INVENTION: Rapid and Sensitive Detection of
; TITLE OF INVENTION: Antibiotic-Resistant Mycobacteria Using Oligonucleotide
; TITLE OF INVENTION: Probes Specific for Ribosomal RNA Precursors
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/745,638
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,602
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/261,068
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 11652-79-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600

```

```
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: rRNA
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium avium
US-08-745-638-53

Query Match          70.0%; Score 15.4; DB 2; Length 27;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCCTTT 19
Db 1 CGAACGGAAGGCCUCU 17

RESULT 50
US-09-738-972-8
; Sequence 8, Application US/09738972
; Patent No. 6747141
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738, 972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-738-972-8

Query Match          70.0%; Score 15.4; DB 3; Length 28;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCCTTT 19
Db 1 CGAACGGAAGGCCCTC 17

RESULT 51
US-09-738-972-15/c
; Sequence 15, Application US/09738972
; Patent No. 6747141
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738, 972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 28

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-738-972-15

Query Match          70.0%; Score 15.4; DB 3; Length 28;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAACGGAAGGCCTTTC 20
Db 27 GACCGGAAGGCCTTTC 43

RESULT 52
US-09-640-211A-60
; Sequence 60, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-60

Query Match          70.0%; Score 15.4; DB 3; Length 455;
Best Local Similarity 94.1%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAACGGAAGGCCTTTC 20
Db 27 GACCGGAAGGCCTTTC 43

RESULT 53
US-09-640-211A-1958
; Sequence 1958, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1958
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-1958

Query Match          70.0%; Score 15.4; DB 3; Length 455;
Best Local Similarity 94.1%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 4 GAACGGAAGGCGCTTTC 20
Db 27 GACCGGAAGGCGCTTTC 43

RESULT 54
US-09-270-767-6474/c
; Sequence 6474, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6474
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-6474

Query Match 70.0%; Score 15.4; DB 3; Length 466;
Best Local Similarity 94.1%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AACGGAAGGCGCTTCG 21
Db 448 AACGTAAGGCGCTTCG 432

RESULT 55
US-09-270-767-21756/c
; Sequence 21756, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21756
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-21756

Query Match 70.0%; Score 15.4; DB 3; Length 466;
Best Local Similarity 94.1%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AACGGAAGGCGCTTCG 21
Db 448 AACGTAAGGCGCTTCG 432

RESULT 56
US-09-540-4420
; Sequence 4420, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

QY 4 GAACGGAAGGCGCTTTC 20
Db 23339 GAACGGAAGGCGCTTTC 23323

RESULT 57
US-09-902-540-1218/c
; Sequence 1218, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1218
; LENGTH: 23677
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1218

Query Match 70.0%; Score 15.4; DB 3; Length 23677;
Best Local Similarity 94.1%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAACGGAAGGCGCTTTC 20
Db 23339 GAACGGAAGGCGCTTTC 23323

RESULT 58
US-09-533-559-1639/c
; Sequence 1639, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 5849.200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1639
```

```
; LENGTH: 409
; TYPE: DNA
; ORGANISM: Fusarium venenatum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(409)
; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-1639

Query Match          69.1%; Score 15.2; DB 3; Length 409;
Best Local Similarity 77.3%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1  GTCCGACGGAAGCCCTTCGG 22
Db      336  GNCGAANGGAAAGTCCTTCGG 315

RESULT 59
US-09-949-016-125682/c
; Sequence 125682, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125682.
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-125682

Query Match          69.1%; Score 15.2; DB 3; Length 601;
Best Local Similarity 85.0%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3  CGAACGGAAGCCCTTCGG 22
Db      382  CGATCAGAAAGCCCTTCAG 363

RESULT 60
US-09-221-017B-580
; Sequence 580, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Ross, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
```

```
; APPLICATION NUMBER: US/09/221,017B
; FILING DATE: 23-DEC-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1182
; FILING DATE: 31-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1546
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP2911
; FILING DATE: 09-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU98/01023
; FILING DATE: 10-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Monroy, Gladys H
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 27340-20021.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 580:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 603 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: UNKNOWN
; ORIGINAL SOURCE:
; ORGANISM: PORPHYROMONAS GINGIVALIS
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1...603
US-09-221-017B-580

Query Match          69.1%; Score 15.2; DB 3; Length 603;
Best Local Similarity 85.0%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3  CGAACGGAAGCCCTTCGG 22
Db      447  CGAACGGAAGTCCTTCGG 466

RESULT 61
US-09-657-289A-21/c
; Sequence 21, Application US/09657289A
; Patent No. 6737245
; GENERAL INFORMATION:
; APPLICANT: Francis, Kevin P.
; APPLICANT: Contag, Pamela R.
; APPLICANT: Joh, Danny J.
; TITLE OF INVENTION: LUCIFERASE EXPRESSION CASSETTES AND METHODS OF USE
; FILE REFERENCE: 9400-0006
; CURRENT APPLICATION NUMBER: US/09/657,289A
; CURRENT FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: base_polymorphism
; LOCATION: 7
; OTHER INFORMATION: /note = "n' represents an a or g or t or c polymorphism at this
; NAME/KEY: base_polymorphism
; LOCATION: 33
```

;
; OTHER INFORMATION: /note = 'n' represents an a or g or t or c polymorphism at this
; NAME/KEY: position
; LOCATION: 97
; OTHER INFORMATION: /note = 'n' represents an a or g or t or c polymorphism at this
; NAME/KEY: position
; LOCATION: 126
; OTHER INFORMATION: /note = 'n' represents an a or g or t or c polymorphism at this
; OTHER INFORMATION: position
; OTHER INFORMATION: Description of Artificial Sequence: pDL289
; OTHER INFORMATION: luxABCDE Spl
US-09-657-289A-21

Query Match 69.1%; Score 15.2; DB 3; Length 622;
Best Local Similarity 81.0%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 2 TCGAACGGAAGGCGCTTTCGG 22
Db 42 TCGAACGCTNAAGCGCTTTCGG 22

RESULT 62
US-09-257-584-1

; Sequence 1, Application US/09257584A
; Patent No. 6177611

; GENERAL INFORMATION:

; APPLICANT: Rice, Douglas A.

; TITLE OF INVENTION: Constitutive Maize Promoters

; FILE REFERENCE: 5718-33, 035718/175218

; CURRENT APPLICATION NUMBER: US/09/257,584A

; CURRENT FILING DATE: 1999-02-25

; EARLIER APPLICATION NUMBER: 60/076,075

; EARLIER FILING DATE: 1998-02-26

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 1392

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: H2B histone promoter

US-09-257-584-1

Query Match 69.1%; Score 15.2; DB 3; Length 1392;
Best Local Similarity 85.0%; Pred. No. 4e+02; Mismatches 3; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCGCTTTCGG 22
Db 1141 CCAAAGGAAGGCGCTTTCGG 1160

RESULT 63

US-09-134-000C-2261

; Sequence 2261, Application US/09134000C

; Patent No. 6617156

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

; FILE REFERENCE: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

; CURRENT APPLICATION NUMBER: US/09/134,000C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/055,778

; PRIOR FILING DATE: 1997-08-15

; NUMBER OF SEQ ID NOS: 6812

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2261

; LENGTH: 1542

; TYPE: DNA

; ORGANISM: Enterococcus faecalis

US-09-134-000C-2261

Query Match 69.1%; Score 15.2; DB 3; Length 1542;
Best Local Similarity 85.0%; Pred. No. 4.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTCG 21
Db 843 TCAAACGGAAGGACTATCG 862

RESULT 64

US-09-949-016-15307/c

; Sequence 15307, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 15307

; LENGTH: 138282

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-15307

Query Match 69.1%; Score 15.2; DB 3; Length 138282;
Best Local Similarity 85.0%; Pred. No. 9.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCGCTTTCGG 22
Db 113452 CGATCAGAAAGGCGCTTTCAG 113433

RESULT 65

US-09-949-016-16038/c

; Sequence 16038, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 16038

; LENGTH: 166698

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(166698)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-16038

Query Match 69.1%; Score 15.2; DB 3; Length 166698;
Best Local Similarity 85.0%; Pred. No. 9.7e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTTC 20
| | | | | | | | | | | | | | | | | | | | | |
Db 116338 GTCGAACGGAAGGCTTTTC 116319

RESULT 66

US-09-531-120-209
; Sequence 209, Application US/09531120
; Patent No. 6972197
; GENERAL INFORMATION:
; APPLICANT: PREUSS, DAPHNE
; APPLICANT: COPENHAVER, GREGORY
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD:309US
; CURRENT APPLICATION NUMBER: US/09/531.120
; CURRENT FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,219
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 209
; LENGTH: 611587
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-531-120-209

Query Match 69.1%; Score 15.2; DB 4; Length 611587;
Best Local Similarity 85.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCTTTTC 21
| | | | | | | | | | | | | | | | | | | | | |
Db 452361 TCGACAGAAAGTCTTTTC 452280

RESULT 67

US-09-023-655-689
; Sequence 689, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023.655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 689:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1429 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: TLYMNOT02
; CLONE: 450088
US-09-023-655-689

Query Match 69.2%; Score 15; DB 3; Length 1429;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GGAAGGCTTTTCG 22
| | | | | | | | | | | | | | | | | | | | | |
Db 264 GGAAGGCTTTTCG 278

RESULT 68

US-08-433-126A-221/c
; Sequence 221, Application US/08433126A
; Patent No. 568935
; GENERAL INFORMATION:
; APPLICANT: STEPHENS, ANDREW
; APPLICANT: SCHNEIDER, DAN
; APPLICANT: GOLD, LARRY
; TITLE OF INVENTION: NUCLEIC ACID LIGANDS OF TISSUE
; TITLE OF INVENTION: TARGET
; NUMBER OF SEQUENCES: 241
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MG
; COMPUTER: IBM pc compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433.126A
; FILING DATE: 03 MAY 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX31.2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 221:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

TOPOLOGY: linear
 FEATURE:
 OTHER INFORMATION: All C's are 2'-F cytosine
 FEATURE:
 OTHER INFORMATION: All U's are 2'-F uracil
 US-08-433-126A-221

Query Match 67.3%; Score 14.8; DB 2; Length 87;
 Best Local Similarity 88.9%; Pred. No. 3.8e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AACGGAAGGCTTCGG 22
 DB 50 ATCGTAAGGCTTCGG 33

RESULT 69
 US-08-433-124A-221/c
 ; Sequence 221, Application US/08433124A
 ; Patent No. 5750342
 ; GENERAL INFORMATION:
 ; APPLICANT: STEPHENS, ANDREW
 ; APPLICANT: SCHNEIDER, DAN
 ; APPLICANT: GOLD, LARRY
 ; TITLE OF INVENTION: NUCLEIC ACID LIGANDS OF TISSUE
 ; TITLE OF INVENTION: TARGET
 ; NUMBER OF SEQUENCES: 241
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Swanson & Bratschun, L.L.C.
 ; STREET: 8400 E. Prentice Avenue, Suite 200
 ; CITY: Englewood
 ; STATE: Colorado
 ; COUNTRY: USA
 ; ZIP: 80111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MG
 COMPUTER: IBM pc compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 6.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/433,124A
 FILING DATE: 03 MAY 1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/714,131
 FILING DATE: 10-JUNE-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/536,428
 FILING DATE: 11-JUNE-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/964,624
 FILING DATE: 21-OCTOBER-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33,215
 REFERENCE/DOCKET NUMBER: NEX31.2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433
 INFORMATION FOR SEQ ID NO: 221:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 87 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 OTHER INFORMATION: All C's are 2'-F cytosine
 FEATURE:
 OTHER INFORMATION: All U's are 2'-F uracil
 US-08-433-124A-221

Query Match 67.3%; Score 14.8; DB 2; Length 87;
 Best Local Similarity 88.9%; Pred. No. 3.8e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5 AACGGAAGGCTTCGG 22
 DB 50 ATCGTAAGGCTTCGG 33

RESULT 70
 US-08-976-413A-221/c
 ; Sequence 221, Application US/08976413A
 ; Patent No. 6127119
 ; GENERAL INFORMATION:
 ; APPLICANT: STEPHENS, ANDREW
 ; APPLICANT: GOLD, LARRY
 ; APPLICANT: SPECK, ULRICH
 ; TITLE OF INVENTION: NUCLEIC ACID LIGANDS OF TISSUE TARGET
 ; NUMBER OF SEQUENCES: 440
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Swanson & Bratschun, L.L.C.
 ; STREET: 8400 E. Prentice Avenue, Suite 200
 ; CITY: Englewood
 ; STATE: Colorado
 ; COUNTRY: USA
 ; ZIP: 80111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MG
 ; COMPUTER: IBM pc compatible
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: WordPerfect 8.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/976,413A
 ; FILING DATE: 21-NOVEMBER-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/433,124
 ; FILING DATE: 03-MAY-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/714,131
 ; FILING DATE: 10-JUNE-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/536,428
 ; FILING DATE: 11-JUNE-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/964,624
 ; FILING DATE: 21-OCTOBER-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Barry J. Swanson
 ; REGISTRATION NUMBER: 33,215
 ; REFERENCE/DOCKET NUMBER: NEX31/CIP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (303) 793-3333
 ; TELEFAX: (303) 793-3433
 ; INFORMATION FOR SEQ ID NO: 221:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 87 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; FEATURE:
 ; OTHER INFORMATION: All C's are 2'-F cytosine
 ; FEATURE:
 ; OTHER INFORMATION: All U's are 2'-F uracil
 US-08-976-413A-221

Query Match 67.3%; Score 14.8; DB 3; Length 87;
 Best Local Similarity 88.9%; Pred. No. 3.8e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AACGGAAGGCTTCGG 22
 DB 50 ATCGTAAGGCTTCGG 33

RESULT 71

PCT-US96-06059-221/c
; Sequence 221, Application PC/TUS9606059
; GENERAL INFORMATION:
; APPLICANT: STEPHENS, ANDREW
; APPLICANT: SCHNEIDER, DAN
; APPLICANT: GOLD, LARRY
; TITLE OF INVENTION: NUCLEIC ACID LIGANDS OF TISSUE
; TITLE OF INVENTION: TARGET
; NUMBER OF SEQUENCES: 241
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MG
; COMPUTER: IBM pc compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/06059
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/433,124
; FILING DATE: 03-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/433,126
; FILING DATE: 03-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX31.2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 221:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: All C's are 2'-F cytosine
; FEATURE:
; OTHER INFORMATION: All U's are 2'-F uracil
PCT-US96-06059-221

Query Match 67.3%; Score 14.8; DB 7; Length 87;
Best Local Similarity 88.9%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AACGGAAGGCTTCGG 22
| | | | | | | | | | | | | | | | | | | | | |
Db 50 ATCGTAGGCGCTTCGG 33

RESULT 72

US-09-016-434-408
; Sequence 408, Application US/09016434
; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 408:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRSTNOT07
; CLONE: 2122627
US-09-016-434-408

Query Match 67.3%; Score 14.8; DB 3; Length 107;
Best Local Similarity 88.9%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGAACGGAAAGGCTTTC 20
| | | | | | | | | | | | | | | | | | | | | |
Db 71 CGAACGGCAAGCCTTTC 88

RESULT 73

US-09-513-999C-2742
; Sequence 2742, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 2742
; LENGTH: 362
; TYPE: DNA

```
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 146..361
US-09-513-999C-2742

Query Match      67.3%; Score 14.8; DB 3; Length 362;
Best Local Similarity 88.9%; Pred. No. 5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CGAACGGAAGGCCTTTC 20
    ||||| |||||
Db 108 CGAACGGAAGGCCTTTC 125

RESULT 74
US-09-270-767-29724/c
; Sequence 29724, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29724
; LENGTH: 532
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-29724

Query Match      67.3%; Score 14.8; DB 3; Length 532;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TCGAACGGAAGGCCTTT 19
    ||||| |||||
Db 248 TCGAACAGAAAGGCTTTT 231

RESULT 75
US-09-252-991A-5578
; Sequence 5578, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5578
; LENGTH: 543
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5578

Query Match      67.3%; Score 14.8; DB 3; Length 543;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAACGGAAGGCCTTTCG 21
    ||||| |||||
Db 145 GAACGGATAGGCTGTCG 162

RESULT 76
US-09-252-991A-5650/c
; Sequence 5650, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5650
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5650

Query Match      67.3%; Score 14.8; DB 3; Length 600;
Best Local Similarity 88.9%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAACGGAAGGCCTTTCG 21
    ||||| |||||
Db 468 GAACGGATAGGCTGTCG 451

RESULT 77
US-09-949-016-82725
; Sequence 82725, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82725
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-82725

Query Match      67.3%; Score 14.8; DB 3; Length 601;
Best Local Similarity 88.9%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTT 18
    ||| |||||
Db 438 GTCGAACGGAAGGCATT 455

RESULT 78
US-09-949-016-82726
; Sequence 82726, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82726
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-82726

Query Match      67.3%; Score 14.8; DB 3; Length 601;
Best Local Similarity 88.9%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTT 18
    ||| |||||
Db 438 GTCGAACGGAAGGCATT 455
```

```
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82726
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-82726

Query Match          67.3%; Score 14.8; DB 3; Length 601;
Best Local Similarity 88.9%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTT 18
   ||| ||||| ||||| |||
Db 205 GTCAACGGAAGGCATT 222

RESULT 79
US-09-949-016-82727
; Sequence 82727, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82727
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-82727

Query Match          67.3%; Score 14.8; DB 3; Length 601;
Best Local Similarity 88.9%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTT 18
   ||| ||||| ||||| |||
Db 46 GTCAACGGAAGGCATT 63

RESULT 80
US-09-949-016-148702/c
; Sequence 148702, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
```

```
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 148702
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-148702

Query Match          67.3%; Score 14.8; DB 3; Length 601;
Best Local Similarity 88.9%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAACGGAAGGCCTTTTCG 21
   ||| ||||| ||||| |||
Db 249 GAACAGAAGGCCTTTGG 232

RESULT 81
US-09-533-559-7113
; Sequence 7113, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 5849.200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7113
; LENGTH: 637
; TYPE: DNA
; ORGANISM: Aspergillus oryzae
US-09-533-559-7113

Query Match          67.3%; Score 14.8; DB 3; Length 637;
Best Local Similarity 88.9%; Pred. No. 5.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTT 18
   ||| ||||| ||||| |||
Db 32 GTCGAACGGAAGGCATT 49

RESULT 82
US-09-248-796A-4578/c
; Sequence 4578, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 4578
```

```
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-4578

Query Match          67.3%; Score 14.8; DB 3; Length 645;
Best Local Similarity 88.9%; Pred. No. 5.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCCTTTC 20
    ||||| ||||| |||||
Db 602 CGAACGGAAGGCATTC 585

RESULT 83
US-09-328-352-3521/c
; Sequence 3521, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: GTC99-03PA
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 3521
; LENGTH: 795
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-3521

Query Match          67.3%; Score 14.8; DB 3; Length 795;
Best Local Similarity 88.9%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCCTTT 19
    ||||| ||||| |||||
Db 453 TCGAACGTACAGGCCTTT 436

RESULT 84
US-09-270-767-13705/c
; Sequence 13705, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13705
; LENGTH: 1160
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13705

Query Match          67.3%; Score 14.8; DB 3; Length 1160;
Best Local Similarity 88.9%; Pred. No. 6.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCCTTT 19
    ||||| ||||| |||||
Db 876 TCGAACAGAGAGGCCTTT 859

RESULT 85
US-09-949-016-2374
; Sequence 2374, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15445
; LENGTH: 4029
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2374

Query Match          67.3%; Score 14.8; DB 3; Length 1945;
Best Local Similarity 88.9%; Pred. No. 6.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCCTTTC 20
    ||||| ||||| |||||
Db 247 CGAACGGCACGCCTTTC 264

RESULT 86
US-09-270-767-163
; Sequence 163, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 163
; LENGTH: 4029
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-163

Query Match          67.3%; Score 14.8; DB 3; Length 4029;
Best Local Similarity 88.9%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTT 18
    ||||| ||||| |||||
Db 1401 GGCGAACGGAAGGCCAT 1418

RESULT 87
US-09-270-767-15445
; Sequence 15445, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15445
; LENGTH: 4029
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2374
```

; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-15445

Query Match 67.3%; Score 14.8; DB 3; Length 4029;
Best Local Similarity 88.9%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAAGGCTT 18
| | | | | | | | | | | | | | | | | |
Db 1401 GCGACGGAAAGGCGCAT 1418

RESULT 88
US-09-949-016-14116
; Sequence 14116, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14116
; LENGTH: 11050
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14116

Query Match 67.3%; Score 14.8; DB 3; Length 11050;
Best Local Similarity 88.9%; Pred. No. 9.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGAACGGAAAGGCTTTC 20
| | | | | | | | | | | | | | | | | |
Db 5117 CGAACGGCAAGCCTTTC 5134

RESULT 89
US-09-949-016-15957/c
; Sequence 15957, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15957
; LENGTH: 35916
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15957

Query Match 67.3%; Score 14.8; DB 3; Length 35916;
Best Local Similarity 88.9%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGAACGGAAAGGCTTTC 20
| | | | | | | | | | | | | | | | | |
Db 4145 CGCACGGCAAGGCTTTC 4128

RESULT 90
US-09-949-016-17095/c
; Sequence 17095, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17095
; LENGTH: 36855
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17095

Query Match 67.3%; Score 14.8; DB 3; Length 36855;
Best Local Similarity 88.9%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAAGGCTTTC 19
| | | | | | | | | | | | | | | | | |
Db 8257 TCGAATCGAAAGGCTTTC 8240

RESULT 91
US-09-949-016-15116/c
; Sequence 15116, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15116
; LENGTH: 83462
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) ... (83462)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15116

Query Match 67.3%; Score 14.8; DB 3; Length 83462;

```
Best Local Similarity 88.9%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCGCTTTC 20
    ||||| ||||| |||||
Db 2869 CGACAGACAGGCGCTTTC 2852

RESULT 92
US-09-949-016-13629
; Sequence 13629, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13629
; LENGTH: 93894
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(93894)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13629

Query Match 67.3%; Score 14.8; DB 3; Length 93894;
Best Local Similarity 88.9%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAACGGAAGGCGCTTTCG 21
    ||||| ||||| |||||
Db 26767 GAACGGAAGGCGCTTTCG 26784

RESULT 93
US-09-949-016-15921/c
; Sequence 15921, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15921
; LENGTH: 124480
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15921

Query Match 67.3%; Score 14.8; DB 3; Length 124480;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Best Local Similarity 88.9%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAACGGAAGGCGCTTTCG 21
    ||||| ||||| |||||
Db 118710 GAACAGAAAGGCGCTTTCG 118693

RESULT 94
US-09-949-016-13845/c
; Sequence 13845, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13845
; LENGTH: 152132
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13845

Query Match 67.3%; Score 14.8; DB 3; Length 152132;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTT 19
    ||||| ||||| |||||
Db 13321 TCGAACGGAAGGCGCTTT 13304

RESULT 95
US-09-949-016-12371/c
; Sequence 12371, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12371
; LENGTH: 152145
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12371

Query Match 67.3%; Score 14.8; DB 3; Length 152145;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTT 19
    ||||| ||||| |||||
Db 13321 TCGAACGGAAGGCGCTTT 13304
```

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RESULT 96
US-09-949-016-12086/c
; Sequence 12086, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12086
; LENGTH: 152582
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(152582)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12086

Query Match      67.3%; Score 14.8; DB 3; Length 152582;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 TCGAACGGAAGGCCCTT 19
Db      60573 TCGAATGGAAGGCCCTT 60556

RESULT 97
US-09-949-016-17390/c
; Sequence 17390, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17390
; LENGTH: 152583
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(152583)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17390

Query Match      67.3%; Score 14.8; DB 3; Length 152583;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 TCGAACGGAAGGCCCTT 19
Db      60573 TCGAATGGAAGGCCCTT 60556

RESULT 98
US-09-949-016-17391/c
; Sequence 17391, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17391
; LENGTH: 152583
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(152583)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17391

Query Match      67.3%; Score 14.8; DB 3; Length 152583;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 TCGAACGGAAGGCCCTT 19
Db      60573 TCGAATGGAAGGCCCTT 60556

RESULT 99
US-09-820-007-3
; Sequence 3, Application US/09820007
; Patent No. 6830900
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; AND USES THEREOF
; FILE REFERENCE: CL001205
; CURRENT APPLICATION NUMBER: US/09/820,007
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 213456
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(213456)
; OTHER INFORMATION: n = A,T,C or G
US-09-820-007-3

Query Match      67.3%; Score 14.8; DB 3; Length 213456;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GTCGAACGGAAGGCCCTT 18
Db      60573 TCGAATGGAAGGCCCTT 60556
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 03:46:33 ; Search time 882.518 Seconds
(without alignments)
306.314 Million cell updates/sec

Title: US-10-665-708-23

Perfect score: 22

Sequence: 1 gtcgaacgaaaggccttcgg 22

Scoring table: IDENTITY_NUC

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Searched: 18892170 seqs, 614381738 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

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Published Applications NA Main:*

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- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
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- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	22	100.0	22	3	US-09-738-274-23
2	22	100.0	22	10	US-10-665-708-23
3	21	95.5	24	3	US-09-738-274-22
4	21	95.5	24	10	US-10-665-708-22
5	21	95.5	25	3	US-09-738-274-21
6	21	95.5	25	10	US-10-665-708-21
7	20.4	92.7	454	7	US-10-438-774-15
8	20.4	92.7	1449	10	US-10-697-802A-6
9	20.4	92.7	1455	10	US-10-697-802A-13
10	20.4	92.7	1482	10	US-10-697-802A-5
11	19	86.4	19	3	US-09-738-274-24
12	19	86.4	19	10	US-10-665-708-24
13	18.8	85.5	1403	10	US-10-522-454-1
14	18.8	85.5	1443	13	US-11-035-296-1
15	18.8	85.5	1443	13	US-11-045-628-1
16	18.8	85.5	1461	10	US-10-697-802A-7
17	18.8	85.5	1480	16	US-11-228-416-5
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					Sequence 22, Appl
					Sequence 21, Appl
					Sequence 20, Appl
					Sequence 19, Appl
					Sequence 18, Appl
					Sequence 17, Appl
					Sequence 16, Appl
					Sequence 15, Appl
					Sequence 14, Appl
					Sequence 13, Appl
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					Sequence 11, Appl
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					Sequence 9, Appl
					Sequence 8, Appl
					Sequence 7, Appl
					Sequence 6, Appl
					Sequence 5, Appl
					Sequence 4, Appl
					Sequence 3, Appl
					Sequence 2, Appl
					Sequence 1, Appl

18	18.8	85.5	1480	16	US-11-228-416-6	Sequence 6, Appl
19	18.8	85.5	1480	16	US-11-228-416-8	Sequence 8, Appl
20	18.8	85.5	1480	16	US-11-228-416-9	Sequence 9, Appl
21	18.8	85.5	1481	16	US-11-228-416-3	Sequence 3, Appl
22	18.8	85.5	1482	16	US-11-228-416-4	Sequence 4, Appl
23	18.8	85.5	1483	16	US-11-228-416-7	Sequence 7, Appl
24	17.8	80.9	1439	9	US-10-230-026-6	Sequence 6, Appl
25	17.8	80.9	1439	9	US-10-486-307-6	Sequence 31, Appl
26	17.4	79.1	25	8	US-10-220-212A-31	Sequence 33, Appl
27	17.4	79.1	25	8	US-10-220-212A-33	Sequence 7, Appl
28	17.4	79.1	32	3	US-09-738-972-7	Sequence 14, Appl
29	17.4	79.1	32	3	US-09-738-972-14	Sequence 7, Appl
30	17.4	79.1	32	9	US-10-862-026-7	Sequence 14, Appl
31	17.4	79.1	32	9	US-10-862-026-14	Sequence 14, Appl
32	17.4	79.1	560	10	US-10-478-633A-23	Sequence 23, Appl
33	17.4	79.1	1421	10	US-10-697-802A-12	Sequence 12, Appl
34	17.4	79.1	1454	10	US-10-697-802A-2	Sequence 2, Appl
35	17.4	79.1	1465	7	US-10-029-397A-32	Sequence 32, Appl
36	17.2	78.2	513	4	US-09-925-065A-544396	Sequence 544396, Appl
37	17.2	78.2	513	4	US-09-925-065A-544397	Sequence 544397, Appl
38	17.2	78.2	513	5	US-09-925-065A-544396	Sequence 544396, Appl
39	17.2	78.2	513	5	US-09-925-065A-544397	Sequence 544397, Appl
40	17.2	78.2	620	8	US-10-437-963-34505	Sequence 34505, A
41	17.2	78.2	638	6	US-10-027-632-292604	Sequence 292604, Appl
42	17.2	78.2	638	6	US-10-027-632-292605	Sequence 292605, Appl
43	17.2	78.2	638	7	US-10-027-632-292604	Sequence 292604, Appl
44	17.2	78.2	638	7	US-10-027-632-292605	Sequence 292605, Appl
45	17.2	78.2	1437	7	US-10-085-871C-1	Sequence 1, Appl
46	17.2	78.2	1437	10	US-10-727-643-1	Sequence 1, Appl
47	17.2	78.2	1471	7	US-10-085-871C-2	Sequence 2, Appl
48	17.2	78.2	1471	10	US-10-727-643-2	Sequence 2, Appl
49	17.2	78.2	1488	9	US-10-756-683-1	Sequence 1, Appl
50	17.2	78.2	1514	9	US-10-875-161-2	Sequence 2, Appl
51	17	77.3	30	11	US-10-831-286A-1517	Sequence 1517, Ap
52	16.4	74.5	30	11	US-10-831-286A-8212	Sequence 8212, Ap
53	16.2	73.6	367	7	US-10-062-674-613	Sequence 613, App
54	16.2	73.6	622	8	US-10-767-701-31297	Sequence 31297, A
55	16.2	73.6	635	9	US-10-425-115-59269	Sequence 59269, A
56	16	72.7	20	11	US-10-831-286A-12801	Sequence 12801, A
57	16	72.7	20	11	US-10-831-286A-23905	Sequence 23905, A
58	16	72.7	23	3	US-09-738-274-27	Sequence 27, Appl
59	16	72.7	23	10	US-10-665-708-27	Sequence 27, Appl
60	16	72.7	26	3	US-09-738-274-28	Sequence 28, Appl
61	16	72.7	26	10	US-10-665-708-28	Sequence 28, Appl
62	16	72.7	80	9	US-10-830-943-11	Sequence 11, Appl
63	16	72.7	560	10	US-10-478-633A-24	Sequence 24, Appl
64	16	72.7	935	10	US-10-779-543-8365	Sequence 8365, Ap
65	16	72.7	1321	10	US-10-697-802A-11	Sequence 11, Appl
66	16	72.7	1415	10	US-10-697-802A-14	Sequence 14, Appl
67	16	72.7	1460	6	US-10-062-777-1	Sequence 1, Appl
68	16	72.7	1460	7	US-10-419-095-1	Sequence 1, Appl
69	16	72.7	1462	10	US-10-697-802A-15	Sequence 15, Appl
70	16	72.7	1484	10	US-10-697-802A-8	Sequence 8, Appl
71	16	72.7	1527	10	US-10-697-802A-18	Sequence 18, Appl
72	15.8	71.8	32	3	US-09-738-274-14	Sequence 14, Appl
73	15.8	71.8	32	10	US-10-665-708-14	Sequence 14, Appl
74	15.8	71.8	170	6	US-10-062-727-254	Sequence 254, App
75	15.8	71.8	305	6	US-10-062-727-376	Sequence 376, App
76	15.8	71.8	381	10	US-10-450-763-13678	Sequence 13678, A
77	15.8	71.8	468	7	US-10-438-774-17	Sequence 17, Appl
78	15.8	71.8	576	10	US-10-450-763-3105	Sequence 3105, Ap
79	15.8	71.8	625	12	US-10-301-480-442948	Sequence 442948, Appl
80	15.8	71.8	625	12	US-10-301-480-1056357	Sequence 1056357, Appl
81	15.8	71.8	634	4	US-09-925-065A-373045	Sequence 373045, Appl
82	15.8	71.8	634	5	US-09-925-065A-373045	Sequence 373045, Appl
83	15.8	71.8	1416	10	US-10-697-802A-17	Sequence 17, Appl
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85	15.8	71.8	1463	10	US-10-697-802A-10	Sequence 10, Appl
86	15.8	71.8	1464	3	US-09-726-774-7	Sequence 7, Appl
87	15.8	71.8	1464	8	US-10-719-633-7	Sequence 7, Appl
88	15.8	71.8	1524	8	US-10-220-212A-34	Sequence 34, Appl
89	15.8	71.8	1536	7	US-10-029-397A-33	Sequence 33, Appl
90	15.8	71.8	1536	7	US-10-029-397A-34	Sequence 34, Appl

c 91	15.8	71.8	2896	10	US-10-488-528-3	Sequence 3, Appli	c 164	15.2	69.1	499	3	US-09-918-995-261	Sequence 261, App
c 92	15.8	71.8	2919	7	US-10-369-493-35634	Sequence 35634, A	165	15.2	69.1	558	16	US-11-096-568A-27724	Sequence 27724, A
c 93	15.8	71.8	2934	10	US-10-488-528-1	Sequence 1, Appli	166	15.2	69.1	561	3	US-09-925-299-10	Sequence 10, Appl
c 94	15.8	71.8	6883	3	US-09-764-877-3363	Sequence 3363, Ap	167	15.2	69.1	561	3	US-09-925-299-10	Sequence 10, Appl
c 95	15.8	71.8	6883	3	US-10-242-515-3363	Sequence 3363, Ap	168	15.2	69.1	603	6	US-10-194-163-580	Sequence 580, App
c 96	15.8	71.8	21126	8	US-10-465-008-10	Sequence 10, Appl	c 169	15.2	69.1	641	4	US-09-925-065A-750529	Sequence 750529,
c 97	15.6	70.9	297	7	US-10-012-697-422	Sequence 422, App	c 170	15.2	69.1	641	5	US-09-925-065A-750529	Sequence 750529,
c 98	15.6	70.9	297	10	US-10-779-543-22422	Sequence 22422, A	171	15.2	69.1	658	4	US-09-925-065A-220788	Sequence 220788,
c 99	15.6	70.9	439	7	US-10-410-681-27	Sequence 27, Appl	172	15.2	69.1	658	5	US-09-925-065A-220788	Sequence 220788,
c 100	15.6	70.9	471	11	US-10-932-182A-77805	Sequence 77805, A	173	15.2	69.1	671	6	US-10-027-632-32863	Sequence 32863, A
c 101	15.6	70.9	524	3	US-09-770-152-949	Sequence 949, App	174	15.2	69.1	671	7	US-10-027-632-32863	Sequence 32863, A
c 102	15.6	70.9	530	8	US-10-767-701-30317	Sequence 30317, A	175	15.2	69.1	693	6	US-10-027-632-102406	Sequence 102406,
c 103	15.6	70.9	600	4	US-09-925-065A-906221	Sequence 906221, A	176	15.2	69.1	693	6	US-10-027-632-102406	Sequence 102406,
c 104	15.6	70.9	600	5	US-09-925-065A-906221	Sequence 906221, A	177	15.2	69.1	693	7	US-10-027-632-102406	Sequence 102406,
c 105	15.6	70.9	600	10	US-10-972-079-86404	Sequence 86404, A	178	15.2	69.1	693	7	US-10-027-632-102406	Sequence 102406,
c 106	15.6	70.9	624	10	US-10-487-804-136	Sequence 804, App	c 179	15.2	69.1	766	4	US-09-925-065A-85410	Sequence 85410, A
c 107	15.6	70.9	654	4	US-09-925-065A-481777	Sequence 481777, A	c 180	15.2	69.1	766	5	US-09-925-065A-85410	Sequence 85410, A
c 108	15.6	70.9	654	5	US-09-925-065A-481777	Sequence 481777, A	c 181	15.2	69.1	766	5	US-09-925-065A-85410	Sequence 85410, A
c 109	15.6	70.9	659	8	US-10-424-599-80785	Sequence 80785, A	c 182	15.2	69.1	766	12	US-10-301-480-186650	Sequence 186650,
c 110	15.6	70.9	786	16	US-11-096-568A-32833	Sequence 32833, A	c 183	15.2	69.1	766	12	US-10-301-480-800059	Sequence 800059,
c 111	15.6	70.9	960	6	US-10-087-132-1004	Sequence 1004, Ap	c 184	15.2	69.1	861	10	US-10-467-657-2959	Sequence 2959, Ap
c 112	15.6	70.9	999	7	US-10-156-761-5559	Sequence 5559, Ap	c 185	15.2	69.1	978	3	US-09-876-143-1060	Sequence 1060, Ap
c 113	15.6	70.9	1062	8	US-10-424-599-55432	Sequence 55432, A	c 186	15.2	69.1	1341	8	US-10-767-701-10349	Sequence 10349, A
c 114	15.6	70.9	1101	7	US-10-369-493-40702	Sequence 40702, A	c 187	15.2	69.1	1420	6	US-10-050-704-89	Sequence 89, Appl
c 115	15.6	70.9	1111	8	US-10-425-114-7767	Sequence 7767, Ap	c 188	15.2	69.1	1420	6	US-10-798-512-89	Sequence 89, Appl
c 116	15.6	70.9	1197	7	US-10-156-761-1373	Sequence 1373, Ap	c 189	15.2	69.1	1632	16	US-11-079-463-4538	Sequence 4538, Ap
c 117	15.6	70.9	1675	7	US-10-369-493-32574	Sequence 32574, A	c 190	15.2	69.1	1736	4	US-09-925-065A-79104	Sequence 79104, A
c 118	15.6	70.9	1718	8	US-10-425-114-72	Sequence 72, Appl	c 191	15.2	69.1	1736	4	US-09-925-065A-79105	Sequence 79105, A
c 119	15.6	70.9	1729	8	US-10-424-599-80784	Sequence 80784, A	c 192	15.2	69.1	1736	4	US-09-925-065A-79106	Sequence 79106, A
c 120	15.6	70.9	2389	3	US-09-938-842A-2525	Sequence 2525, Ap	c 193	15.2	69.1	1736	5	US-09-925-065A-79105	Sequence 79105, A
c 121	15.6	70.9	3096	9	US-10-425-115-40860	Sequence 40860, A	c 194	15.2	69.1	1736	5	US-09-925-065A-79105	Sequence 79105, A
c 122	15.6	70.9	3257	7	US-10-410-681-39	Sequence 39, Appl	c 195	15.2	69.1	1736	5	US-09-925-065A-79106	Sequence 79106, A
c 123	15.6	70.9	3913	9	US-10-425-115-85383	Sequence 85383, A	c 196	15.2	69.1	1736	12	US-10-301-480-180343	Sequence 180343,
c 124	15.6	70.9	2427	8	US-10-856-499-190	Sequence 190, App	c 197	15.2	69.1	1736	12	US-10-301-480-180344	Sequence 180344,
c 125	15.6	70.9	2982	3	US-09-938-842A-2525	Sequence 2525, Ap	c 198	15.2	69.1	1736	12	US-10-301-480-180345	Sequence 180345,
c 126	15.6	70.9	3257	7	US-10-410-681-39	Sequence 39, Appl	c 199	15.2	69.1	1736	12	US-10-301-480-793752	Sequence 793752,
c 127	15.6	70.9	3257	7	US-10-410-681-39	Sequence 39, Appl	c 200	15.2	69.1	1736	12	US-10-301-480-793753	Sequence 793753,
c 128	15.6	70.9	3913	9	US-10-425-115-85383	Sequence 85383, A	c 201	15.2	69.1	1736	12	US-10-301-480-793754	Sequence 793754,
c 129	15.6	70.9	12368	10	US-10-893-671-81	Sequence 83, Appl	c 202	15.2	69.1	2635	6	US-10-128-714-1270	Sequence 1270, Ap
c 130	15.6	70.9	43800	6	US-10-087-192-1003	Sequence 1003, Ap	c 203	15.2	69.1	2937	8	US-10-282-122A-11160	Sequence 1160, Ap
c 131	15.6	70.9	268685	7	US-10-265-071-22	Sequence 22, Appl	c 204	15.2	69.1	2964	6	US-10-128-714-6270	Sequence 6270, Ap
c 132	15.6	70.9	268685	7	US-10-025-966A-22	Sequence 22, Appl	c 205	15.2	69.1	3485	3	US-09-070-927A-283	Sequence 283, App
c 133	15.6	70.9	268685	10	US-10-933-025-22	Sequence 22, Appl	c 206	15.2	69.1	4635	6	US-10-128-714-270	Sequence 270, App
c 134	15.6	70.9	268685	16	US-11-219-360-22	Sequence 22, Appl	c 207	15.2	69.1	4964	6	US-10-128-714-5270	Sequence 5270, Ap
c 135	15.6	70.9	387780	10	US-10-995-561-13559	Sequence 13259, A	c 208	15.2	69.1	5694	8	US-10-437-963-9516	Sequence 9516, Ap
c 136	15.6	70.9	495269	8	US-10-398-221-8	Sequence 8, Appli	c 209	15.2	69.1	5913	8	US-10-437-963-9516	Sequence 9516, Ap
c 137	15.6	70.9	3011208	8	US-10-398-221-2058	Sequence 2058, Ap	c 210	15.2	69.1	42104	6	US-10-087-192-1138	Sequence 1138, Ap
c 138	15.6	70.9	9025608	7	US-10-156-761-1	Sequence 15, Appl	c 211	15.2	69.1	89328	3	US-09-873-367C-332	Sequence 332, App
c 139	15.4	70.0	25	9	US-10-719-900-43767	Sequence 43767, A	c 212	15.2	69.1	89328	6	US-10-843-641A-332	Sequence 332, App
c 140	15.4	70.0	28	3	US-09-738-972-8	Sequence 8, Appli	c 213	15.2	69.1	105305	6	US-10-087-192-1369	Sequence 1369, App
c 141	15.4	70.0	28	3	US-09-738-972-15	Sequence 8, Appli	c 214	15.2	69.1	170489	8	US-10-322-281-380	Sequence 380, App
c 142	15.4	70.0	28	9	US-10-862-036-8	Sequence 15, Appl	c 215	15.2	69.1	259903	10	US-10-756-149-3550	Sequence 3550, Ap
c 143	15.4	70.0	28	9	US-10-862-036-15	Sequence 15, Appl	c 216	15.2	69.1	260549	9	US-10-741-600-17723	Sequence 17723, A
c 144	15.4	70.0	28	9	US-10-862-036-15	Sequence 15, Appl	c 217	15.2	69.1	611587	15	US-11-117-187-209	Sequence 209, App
c 145	15.4	70.0	30	11	US-10-831-286A-4562	Sequence 4562, Ap	c 218	15.2	69.1	1163020	8	US-10-398-221-10	Sequence 10, Appl
c 146	15.4	70.0	455	9	US-10-856-499-60	Sequence 60, Appl	c 219	15.2	69.1	1694969	12	US-10-506-454-1590	Sequence 1690, Ap
c 147	15.4	70.0	1164	9	US-10-856-499-3958	Sequence 1358, Ap	c 220	15.2	69.1	264428	16	US-11-045-004-1	Sequence 1, Appli
c 148	15.4	70.0	1187	10	US-10-369-493-32250	Sequence 42960, A	c 221	15.2	69.1	3011208	8	US-10-398-221-2058	Sequence 2058, Ap
c 149	15.4	70.0	1187	10	US-10-750-185-42960	Sequence 42960, A	c 222	15.2	69.1	20	11	US-10-831-286A-11940	Sequence 11940, A
c 150	15.4	70.0	2642	13	US-11-097-143-31768	Sequence 31768, A	c 223	15.2	69.1	20	11	US-10-831-286A-14889	Sequence 14889, A
c 151	15.4	70.0	2642	13	US-10-750-185-34543	Sequence 34543, A	c 224	15.2	69.1	20	11	US-10-831-286A-24565	Sequence 24565, A
c 152	15.4	70.0	2665	10	US-10-750-623-34543	Sequence 34543, A	c 225	15.2	69.1	243	8	US-10-424-599-53002	Sequence 53002, A
c 153	15.4	70.0	3581	13	US-11-097-143-31795	Sequence 31795, A	c 226	15.2	69.1	301	9	US-10-425-115-24598	Sequence 24598, A
c 154	15.4	70.0	5433	13	US-11-097-143-3737	Sequence 3737, Ap	c 227	15.2	69.1	1429	8	US-10-029-386-13162	Sequence 13162, A
c 155	15.4	70.0	7162	13	US-11-097-143-3736	Sequence 3736, Ap	c 228	15.2	69.1	1429	8	US-10-641-643-689	Sequence 689, App
c 156	15.2	69.1	25	13	US-11-036-317-106689	Sequence 106689, A	c 229	15.2	69.1	2173	8	US-10-296-115-424	Sequence 424, App
c 157	15.2	69.1	201	9	US-10-741-600-48545	Sequence 48545, A	c 230	15.2	69.1	2196	15	US-10-221-625-108	Sequence 108, App
c 158	15.2	69.1	201	9	US-10-741-600-48545	Sequence 48545, A	c 231	15.2	69.1	2196	15	US-11-000-688-253	Sequence 253, App
c 159	15.2	69.1	365	8	US-10-717-897-63	Sequence 63, Appl	c 232	15.2	69.1	3003	13	US-11-097-143-7973	Sequence 7973, Ap
c 160	15.2	69.1	409	9	US-10-653-047-1639	Sequence 1639, Ap	c 233	15.2	69.1	3293	3	US-09-764-864-123	Sequence 123, App
c 161	15.2	69.1	414	10	US-10-779-543-10690	Sequence 10690, A	c 234	15.2	69.1	8544	13	US-11-097-143-7972	Sequence 7972, Ap
c 162	15.2	69.1	475	3	US-09-867-701-1093	Sequence 1093, Ap	c 235	14.8	67.3	9025608	7	US-10-156-761-1	Sequence 1, Appli
c 163	15.2	69.1	489	8	US-10-437-963-44760	Sequence 44760, A	c 236	14.8	67.3	20	11	US-10-831-286A-38180	Sequence 38180, A
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[illegible]

US-09-738-274-22
; Sequence 22, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-22

Query Match 95.5%; Score 21; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 4 GTCGAACGGAAGGCGTTTCG 24

RESULT 4
US-10-665-708-22
; Sequence 22, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-10-665-708-22

Query Match 95.5%; Score 21; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGTTTCG 21
|||||
Db 4 GTCGAACGGAAGGCGTTTCG 24

RESULT 5
US-09-738-274-21
; Sequence 21, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-21

Query Match 95.5%; Score 21; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGTTTCG 21
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Db 5 GTCGAACGGAAGGCGTTTCG 25

RESULT 6
US-10-665-708-21
; Sequence 21, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-10-665-708-21

Query Match 95.5%; Score 21; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTCGAACGGAAGGCGCTTTCG 21
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DB 5 GTCGAACGGAAGGCGCTTTCG 25

RESULT 7

US-10-438-774-15
; Sequence 15, Application US/10438774
; Publication No. US20040010504A1
; GENERAL INFORMATION:
; APPLICANT: Mohammed, Steven
; APPLICANT: Ali, Hesham
; APPLICANT: Kuyper, Dan
; TITLE OF INVENTION: Custom Sequence Databases and Methods of
; FILE REFERENCE: UNMC.63174-US
; CURRENT APPLICATION NUMBER: US/10/438,774
; PRIOR FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: 60/381,015
; PRIOR FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-438-774-15

Query Match 92.7%; Score 20.4; DB 7; Length 454;
Best Local Similarity 95.5%; Pred. No. 4.6;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTCGAACGGAAGGCGCTTTCG 22
|||||
DB 1 GTCGAACGGAAGGCGCTTTCG 22

RESULT 8

US-10-697-802A-6
; Sequence 6, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 6
; LENGTH: 1449
; TYPE: DNA
; ORGANISM: Mycobacterium fortuitum
US-10-697-802A-6

Query Match 92.7%; Score 20.4; DB 10; Length 1449;
Best Local Similarity 95.5%; Pred. No. 4.7;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTCGAACGGAAGGCGCTTTCG 22
|||||
DB 24 GTCGAACGGAAGGCGCTTTCG 45

RESULT 9

US-10-697-802A-13
; Sequence 13, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG

; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 13
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Mycobacterium mucogenicum
US-10-697-802A-13

Query Match 92.7%; Score 20.4; DB 10; Length 1455;
Best Local Similarity 95.5%; Pred. No. 4.7;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTCGAACGGAAGGCGCTTTCG 22
|||||
DB 34 GTCGAACGGAAGGCGCTTTCG 55

RESULT 10

US-10-697-802A-5
; Sequence 5, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 5
; LENGTH: 1482
; TYPE: DNA
; ORGANISM: Mycobacterium farcinogenes
US-10-697-802A-5

Query Match 92.7%; Score 20.4; DB 10; Length 1482;
Best Local Similarity 95.5%; Pred. No. 4.7;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTCGAACGGAAGGCGCTTTCG 22
|||||
DB 32 GTCGAACGGAAGGCGCTTTCG 53

RESULT 11

US-09-738-274-24
; Sequence 24, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer

; OTHER INFORMATION: oligonucleotide
US-09-738-274-24

Query Match 86.4%; Score 19; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAACGGAAGGCGCTTTTCGG 22
|||||
Db 1 GAACGGAAGGCGCTTTTCGG 19

RESULT 12

US-10-665-708-24
; Sequence 1, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GPI07-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-10-665-708-24

Query Match 86.4%; Score 19; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAACGGAAGGCGCTTTTCGG 22
|||||
Db 1 GAACGGAAGGCGCTTTTCGG 19

RESULT 13

US-10-522-454-1
; Sequence 1, Application US/10522454
; Publication No. US20050244938A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Russell T.
; APPLICANT: Hamann, Mark T.
; APPLICANT: Peraud, Olivier
; APPLICANT: Kasaanah, Noer
; TITLE OF INVENTION: MANZAMINE-PRODUCING ACTINOMYCETES
; FILE REFERENCE: 4115-180
; CURRENT APPLICATION NUMBER: US/10/522,454
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: PCT/USO3/24238
; PRIOR FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 1403
; TYPE: DNA
; ORGANISM: Actinomyces sp.
US-10-522-454-1

Query Match 85.5%; Score 18.8; DB 10; Length 1403;
Best Local Similarity 90.9%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTTCGG 22
|||||
Db 29 GTCGAGCGGAAGGCGCTTCGG 50

RESULT 14

US-11-035-296-1
; Sequence 1, Application US/11035296
; Publication No. US20050203005A1
; GENERAL INFORMATION:
; APPLICANT: VICURON PHARMACEUTICALS INC.
; APPLICANT: LAZZARINI, Ameriga
; APPLICANT: GASTALDO, Luciano
; APPLICANT: CANDIANI, Gianpaolo
; APPLICANT: CICILIATO, Ismaela
; APPLICANT: LOSI, Daniele
; APPLICANT: MARINELLI, Flavia
; APPLICANT: SELVA, Enrico
; APPLICANT: PARENTI, Franco
; TITLE OF INVENTION: ANTIBIOTIC 107891, ITS FACTORS A1 AND A2, PHARMACEUTICALLY
; FILE REFERENCE: 892,280-195
; CURRENT APPLICATION NUMBER: US/11/035,296
; CURRENT FILING DATE: 2005-01-12
; PRIOR APPLICATION NUMBER: US 10/521,336
; PRIOR FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: PCT/EP2004/007658
; PRIOR FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: EP 03016306.7
; PRIOR FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Microbispora sp. ATCC PTA-5024
US-11-035-296-1

Query Match 85.5%; Score 18.8; DB 13; Length 1443;
Best Local Similarity 90.9%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTTCGG 22
|||||
Db 34 GTCGAGCGGAAGGCGCTTCGG 55

RESULT 15

US-11-045-628-1
; Sequence 1, Application US/11045628
; Publication No. US20050233952A1
; GENERAL INFORMATION:
; APPLICANT: VICURON PHARMACEUTICALS INC.
; APPLICANT: LAZZARINI, Ameriga
; APPLICANT: GASTALDO, Luciano
; APPLICANT: CANDIANI, Gianpaolo
; APPLICANT: CICILIATO, Ismaela
; APPLICANT: LOSI, Daniele
; APPLICANT: MARINELLI, Flavia
; APPLICANT: SELVA, Enrico
; APPLICANT: PARENTI, Franco
; TITLE OF INVENTION: ANTIBIOTIC 107891, ITS FACTORS A1 AND A2, PHARMACEUTICALLY
; FILE REFERENCE: 892,280-500
; CURRENT APPLICATION NUMBER: US/11/045,628
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: US 11/035,296
; PRIOR FILING DATE: 2005-01-12

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; PRIOR APPLICATION NUMBER: US 10/521,336
; PRIOR FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: PCT/EP2004/007658
; PRIOR FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: EP 03016306.7
; PRIOR FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Microbispora sp. ATCC PTA-5024
US-11-045-628-1

Query Match      85.5%; Score 18.8; DB 13; Length 1443;
Best Local Similarity 90.9%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1  GTCGAACGGAAGGCTTTCGG 22
      ||||| ||||| ||||| |||||
Db  34  GTCGAGCGGAAGGCTTTCGG 55

RESULT 16
US-10-697-802A-7
; Sequence 7, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 7
; LENGTH: 1461
; TYPE: DNA
; ORGANISM: Mycobacterium goodnae
US-10-697-802A-7

Query Match      85.5%; Score 18.8; DB 10; Length 1461;
Best Local Similarity 90.9%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1  GTCGAACGGAAGGCTTTCGG 22
      ||||| ||||| ||||| |||||
Db  24  GTCGAACGTAAGGCTTTCGG 45

RESULT 17
US-11-228-416-5
; Sequence 5, Application US/11228416
; Publication No. US20060008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1480
; TYPE: DNA
; ORGANISM: Salinospora sp. CNH898 16S ribosomal RNA gene, partial sequence
```

```
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1423)..(1423)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
US-11-228-416-5

Query Match      85.5%; Score 18.8; DB 16; Length 1480;
Best Local Similarity 90.9%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1  GTCGAACGGAAGGCTTTCGG 22
      ||||| ||||| ||||| |||||
Db  54  GTCGAGCGGAAGGCTTTCGG 75

RESULT 18
US-11-228-416-6
; Sequence 6, Application US/11228416
; Publication No. US20060008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1480
; TYPE: DNA
; ORGANISM: Salinospora sp. CNH440 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1423)..(1423)
```


; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
US-11-228-416-6

Query Match 85.5%; Score 18.8; DB 16; Length 1480;

Best Local Similarity 90.9%; Pred. No. 30; Mismatches 2; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCCCTTCGG 22
|||||

Db 54 GTCGAGCGGAAAGCCCTTCGG 75

RESULT 19

US-11-228-416-8

; Sequence 8, Application US/11228416

; Publication No. US20060008852A1

; GENERAL INFORMATION:

; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO

; APPLICANT: FENICAL, William

; APPLICANT: JENSEN, Paul R.

; APPLICANT: MINCER, Tracy J.

; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO

; FILE REFERENCE: UCSD1630-1

; CURRENT APPLICATION NUMBER: US/11/228,416

; CURRENT FILING DATE: 2005-09-15

; PRIOR APPLICATION NUMBER: US/09/991,518B

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: US 60/249,356

; PRIOR FILING DATE: 2000-11-16

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8

; LENGTH: 1480

; TYPE: DNA

; ORGANISM: Salinospora sp. CNH725 16S ribosomal RNA gene, partial sequence

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (198)..(198)

; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (351)..(351)

; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (442)..(442)

; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (443)..(443)

; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1423)..(1423)

; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA

US-11-228-416-8

Query Match

Best Local Similarity 85.5%; Score 18.8; DB 16; Length 1480;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCCCTTCGG 22

|||||

Db 54 GTCGAGCGGAAAGCCCTTCGG 75

RESULT 20

US-11-228-416-9

; Sequence 9, Application US/11228416

; Publication No. US20060008852A1

; GENERAL INFORMATION:

; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO

; APPLICANT: FENICAL, William

; APPLICANT: JENSEN, Paul R.

; APPLICANT: MINCER, Tracy J.

; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO

; FILE REFERENCE: UCSD1630-1

; CURRENT APPLICATION NUMBER: US/11/228,416

; CURRENT FILING DATE: 2005-09-15

; PRIOR APPLICATION NUMBER: US/09/991,518B

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: US 60/249,356

; PRIOR FILING DATE: 2000-11-16

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 9

; LENGTH: 1480

; TYPE: DNA

; ORGANISM: Salinospora sp. CNH964 16S ribosomal RNA gene, partial sequence

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (198)..(198)

; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (351)..(351)

; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (442)..(442)

; OTHER INFORMATION: n is signature nucleotide t position 467 of 16S rDNA

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (443)..(443)

; OTHER INFORMATION: n is signature nucleotide t position 468 of 16S rDNA

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1423)..(1423)

; OTHER INFORMATION: n is signature nucleotide g position 1456 of 16S rDNA

US-11-228-416-9

Query Match

Best Local Similarity 85.5%; Score 18.8; DB 16; Length 1480;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCCCTTCGG 22

|||||

Db 54 GTCGAGCGGAAAGCCCTTCGG 75

RESULT 21

US-11-228-416-3

; Sequence 3, Application US/11228416

; Publication No. US20060008852A1

; GENERAL INFORMATION:

; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO

; APPLICANT: FENICAL, William

; APPLICANT: JENSEN, Paul R.

; APPLICANT: MINCER, Tracy J.

; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO

; FILE REFERENCE: UCSD1630-1

; CURRENT APPLICATION NUMBER: US/11/228,416

; CURRENT FILING DATE: 2005-09-15

; PRIOR APPLICATION NUMBER: US/09/991,518B

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: US 60/249,356

; PRIOR FILING DATE: 2000-11-16

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 1481

; TYPE: DNA

; ORGANISM: Salinospora sp. CNH643 16S ribosomal RNA gene, partial sequence

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (198)..(198)

OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: (352)..(352)
OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: (443)..(443)
OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: (444)..(444)
OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1424)..(1424)
OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
US-11-228-416-3

Query Match 85.5%; Score 18.8; DB 16; Length 1481;
Best Local Similarity 90.9%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GTCGACGGAAGGCCCTTCGG 22
Db 54 GTCGAGCGGAAGGCCCTTCGG 75

RESULT 22
US-11-228-416-4
; Sequence 4, Application US/11228416
; Publication No. US2006000852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1482
; TYPE: DNA
; ORGANISM: Salinospora sp. CNH646 16S ribosomal RNA gene, partial sequence
; FEATURE:
NAME/KEY: misc_feature
LOCATION: (198)..(198)
OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: (351)..(351)
OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: (442)..(442)
OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: (443)..(443)
OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1425)..(1425)
OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
US-11-228-416-4

Query Match 85.5%; Score 18.8; DB 16; Length 1482;
Best Local Similarity 90.9%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GTCGACGGAAGGCCCTTCGG 22
Db 54 GTCGAGCGGAAGGCCCTTCGG 75

RESULT 23
US-11-228-416-7
; Sequence 7, Application US/11228416
; Publication No. US2006000852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1483
; TYPE: DNA
; ORGANISM: Salinospora sp. CNH536 16S ribosomal RNA gene, partial sequence
; FEATURE:
NAME/KEY: misc_feature
LOCATION: (198)..(198)
OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: (351)..(351)
OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: (443)..(443)
OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: (444)..(444)
OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1426)..(1426)
OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
US-11-228-416-7

Query Match 85.5%; Score 18.8; DB 16; Length 1483;
Best Local Similarity 90.9%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GTCGACGGAAGGCCCTTCGG 22
Db 54 GTCGAGCGGAAGGCCCTTCGG 75

RESULT 24
US-10-230-026-6
; Sequence 6, Application US/10230026
; Publication No. US20030124695A1
; GENERAL INFORMATION:
; APPLICANT: MICHAEL G. BRAMUCCI
; APPLICANT: PATRICIA C. BRZOSTOWICZ
; APPLICANT: KRISTY N. KOSTICHKA
; APPLICANT: VASANTHA NAGARAJAN
; APPLICANT: PIERRE E. ROUVIERE

```
; APPLICANT: STUART M. THOMAS
; TITLE OF INVENTION: GENES ENCODING BAAYER-VILLIGER MONOOXYGENASES
; FILE REFERENCE: C11789 US NA
; CURRENT APPLICATION NUMBER: US/10/230,026
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 60/315,546
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 1439
; TYPE: DNA
; ORGANISM: Rhodococcus erythropolis AN12
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1417)..(1417)
; OTHER INFORMATION: N = G or A or T or C
US-10-230-026-6
Query Match      80.9%; Score 17.8; DB 7; Length 1439;
Best Local Similarity 90.5%; Pred. No. 97;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2  TCGAACGGAAGGCGCTTTTCGG 22
Db  36  TCGAGCGGTAAGGCGCTTTTCGG 56

RESULT 25
US-10-486-307-6
; Sequence 6, Application US/10486307
; Publication No. US20040267001A1
; GENERAL INFORMATION:
; APPLICANT: E. I. duPont de Nemours, Inc.
; TITLE OF INVENTION: GENES ENCODING BAAYER-VILLIGER MONOOXYGENASES
; FILE REFERENCE: C11789 PCT
; CURRENT APPLICATION NUMBER: US/10/486,307
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: 60/315,546
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 1439
; TYPE: DNA
; ORGANISM: Rhodococcus erythropolis AN12
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1417)..(1417)
; OTHER INFORMATION: N = G or A or T or C
US-10-486-307-6
Query Match      80.9%; Score 17.8; DB 9; Length 1439;
Best Local Similarity 90.5%; Pred. No. 97;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2  TCGAACGGAAGGCGCTTTTCGG 22
Db  36  TCGAGCGGTAAGGCGCTTTTCGG 56

RESULT 26
US-10-220-212A-31
; Sequence 31, Application US/10220212A
; Publication No. US20040110129A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America as represented by the
; APPLICANT: Secretary, Department of Health & Human Services, the National Institutes
; APPLICANT: Health
; APPLICANT: Beckman Coulter, Inc.
; TITLE OF INVENTION: Multiplex Hybridization System for the Identification of Pathogen
; TITLE OF INVENTION: Mycobacterium and Method of Use
; FILE REFERENCE: 4239-58135
```

```
; CURRENT APPLICATION NUMBER: US/10/220,212A
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/186,840
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mycobacterium-specific oligonucleotide
US-10-220-212A-31
Query Match      79.1%; Score 17.4; DB 8; Length 25;
Best Local Similarity 94.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  4  GAACGGAAGGCGCTTTTCGG 22
Db  1  GAACGGAAGGCGCTTTTCGG 19

RESULT 27
US-10-220-212A-33
; Sequence 33, Application US/10220212A
; Publication No. US20040110129A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America as represented by the
; APPLICANT: Secretary, Department of Health & Human Services, the National Institutes
; APPLICANT: Health
; APPLICANT: Beckman Coulter, Inc.
; TITLE OF INVENTION: Multiplex Hybridization System for the Identification of Pathogen
; FILE REFERENCE: 4239-58135
; CURRENT APPLICATION NUMBER: US/10/220,212A
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/186,840
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mycobacterium-specific oligonucleotide
US-10-220-212A-33
Query Match      79.1%; Score 17.4; DB 8; Length 25;
Best Local Similarity 94.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  4  GAACGGAAGGCGCTTTTCGG 22
Db  1  GAACGGAAGGCGCTTTTCGG 19

RESULT 28
US-09-738-972-7
; Sequence 7, Application US/09738972
; Patent No. US20020012918A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
```

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: primer
US-09-738-972-7

Query Match          79.1%; Score 17.4; DB 3; Length 32;
Best Local Similarity 94.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19
    |||||
Db 5 GTCGAACGGAAGGCCTCT 23
    |||||

RESULT 29
US-09-738-972-14/c
; Sequence 14, Application US/09738972
; Patent No. US20020012918A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; TITLE OF INVENTION: AVIUM COMPLEX SPECIES
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: probe
US-09-738-972-14

Query Match          79.1%; Score 17.4; DB 3; Length 32;
Best Local Similarity 94.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19
    |||||
Db 28 GTCGAACGGAAGGCCTCT 10
    |||||

RESULT 30
US-10-862-026-7
; Sequence 7, Application US/10862026
; Publication No. US20040224348A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; TITLE OF INVENTION: AVIUM COMPLEX SPECIES
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/10/862,026
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: primer
US-10-862-026-7

Query Match          79.1%; Score 17.4; DB 9; Length 32;
Best Local Similarity 94.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19
    |||||
Db 5 GTCGAACGGAAGGCCTCT 23
    |||||

RESULT 31
US-10-862-026-14/c
; Sequence 14, Application US/10862026
; Publication No. US20040224348A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; TITLE OF INVENTION: AVIUM COMPLEX SPECIES
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/10/862,026
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: probe
US-10-862-026-14

Query Match          79.1%; Score 17.4; DB 9; Length 32;
Best Local Similarity 94.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19
    |||||
Db 28 GTCGAACGGAAGGCCTCT 10
    |||||

RESULT 32
US-10-478-633A-23
; Sequence 23, Application US/10478633A
; Publication No. US20050059000A1
; GENERAL INFORMATION:
; APPLICANT: TAKARA BIO INC.
; TITLE OF INVENTION: A stabilization method and a preservation method for a reagent fo
; FILE REFERENCE: 663232
; CURRENT APPLICATION NUMBER: US/10/478,633A
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: JP 2001-177737
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2001-249689
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 23
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-10-478-633A-23

Query Match          79.1%; Score 17.4; DB 10; Length 560;
Best Local Similarity 94.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 GTCGAACGGAAGGCCTTT 19
Db 34 GTCGAACGGAAGGCCTCT 52

RESULT 33
US-10-697-802A-12
; Sequence 12, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 12
; LENGTH: 1421
; TYPE: DNA
; ORGANISM: Mycobacterium lentiflavum
US-10-697-802A-12

Query Match 79.1%; Score 17.4; DB 10; Length 1421;
Best Local Similarity 94.7%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19
Db 24 GTCGAACGGAAGGCCTCT 42

RESULT 34
US-10-697-802A-2
; Sequence 2, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 2
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-10-697-802A-2

Query Match 79.1%; Score 17.4; DB 10; Length 1454;
Best Local Similarity 94.7%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19
Db 34 GTCGAACGGAAGGCCTCT 52

RESULT 35
US-10-029-397A-32
; Sequence 32, Application US/10029397A
; Publication No. US20030175709A1
; GENERAL INFORMATION:
; APPLICANT: MURPHY, GEORGE L.
; APPLICANT: WHITLEY, J. PENN
; TITLE OF INVENTION: METHOD AND SYSTEM FOR DEPLETING rRNA POPULATIONS
; FILE REFERENCE: AMBI-076US
; CURRENT APPLICATION NUMBER: US/10/029,397A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 32
; LENGTH: 1465
; TYPE: DNA
; ORGANISM: Mycobacterium avium
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (298)..(881)
; OTHER INFORMATION: N = A, C, G or T/U
US-10-029-397A-32

Query Match 79.1%; Score 17.4; DB 7; Length 1465;
Best Local Similarity 94.7%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19
Db 24 GTCGAACGGAAGGCCTCT 42

RESULT 36
US-09-925-065A-544396
; Sequence 544396, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 544396
; LENGTH: 513
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-544396

Query Match 78.2%; Score 17.2; DB 4; Length 513;
Best Local Similarity 86.4%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTTCGG 22
Db 223 GTCGAAGGGAAGGCCATTCCG 244

RESULT 37
US-09-925-065A-544397
; Sequence 544397, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
```

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RESULT 39
US-09-925-065A-544397
; Sequence 544397, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24

```

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RESULT 41
US-10-027-632-292604
; Sequence 292604, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome

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Qy 1 GTCGAACGGAAAGGCCTTTTCGG 22

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; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 292605

```



```
; GENERAL INFORMATION:
; APPLICANT: Korea Chungang Educational Foundation
; APPLICANT: Hwang, Byong Kook
; APPLICANT: Lee, Jung Yeop
; TITLE OF INVENTION: Thiobactin and Antifungal Composition for Controlling Plant
; TITLE OF INVENTION: Diseases Using the Same
; FILE REFERENCE: 4228-102
; CURRENT APPLICATION NUMBER: US/10/756,683
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: KP 10-2003-0015628
; PRIOR FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: KP 10-2003-0015629
; PRIOR FILING DATE: 2003-03-13
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1488
; TYPE: DNA
; ORGANISM: Lechevalieria aerocolonigenes
US-10-756-683-1

Query Match          78.2%; Score 17.2; DB 9; Length 1488;
Best Local Similarity 86.4%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCCCTTCGG 22
   ||||| ||||| ||||| ||||| |||||
Db 46 GTCGAGCGGTAAGGCCCTTCGG 67

RESULT 50
US-10-875-161-2
; Sequence 2, Application US/10875161
; Publication No. US20050009151A1
; GENERAL INFORMATION:
; APPLICANT: Chase, Matthew
; APPLICANT: Clayton, Robert
; APPLICANT: Landis, Bryan
; APPLICANT: Banerjee, Amit
; TITLE OF INVENTION: Methods for the Stereoselective Synthesis and Enantiomeric
; TITLE OF INVENTION: Enrichment of Beta-Amino Acids
; FILE REFERENCE: SO-3262-2-PR-US
; CURRENT APPLICATION NUMBER: US/10/875,161
; CURRENT FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 1514
; TYPE: DNA
; ORGANISM: Rhodococcus opacus
; FEATURE:
; NAME/KEY: rRNA
; LOCATION: (1)..(1514)
; OTHER INFORMATION: 16s rRNA gene (rDNA) from Rhodococcus opacus
; FEATURE:
; NAME/KEY: misc difference
; LOCATION: (1)..(1514)
; OTHER INFORMATION: Alignment 0.17% different from 16s rRNA gene (rDNA) of
; OTHER INFORMATION: Rhodococcus opacus
US-10-875-161-2

Query Match          78.2%; Score 17.2; DB 9; Length 1514;
Best Local Similarity 86.4%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCCCTTCGG 22
   ||||| ||||| ||||| ||||| |||||
Db 57 GTCGAGCGGTAAGGCCCTTCGG 78

RESULT 51
US-10-831-286A-1517
; Sequence 1517, Application US/10831286A
```

```
; Publication No. US20060046246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, QIANDONG
; APPLICANT: CHATELLIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001
; CURRENT APPLICATION NUMBER: US/10/831,286A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/464,955
; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1517
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Corynebacterium diphtheriae
US-10-831-286A-1517

Query Match          77.3%; Score 17; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGGCCT 17
   ||||| ||||| ||||| |||||
Db 4  GTCGAACGGAAAGGCCT 20

RESULT 52
US-10-831-286A-8212
; Sequence 8212, Application US/10831286A
; Publication No. US20060046246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, QIANDONG
; APPLICANT: CHATELLIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001
; CURRENT APPLICATION NUMBER: US/10/831,286A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/464,955
; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8212
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Corynebacterium kutscheri
US-10-831-286A-8212

Query Match          74.5%; Score 16.4; DB 11; Length 30;
Best Local Similarity 94.4%; Pred. No. 4.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGGCCTT 18
   ||||| ||||| ||||| |||||
Db 4  GTCGAACGGAAAGGCCTT 21

RESULT 53
US-10-062-674-613/c
; Sequence 613, Application US/10062674
; Publication No. US20040005559A1
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.
; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
; FILE REFERENCE: PA-0026-1 CIP
; CURRENT APPLICATION NUMBER: US/10/062,674
; CURRENT FILING DATE: 2002-01-30
```

; PRIOR APPLICATION NUMBER: US 09/625,102
; PRIOR FILING DATE: 2000-07-24
; NUMBER OF SEQ ID NOS: 2217
; SOFTWARE: PERL Program
; SEQ ID NO 613
; LENGTH: 367
; TYPE: DNA
; ORGANISM: Mus musculus
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040005559A1 g2292157
US-10-062-674-613

Query Match 73.6%; Score 16.2; DB 7; Length 367;
Best Local Similarity 85.7%; Pred. No. 6.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTCG 22
| | | | | | | | | | | | | | | | | |
Db 39 TTGAATGGAGAGCGCTTTCG 19

RESULT 54

US-10-767-701-31297
; Sequence 31297, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 31297
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 18066455
US-10-767-701-31297

Query Match 73.6%; Score 16.2; DB 8; Length 622;
Best Local Similarity 85.7%; Pred. No. 6.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTCG 21
| | | | | | | | | | | | | | | | | |
Db 32 GTCGAGAGGAATGGCGCTTTCG 52

RESULT 55

US-10-425-115-59269
; Sequence 59269, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 59269
; LENGTH: 635
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 18066455
US-10-767-701-31297

; OTHER INFORMATION: Clone ID: MRT4577_15404C.1
US-10-425-115-59269

Query Match 73.6%; Score 16.2; DB 9; Length 635;
Best Local Similarity 85.7%; Pred. No. 6.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTCG 22
| | | | | | | | | | | | | | | | | |
Db 452 TTGAGCGGAAGGCGCTTTCG 472

RESULT 56

US-10-831-286A-12801
; Sequence 12801, Application US/10831286A
; Publication No. US20060046246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, QIANDONG
; APPLICANT: CHATELLIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001
; CURRENT APPLICATION NUMBER: US/10/831,286A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/464,955
; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12801
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Corynebacterium ulcerans
US-10-831-286A-12801

Query Match 72.7%; Score 16; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16
| | | | | | | | | | | | | | | | | |
Db 5 GTCGAACGGAAGGCC 20

RESULT 57

US-10-831-286A-23905
; Sequence 23905, Application US/10831286A
; Publication No. US20060046246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, QIANDONG
; APPLICANT: CHATELLIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001
; CURRENT APPLICATION NUMBER: US/10/831,286A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/464,955
; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23905
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Corynebacterium ulcerans
US-10-831-286A-23905

Query Match 72.7%; Score 16; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16
| | | | | | | | | | | | | | | | | |
Db 4 GTCGAACGGAAGGCC 19

RESULT 58

US-09-738-274-27
; Sequence 27, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-27

Query Match 72.7%; Score 16; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16
| | | | | | | | | | | | | | | | | |
Db 4 GTCGAACGGAAGGCC 19

RESULT 59

US-10-665-708-27
; Sequence 27, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-10-665-708-27

Query Match 72.7%; Score 16; DB 10; Length 23;

Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16
| | | | | | | | | | | | | | | | | |
Db 4 GTCGAACGGAAGGCC 19

RESULT 60

US-09-738-274-28
; Sequence 28, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-28

Query Match 72.7%; Score 16; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16
| | | | | | | | | | | | | | | | | |
Db 1 GTCGAACGGAAGGCC 16

RESULT 61

US-10-665-708-28
; Sequence 28, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide

US-10-665-708-28

Query Match 72.7%; Score 16; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16
|||||
Db 1 GTCGAACGGAAGGCC 16

RESULT 62

US-10-830-943-11
; Sequence 11, Application US/10830943
; Publication No. US2005009053A1
; GENERAL INFORMATION:
; APPLICANT: Boecker, Sebastian
; APPLICANT: van den Boom, Dirk
; TITLE OF INVENTION: FRAGMENTATION-BASED METHODS AND SYSTEMS
; TITLE OF INVENTION: FOR DE NOVO SEQUENCING
; FILE REFERENCE: 17082-079001
; CURRENT APPLICATION NUMBER: US/10/830,943
; CURRENT FILING DATE: 2004-04-22
; PRIOR APPLICATION NUMBER: US 60/466,006
; PRIOR FILING DATE: 2003-04-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: amplicon sequence

US-10-830-943-11

Query Match 72.7%; Score 16; DB 9; Length 80;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16
|||||
Db 54 GTCGAACGGAAGGCC 69

RESULT 63

US-10-478-633A-24
; Sequence 24, Application US/10478633A
; Publication No. US2005005900A1
; GENERAL INFORMATION:
; APPLICANT: TAKARA BIO INC.
; TITLE OF INVENTION: A stabilization method and a preservation method for a reagent for
; TITLE OF INVENTION: acid amplification or detection reaction
; FILE REFERENCE: 663232
; CURRENT APPLICATION NUMBER: US/10/478,633A
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: JP 2001-177737
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2001-249689
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 24
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Mycobacterium intracellulare

US-10-478-633A-24

Query Match 72.7%; Score 16; DB 10; Length 560;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16
|||||
Db 46 GTCGAACGGAAGGCC 61

RESULT 64

US-10-779-543-8365
; Sequence 8365, Application US/10779543
; Publication No. US20050227917A1
; GENERAL INFORMATION:
; APPLICANT: Williams et al
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
; FILE REFERENCE: 2300-21302
; CURRENT APPLICATION NUMBER: US/10/779,543
; CURRENT FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 10/076,555
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 09/217,471
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/068,755
; PRIOR FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: 60/080,664
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/105,234
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 09/297,648
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: PCT/US99/01619
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: 60/072,910
; PRIOR FILING DATE: 1998-01-28
; PRIOR APPLICATION NUMBER: 60/075,954
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/080,114
; PRIOR FILING DATE: 1998-03-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 23767
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8365
; LENGTH: 935
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 13, 17, 18, 20, 21, 25, 35, 37, 43, 46, 48, 52, 57, 81, 89,
; LOCATION: 108, 116, 127, 138, 139, 142, 144, 168, 169, 172, 178, 179,
; LOCATION: 184, 185, 204, 222, 231, 234, 242, 248, 258, 263, 279, 287,
; LOCATION: 291, 304, 310, 317, 319, 328, 335, 337, 350, 357, 362
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 363, 365, 375, 387, 390, 391, 401, 433, 434, 436, 455, 460,
; LOCATION: 468, 476, 479, 489, 495, 500, 502, 506, 515, 529, 530, 534,
; LOCATION: 543, 553, 563, 564, 565, 566, 592, 627, 628, 631, 642, 645,
; LOCATION: 650, 653, 662, 668, 670, 680, 681, 682, 684, 685, 691
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 696, 703, 707, 741, 745, 752, 756, 763, 767, 770, 771, 779,
; LOCATION: 795, 823, 824, 829, 830, 846, 850, 854, 855, 873, 874, 878,
; LOCATION: 887, 890, 894, 907, 910, 920, 922, 929, 935
; OTHER INFORMATION: n = A,T,C or G

US-10-779-543-8365

Query Match 72.7%; Score 16; DB 10; Length 935;
Best Local Similarity 84.2%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GAACGGAAGCCCTTCGG 22
|||||
Db 452 GAAGGAAGCCCTTTNGG 470

RESULT 65

US-10-697-802A-11

```
; Sequence 11, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 11
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Mycobacterium kubicacae
US-10-697-802A-11

Query Match          72.7%; Score 16; DB 10; Length 1321;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GTCGAACGGAAAGGCC 16
        |||||
Db      18  GTCGAACGGAAAGGCC 33

RESULT 66
US-10-697-802A-14
; Sequence 14, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 14
; LENGTH: 1415
; TYPE: DNA
; ORGANISM: Mycobacterium paraffinicum
US-10-697-802A-14

Query Match          72.7%; Score 16; DB 10; Length 1415;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GTCGAACGGAAAGGCC 16
        |||||
Db      19  GTCGAACGGAAAGGCC 34

RESULT 67
US-10-062-777-1
; Sequence 1, Application US/10062777
; Publication No. US20020119514A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: A PROCESS FOR PRODUCING A BRAN PICKLES FLAVORING SOLUTION
; FILE REFERENCE: 11142W0
; CURRENT APPLICATION NUMBER: US/10/062,777
; CURRENT FILING DATE: 2002-02-05
; PRIOR FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/463,618
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Corynebacterium sp.NK-1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (166)
; OTHER INFORMATION: n is "a" or "g" or "c" or "t".
US-10-062-777-1

Query Match          72.7%; Score 16; DB 6; Length 1460;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GTCGAACGGAAAGGCC 16
        |||||
Db      42  GTCGAACGGAAAGGCC 57

RESULT 68
US-10-419-095-1
; Sequence 1, Application US/10419095
; Publication No. US20030162244A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: A PROCESS FOR PRODUCING A BRAN PICKLES FLAVORING SOLUTION
; FILE REFERENCE: 11142W0
; CURRENT APPLICATION NUMBER: US/10/419,095
; CURRENT FILING DATE: 2003-04-21
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: H10-166226
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Corynebacterium sp.NK-1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (166)
; OTHER INFORMATION: n is "a" or "g" or "c" or "t".
US-10-419-095-1

Query Match          72.7%; Score 16; DB 7; Length 1460;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GTCGAACGGAAAGGCC 16
        |||||
Db      42  GTCGAACGGAAAGGCC 57

RESULT 69
US-10-697-802A-16
; Sequence 16, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 16
; LENGTH: 1462
; TYPE: DNA
; ORGANISM: Mycobacterium szulgai
US-10-697-802A-16

Query Match          72.7%; Score 16; DB 10; Length 1462;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GTCGAACGGAAAGGCC 16
        |||||
Db      24  GTCGAACGGAAAGGCC 39
```

```
RESULT 70
US-10-697-802A-15
; Sequence 15, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 15
; LENGTH: 1484
; TYPE: DNA
; ORGANISM: Mycobacterium simiae
US-10-697-802A-15
Query Match 72.7%; Score 16; DB 10; Length 1484;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16
Db 24 GTCGAACGGAAGGCC 39

RESULT 71
US-10-697-802A-8
; Sequence 8, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 8
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Mycobacterium heckeshornense
US-10-697-802A-8
Query Match 72.7%; Score 16; DB 10; Length 1527;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16
Db 48 GTCGAACGGAAGGCC 63

RESULT 72
US-09-738-274-14
; Sequence 14, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-665-708-14
Query Match 71.8%; Score 15.8; DB 10; Length 32;
Best Local Similarity 89.5%; Pred. No. 9.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19
Db 5 GTCGAACGGAAGGCTCTCT 23

RESULT 73
US-10-665-708-14
; Sequence 14, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-665-708-14
Query Match 71.8%; Score 15.8; DB 10; Length 32;
Best Local Similarity 89.5%; Pred. No. 9.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19
Db 5 GTCGAACGGAAGGCTCTCT 23

RESULT 74
US-10-062-727-254
; Sequence 254, Application US/10062727
; Publication No. US20030018185A1
; GENERAL INFORMATION:
; APPLICANT: Havukala, Ilkka
; APPLICANT: Bloksberg, Leonard
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Plant Microsatellite Markers and Methods
; TITLE OF INVENTION: for their Use
; FILE REFERENCE: 11000.1006CIP
; CURRENT APPLICATION NUMBER: US/10/062,727
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 09/105,307
; PRIOR FILING DATE: 1998-06-25
```

```
; NUMBER OF SEQ ID NOS: 1057
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254
; LENGTH: 170
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
; NAME/KEY: misc feature
; LOCATION: (1)-(170)
; OTHER INFORMATION: n = A,T,C or G
US-10-062-727-254

Query Match          71.8%; Score 15.8; DB 6; Length 170;
Best Local Similarity 89.5%; Pred. No. 9.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAACGGAAAGCCCTTCGG 22
    ||| ||||| ||||| |||
Db 69 GAAGGAAAGCCCTTAGG 87

RESULT 75
US-10-062-727-376
; Sequence 376, Application US/10062727
; Publication No. US20030018185A1
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka
; APPLICANT: Bloksberg, Leonard
; TITLE OF INVENTION: Plant Microsatellite Markers and Methods
; FILE REFERENCE: 11000.1006CIP
; CURRENT APPLICATION NUMBER: US/10/062,727
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 09/105,307
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 1057
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 376
; LENGTH: 305
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-062-727-376

Query Match          71.8%; Score 15.8; DB 6; Length 305;
Best Local Similarity 89.5%; Pred. No. 9.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAACGGAAAGCCCTTCGG 22
    ||| ||||| ||||| |||
Db 70 GAAGGAAAGCCCTTAGG 88

RESULT 76
US-10-450-763-13678/c
; Sequence 13678, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 13678
; LENGTH: 381

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1)..(372)
; OTHER INFORMATION: 100% homologous to Escherichia coli K12 orf, hypothetical
; OTHER INFORMATION: protein, accession number AE000223, Smith-Waterman Score=635.
US-10-450-763-13678

Query Match          71.8%; Score 15.8; DB 10; Length 381;
Best Local Similarity 89.5%; Pred. No. 9.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCCCTTT 19
    ||| ||||| ||||| |||
Db 160 GACGAACGGAAAGCGTTT 142

RESULT 77
US-10-438-774-17
; Sequence 17, Application US/10438774
; Publication No. US20040010504A1
; GENERAL INFORMATION:
; APPLICANT: Hinrichs, Steven
; APPLICANT: Mohammed, Amr
; APPLICANT: Ali, Hesham
; APPLICANT: Kuyper, Dan
; TITLE OF INVENTION: Custom Sequence Databases and Methods of
; FILE OF INVENTION: Use Thereof
; FILE REFERENCE: UNMC.63174-US
; CURRENT APPLICATION NUMBER: US/10/438,774
; CURRENT FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: 60/381,015
; PRIOR FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-438-774-17

Query Match          71.8%; Score 15.8; DB 7; Length 468;
Best Local Similarity 89.5%; Pred. No. 9.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCCCTTT 19
    ||| ||||| ||||| |||
Db 1 GTCGAACGGAAAGGTCTCT 19

RESULT 78
US-10-450-763-3105
; Sequence 3105, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 3105
; LENGTH: 576
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (419)..(3)
; OTHER INFORMATION: 32% homologous to Santalum album proline rich
; OTHER INFORMATION: protein,accession number AF020261,Smith-Waterman score=109.
US-10-450-763-3105

Query Match          71.8%; Score 15.8; DB 10; Length 576;
Best Local Similarity 89.5%; Pred. No. 9.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAACGGAAGGCGCTTCG 22
Db 512 GAATGGAAGGCTTCGG 530

RESULT 79
US-10-301-480-442948
; Sequence 442948, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 442948
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-442948

Query Match          71.8%; Score 15.8; DB 12; Length 625;
Best Local Similarity 89.5%; Pred. No. 9.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTC 20
Db 275 TGGAAACGGAAGGCTTTC 293

RESULT 80
US-10-301-480-1056357
; Sequence 1056357, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1056357
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1056357
```

```
Query Match          71.8%; Score 15.8; DB 12; Length 625;
Best Local Similarity 89.5%; Pred. No. 9.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTC 20
Db 275 TGGAAACGGAAGGCTTTC 293

RESULT 81
US-09-925-065A-373045
; Sequence 373045, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 373045
; LENGTH: 634
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-373045

Query Match          71.8%; Score 15.8; DB 4; Length 634;
Best Local Similarity 89.5%; Pred. No. 9.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTC 20
Db 284 TGGAAACGGAAGGCTTTC 302

RESULT 82
US-09-925-065A-373045
; Sequence 373045, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 373045
; LENGTH: 634
; TYPE: DNA
```



```
; ORGANISM: Homo sapiens
US-09-925-065A-373045

Query Match      71.8%; Score 15.8; DB 5; Length 634;
Best Local Similarity 89.5%; Pred. No. 9.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 TCGAACGGAAGGCGCTTC 20
      | ||||| ||||| |||||
DB      284 TCGAACGGAAGGCTCTTC 302

RESULT 83
US-10-697-802A-17
; Sequence 17, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 17
; LENGTH: 1416
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-697-802A-17

Query Match      71.8%; Score 15.8; DB 10; Length 1416;
Best Local Similarity 89.5%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GTCGAACGGAAGGCGCTTT 19
      | ||||| ||||| |||||
DB      24 GTCGAACGGAAGGTCTCT 42

RESULT 84
US-10-697-802A-3
; Sequence 3, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 3
; LENGTH: 1421
; TYPE: DNA
; ORGANISM: Mycobacterium bovis
US-10-697-802A-3

Query Match      71.8%; Score 15.8; DB 10; Length 1421;
Best Local Similarity 89.5%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GTCGAACGGAAGGCGCTTT 19
      | ||||| ||||| |||||
DB      24 GTCGAACGGAAGGTCTCT 42

RESULT 85
US-10-697-802A-10
; Sequence 10, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
```

```
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 10
; LENGTH: 1463
; TYPE: DNA
; ORGANISM: Mycobacterium kansasii
US-10-697-802A-10

Query Match      71.8%; Score 15.8; DB 10; Length 1463;
Best Local Similarity 89.5%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GTCGAACGGAAGGCGCTTT 19
      | ||||| ||||| |||||
DB      23 GTCGAACGGAAGGTCTCT 41

RESULT 86
US-09-726-774-7
; Sequence 7, Application US/09726774
; Patent No. US20020082226A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; TITLE OF INVENTION: Composition
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/09/726,774
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-726-774-7

Query Match      71.8%; Score 15.8; DB 3; Length 1464;
Best Local Similarity 89.5%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GTCGAACGGAAGGCGCTTT 19
      | ||||| ||||| |||||
DB      24 GTCGAACGGAAGGTCTCT 42

RESULT 87
US-10-719-633-7
; Sequence 7, Application US/10719633
; Publication No. US20040137485A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; TITLE OF INVENTION: Composition
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/10/719,633
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/09/726,774
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-719-633-7
```

```
Query Match      71.8%; Score 15.8; DB 8; Length 1464;
Best Local Similarity 89.5%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTT 19
   |||||
Db 24 GTCGAACGGAAGGCTCT 42

RESULT 88
US-10-220-212A-34
; Sequence 34, Application US/10220212A
; Publication No. US20040110129A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America as represented by the
; APPLICANT: Secretary, Department of Health & Human Services, the National Institutes
; APPLICANT: Health
; APPLICANT: Beckman Coulter, Inc.
; TITLE OF INVENTION: Multiplex Hybridization System for the Identification of Pathogen
; FILE REFERENCE: 4239-58135
; CURRENT APPLICATION NUMBER: US/10/220,212A
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/186,840
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-220-212A-34

Query Match      71.8%; Score 15.8; DB 8; Length 1524;
Best Local Similarity 89.5%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTT 19
   |||||
Db 54 GTCGAACGGAAGGCTCT 72

RESULT 89
US-10-029-397A-33
; Sequence 33, Application US/10029397A
; Publication No. US20030175709A1
; GENERAL INFORMATION:
; APPLICANT: MURPHY, GEORGE L.
; APPLICANT: WHITLEY, J. PENN
; TITLE OF INVENTION: METHOD AND SYSTEM FOR DEPLETING rRNA POPULATIONS
; FILE REFERENCE: AMBI:076US
; CURRENT APPLICATION NUMBER: US/10/029,397A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-029-397A-33

Query Match      71.8%; Score 15.8; DB 7; Length 1536;
Best Local Similarity 89.5%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTT 19
   |||||
Db 63 GTCGAACGGAAGGCTCT 81

RESULT 90
US-10-029-397A-34
; Sequence 34, Application US/10029397A
```

```
; Publication No. US20030175709A1
; GENERAL INFORMATION:
; APPLICANT: MURPHY, GEORGE L.
; APPLICANT: WHITLEY, J. PENN
; TITLE OF INVENTION: METHOD AND SYSTEM FOR DEPLETING rRNA POPULATIONS
; FILE REFERENCE: AMBI:076US
; CURRENT APPLICATION NUMBER: US/10/029,397A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-029-397A-34

Query Match      71.8%; Score 15.8; DB 7; Length 1536;
Best Local Similarity 89.5%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTT 19
   |||||
Db 63 GTCGAACGGAAGGCTCT 81

RESULT 91
US-10-488-528-3
; Sequence 3, Application US/10488528
; Publication No. US20050119459A1
; GENERAL INFORMATION:
; APPLICANT: Kaplan, Feige
; APPLICANT: Swezey, Neil B.
; TITLE OF INVENTION: Late Gestation Lung Genes, Fragments and Uses Thereof
; FILE REFERENCE: 457-110pct
; CURRENT APPLICATION NUMBER: US/10/488,528
; CURRENT FILING DATE: 2004-03-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2896
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (32)...(1525)
US-10-488-528-3

Query Match      71.8%; Score 15.8; DB 10; Length 2896;
Best Local Similarity 89.5%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAACGGAAGGCGCTTTCGG 22
   |||||
Db 1486 GAACGGAAGGCTTTCGG 1504

RESULT 92
US-10-369-493-35634/c
; Sequence 35634, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR-FILING DATE: 2002-02-21
```

```
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 35634
; LENGTH: 2919
; TYPE: DNA
; ORGANISM: Mesorhizobium loti
US-10-369-493-35634

Query Match          71.8%; Score 15.8; DB 7; Length 2919;
Best Local Similarity 89.5%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGCCCTTT 19
| | | | | | | | | | | | | | | | | | | | |
Db 2382 GCGCAACGCAAGGCCCTTT 2364

RESULT 93
US-10-488-528-1
; Sequence 1, Application US/10488528
; Publication No. US20050119459A1
; GENERAL INFORMATION:
; APPLICANT: Kaplan, Feige
; APPLICANT: Swezey, Neil B.
; TITLE OF INVENTION: Late Gestation Lung Genes, Fragments and Uses Thereof
; FILE REFERENCE: 457-110pct
; CURRENT APPLICATION NUMBER: US/10/488,528
; CURRENT FILING DATE: 2004-03-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3054
; TYPE: DNA
; ORGANISM: rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (86)...(1576)
US-10-488-528-1

Query Match          71.8%; Score 15.8; DB 10; Length 3054;
Best Local Similarity 89.5%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAACGGAAGCCCTTTCCGG 22
| | | | | | | | | | | | | | | | | | | | |
Db 1540 GAACGGAAGCCCTTTCCGG 1558

RESULT 94
US-09-764-877-3363
; Sequence 3363, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3363
; LENGTH: 6883
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3363

Query Match          71.8%; Score 15.8; DB 3; Length 6883;
Best Local Similarity 89.5%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAACGGAAGCCCTTTCCGG 22
| | | | | | | | | | | | | | | | | | | | |
Db 478 GAATGGAAGGCTCTTCGG 496

RESULT 95
US-10-242-515-3363
; Sequence 3363, Application US/10242515
; Publication No. US20040009488A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005C1
; CURRENT APPLICATION NUMBER: US/10/242,515
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/764,877
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3363
; LENGTH: 6883
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-242-515-3363

Query Match          71.8%; Score 15.8; DB 7; Length 6883;
Best Local Similarity 89.5%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAACGGAAGCCCTTTCCGG 22
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Db 478 GAATGGAAGGCTCTTCGG 496

RESULT 96
US-10-465-008-10
; Sequence 10, Application US/10465008
; Publication No. US20040016016A1
; GENERAL INFORMATION:
; APPLICANT: MANKIN, LUKE S.
; APPLICANT: DA COSTA E SILVA, OSWALDO
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING PLANT PERFORMANCE
; FILE REFERENCE: 16313-0232
; CURRENT APPLICATION NUMBER: US/10/465,008
; CURRENT FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: 60/389,982
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 21126
; TYPE: DNA
; ORGANISM: Agrobacterium rhizogenes
US-10-465-008-10

Query Match          71.8%; Score 15.8; DB 8; Length 21126;
Best Local Similarity 89.5%; Pred. No. 1e+03;
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Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTT 19
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Db 5577 GTCGAACGACAGGCTTT 5595
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RESULT 97

US-10-012-697-422/c
; Sequence 422, Application US/10012697
; Publication No. US20030215803A1

GENERAL INFORMATION:

; APPLICANT: Escobedo, Jaime
; APPLICANT: Garcia, Pablo Dominguez
; APPLICANT: Kassam, Altaf
; APPLICANT: Lamson, George
; APPLICANT: Scott, Beth
; APPLICANT: Drmanac, Radoje
; APPLICANT: Crkvenjakov, Radomir
; APPLICANT: Dickson, Mark
; APPLICANT: Drmanac, Snezana
; APPLICANT: Labat, Ivan
; APPLICANT: Leehkowitz, Dena
; APPLICANT: Kita, David
; APPLICANT: Garcia, Veronica
; APPLICANT: Jones, Lee William
; APPLICANT: Stache-Crain, Birgit

; TITLE OF INVENTION: HUMAN GENES AND GENE EXPRESSION PRODUCTS

; FILE REFERENCE: 2300-16252

; CURRENT APPLICATION NUMBER: US/10/012,697
; CURRENT FILING DATE: 2003-01-21

; PRIOR APPLICATION NUMBER: 60/254,648

; PRIOR FILING DATE: 2000-12-07

; PRIOR APPLICATION NUMBER: 60/275,668

; PRIOR FILING DATE: 2001-03-13

; NUMBER OF SEQ ID NOS: 1568

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 422

; LENGTH: 297

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 124, 150, 151, 180, 193, 218, 221, 229, 236, 237, 239, 241,

; LOCATION: 243, 250, 252, 260, 278, 281, 285, 286, 297

; OTHER INFORMATION: n = A,T,C or G

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 124, 150, 151, 180, 193, 218, 221, 229, 236, 237, 239, 241,

; LOCATION: 243, 250, 252, 260, 278, 281, 285, 286, 297

; OTHER INFORMATION: n = A,T,C or G

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 124, 150, 151, 180, 193, 218, 221, 229, 236, 237, 239, 241,

; LOCATION: 243, 250, 252, 260, 278, 281, 285, 286, 297

; OTHER INFORMATION: n = A,T,C or G

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 124, 150, 151, 180, 193, 218, 221, 229, 236, 237, 239, 241,

; LOCATION: 243, 250, 252, 260, 278, 281, 285, 286, 297

; OTHER INFORMATION: n = A,T,C or G

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 124, 150, 151, 180, 193, 218, 221, 229, 236, 237, 239, 241,

; LOCATION: 243, 250, 252, 260, 278, 281, 285, 286, 297

; OTHER INFORMATION: n = A,T,C or G

; FEATURE:

; NAME/KEY: misc_feature

; FILE REFERENCE: B1370 US NA

; CURRENT APPLICATION NUMBER: US/10/410,681

; CURRENT FILING DATE: 2003-04-10

; PRIOR APPLICATION NUMBER: US/09/585,173B

Query Match 70.9%; Score 15.6; DB 7; Length 297;

Best Local Similarity 81.8%; Pred. No. 1.2e+03;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTGG 22
|||
Db 82 GTGTACAGGAAGGCTTTGG 61
|||

RESULT 98

US-10-779-543-22422/c

; Sequence 22422, Application US/10779543

; Publication No. US20050227917A1

; GENERAL INFORMATION:

; APPLICANT: Williams et al

; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED

; FILE REFERENCE: 2300-21302

; CURRENT APPLICATION NUMBER: US/10/779,543

; CURRENT FILING DATE: 2004-02-12

; PRIOR APPLICATION NUMBER: 10/076,555

; PRIOR FILING DATE: 2002-02-15

; PRIOR APPLICATION NUMBER: 09/217,471

; PRIOR FILING DATE: 1998-12-21

; PRIOR APPLICATION NUMBER: 60/068,755

; PRIOR FILING DATE: 1997-12-23

; PRIOR APPLICATION NUMBER: 60/080,664

; PRIOR FILING DATE: 1998-04-03

; PRIOR APPLICATION NUMBER: 60/105,234

; PRIOR FILING DATE: 1998-10-21

; PRIOR APPLICATION NUMBER: 09/297,648

; PRIOR FILING DATE: 2000-04-10

; PRIOR APPLICATION NUMBER: PCT/US99/01619

; PRIOR FILING DATE: 1999-01-28

; PRIOR APPLICATION NUMBER: 60/072,910

; PRIOR FILING DATE: 1998-01-28

; PRIOR APPLICATION NUMBER: 60/075,954

; PRIOR FILING DATE: 1998-02-24

; PRIOR APPLICATION NUMBER: 60/080,114

; PRIOR FILING DATE: 1998-03-31

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 23767

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 22422

; LENGTH: 297

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 124, 150, 151, 180, 193, 218, 221, 229, 236, 237, 239, 241,

; LOCATION: 243, 250, 252, 260, 278, 281, 285, 286, 297

; OTHER INFORMATION: n = A,T,C or G

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 124, 150, 151, 180, 193, 218, 221, 229, 236, 237, 239, 241,

; LOCATION: 243, 250, 252, 260, 278, 281, 285, 286, 297

; OTHER INFORMATION: n = A,T,C or G

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 124, 150, 151, 180, 193, 218, 221, 229, 236, 237, 239, 241,

; LOCATION: 243, 250, 252, 260, 278, 281, 285, 286, 297

; OTHER INFORMATION: n = A,T,C or G

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 124, 150, 151, 180, 193, 218, 221, 229, 236, 237, 239, 241,

; LOCATION: 243, 250, 252, 260, 278, 281, 285, 286, 297

; OTHER INFORMATION: n = A,T,C or G

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 124, 150, 151, 180, 193, 218, 221, 229, 236, 237, 239, 241,

; LOCATION: 243, 250, 252, 260, 278, 281, 285, 286, 297

; OTHER INFORMATION: n = A,T,C or G

; FEATURE:

; NAME/KEY: misc_feature

; FILE REFERENCE: B1370 US NA

; CURRENT APPLICATION NUMBER: US/10/410,681

; CURRENT FILING DATE: 2003-04-10

; PRIOR APPLICATION NUMBER: US/09/585,173B

Query Match 70.9%; Score 15.6; DB 7; Length 297;

Best Local Similarity 81.8%; Pred. No. 1.2e+03;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/137,461
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 27
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Zea mays
US-10-410-681-27

Query Match      70.9%; Score 15.6; DB 7; Length 439;
Best Local Similarity 81.8%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1  GTCGACGGAAAGCCCTTCGG 22
Db      182  GTCGACGGAAAGGACTTGCGG 161

RESULT 100
US-10-932-182A-77805
; Sequence 77805, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77805
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-77805

Query Match      70.9%; Score 15.6; DB 11; Length 471;
Best Local Similarity 81.8%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1  GTCGACGGAAAGCCCTTCGG 22
Db      152  GTCCACGGAAAGCCGTCGG 173

Search completed: May 19, 2006, 06:10:29
Job time : 899.518 secs
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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 03:57:04 ; Search time 13.6506 Seconds
(without alignments)
113.711 Million cell updates/sec

Title: US-10-665-708-23

Perfect score: 22

Sequence: 1 gtcgaacggaaggccttcgg 22

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 224314 seqs, 35277956 residues

Total number of hits satisfying chosen parameters: 448623

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.6	70.9	471	7	US-11-217-529-77805 Sequence 77805, A
2	15.6	70.9	2397	7	US-11-217-529-254 Sequence 254, App
3	14.6	66.4	25	7	US-11-217-529-110320 Sequence 110320, A
4	14.6	66.4	1242	7	US-11-217-529-78935 Sequence 78935, A
5	14.6	66.4	1824	7	US-11-217-529-79690 Sequence 79690, A
6	14.6	66.4	1950	7	US-11-217-529-77876 Sequence 77876, A
7	14.4	65.5	2454	7	US-11-217-529-6038 Sequence 6038, App
8	14.2	64.5	858	7	US-11-217-529-1257 Sequence 1257, App
9	14.2	64.5	858	7	US-11-217-529-77141 Sequence 77141, A
10	14.2	64.5	1260	7	US-11-217-529-5375 Sequence 5375, App
11	14	63.6	438	7	US-11-217-529-78815 Sequence 78815, A
12	14	63.6	1224	7	US-11-217-529-3863 Sequence 3863, App
13	14	63.6	1758	7	US-11-217-529-1422 Sequence 1422, App
14	14	63.6	5900	6	US-10-505-928-182 Sequence 182, App
15	13.8	62.7	1931	1	US-09-949-925-78 Sequence 78, Appl
16	13.8	62.7	1932	1	US-09-949-925-12 Sequence 12, Appl
17	13.6	61.8	829	7	US-11-252-080-11 Sequence 11, Appl
18	13.6	61.8	903	7	US-11-217-529-4440 Sequence 4440, App
19	13.6	61.8	1326	7	US-11-217-529-80747 Sequence 80747, A
20	13.6	61.8	1872	7	US-11-217-529-3010 Sequence 3010, App
21	13.6	61.8	2952	7	US-11-217-529-4946 Sequence 4946, App
22	13.6	61.8	3102	7	US-11-217-529-82302 Sequence 82302, A
23	13.4	60.9	497	6	US-10-488-619-2075 Sequence 2075, App
24	13.4	60.9	599	6	US-10-488-619-2156 Sequence 2156, App
25	13.4	60.9	762	7	US-11-217-529-5130 Sequence 5130, App

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Sequence 4877, App
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Sequence 1455, App
Sequence 1859, App
Sequence 120, App
Sequence 490, App


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c 272 12.2 55.5 192 1 US-09-756-097B-92
c 273 12.2 55.5 366 7 US-11-217-529-77191
c 274 12.2 55.5 378 7 US-11-301-554-889
c 275 12.2 55.5 390 7 US-11-301-554-1419
c 276 12.2 55.5 402 7 US-11-217-529-173452
c 277 12.2 55.5 410 6 US-10-488-619-466
c 278 12.2 55.5 447 6 US-10-473-173-139
c 279 12.2 55.5 462 6 US-10-488-619-319
c 280 12.2 55.5 480 7 US-11-217-529-75552
c 281 12.2 55.5 573 7 US-11-217-529-81230
c 282 12.2 55.5 585 7 US-11-217-529-79588
c 283 12.2 55.5 606 7 US-11-217-529-77702
c 284 12.2 55.5 883 6 US-10-488-619-2064
c 285 12.2 55.5 906 7 US-11-217-529-2768
c 286 12.2 55.5 909 7 US-11-217-529-1523
c 287 12.2 55.5 933 7 US-11-217-529-4222
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c 289 12.2 55.5 1029 7 US-11-217-529-81270
c 290 12.2 55.5 1082 6 US-10-511-937-2916
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c 292 12.2 55.5 1143 7 US-11-217-529-3940
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c 295 12.2 55.5 1212 7 US-11-217-529-77899
c 296 12.2 55.5 1344 7 US-11-217-529-4610
c 297 12.2 55.5 1359 7 US-11-217-529-79910
c 298 12.2 55.5 1398 7 US-11-217-529-2602
c 299 12.2 55.5 1410 6 US-10-511-937-447
c 300 12.2 55.5 1422 7 US-11-136-524-69
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ALIGNMENTS

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RESULT 1
US-11-217-529-77805
; Sequence 77805, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

Query Match 70.9%; Score 15.6; DB 7; Length 471;
Best Local Similarity 81.8%; Pred. No. 7.1;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTCGG 22
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Db 152 GTCACACGGAAGGCGGTCGG 173

RESULT 2
US-11-217-529-254
; Sequence 254, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

Query Match 70.9%; Score 15.6; DB 7; Length 2397;
Best Local Similarity 81.8%; Pred. No. 8.5;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTCGG 22
||| ||||| ||| |||
Db 400 GTCGACGGAAGGCGCTTCGG 421

RESULT 3
US-11-217-529-110320
; Sequence 110320, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

Query Match 70.9%; Score 15.6; DB 7; Length 2397;
Best Local Similarity 81.8%; Pred. No. 8.5;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTCGG 22
||| ||||| ||| |||
Db 400 GTCGACGGAAGGCGCTTCGG 421
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; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 110320
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-110320

Query Match      66.4%; Score 14.6; DB 7; Length 25;
Best Local Similarity 81.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCGCTTTTCG 21
    ||||| ||||| ||||| |||||
Db 5 GTCCACGGAAGAACCGGTCG 25

RESULT 4
US-11-217-529-78935
; Sequence 78935, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78935
; LENGTH: 1242
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78935

Query Match      66.4%; Score 14.6; DB 7; Length 1242;
Best Local Similarity 81.0%; Pred. No. 26;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TCGAACGGAAGGCGCTTTTCG 22
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Db 63 TCGAACAGTAAGGCTTTTTCG 83

RESULT 5
US-11-217-529-79690/c
; Sequence 79690, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79690
; LENGTH: 1824
; TYPE: DNA

```

```

; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79690

Query Match      66.4%; Score 14.6; DB 7; Length 1824;
Best Local Similarity 81.0%; Pred. No. 27;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TCGAACGGAAGGCGCTTTTCG 22
    ||||| ||||| ||||| |||||
Db 748 TCGACGGAATAACTTACGG 728

RESULT 6
US-11-217-529-77876
; Sequence 77876, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77876
; LENGTH: 1950
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77876

Query Match      66.4%; Score 14.6; DB 7; Length 1950;
Best Local Similarity 81.0%; Pred. No. 28;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TCGAACGGAAGGCGCTTTTCG 22
    ||||| ||||| ||||| |||||
Db 1232 TCGAACTGAAAGGCTTTTCG 1252

RESULT 7
US-11-217-529-6038
; Sequence 6038, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6038
; LENGTH: 2454
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (2284)..(2317)
; OTHER INFORMATION: a, c, g, t, unknown, or other

```

US-11-217-529-6038

Query Match 65.5%; Score 14.4; DB 7; Length 2454;
Best Local Similarity 93.8%; Pred. No. 36;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AACGGAAGGCTTTC 20
||| ||||| ||||| |||||
Db 1022 AATGGAAGGCTTTC 1037

RESULT 8

US-11-217-529-1257/c
; Sequence 1257, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1257
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1257

Query Match 64.5%; Score 14.2; DB 7; Length 858;
Best Local Similarity 84.2%; Pred. No. 40;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCTTTC 20
||| ||||| ||||| |||||
Db 187 TCGAAGAGAAAGGCTTTC 169

RESULT 9

US-11-217-529-77141/c
; Sequence 77141, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77141
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77141

Query Match 64.5%; Score 14.2; DB 7; Length 858;
Best Local Similarity 84.2%; Pred. No. 40;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCTTTC 20
||| ||||| ||||| |||||
Db 187 TCGAAGAGAAAGGCTTTC 169

RESULT 10
US-11-217-529-5375/c
; Sequence 5375, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5375
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5375

Query Match 64.5%; Score 14.2; DB 7; Length 1260;
Best Local Similarity 84.2%; Pred. No. 42;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTT 19
||| ||||| ||||| |||||
Db 414 GTGGAACGGAAGGCTTTT 396

RESULT 11

US-11-217-529-78815
; Sequence 78815, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78815
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78815

Query Match 63.6%; Score 14; DB 7; Length 438;
Best Local Similarity 77.3%; Pred. No. 47;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTCGG 22
||| ||||| ||||| |||||
Db 3 GTCGAAGGGAAGGTTTGTCTG 24

```
RESULT 12
US-11-217-529-3863
; Sequence 3863, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3863
; LENGTH: 1224
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3863

Query Match      63.6%; Score 14; DB 7; Length 1224;
Best Local Similarity 77.3%; Pred. No. 53;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTTTCGG 22
Db 309 GTCGAAGGAGGAGCCTTGCG 330

RESULT 13
US-11-217-529-1422/c
; Sequence 1422, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1422
; LENGTH: 1758
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1422

Query Match      63.6%; Score 14; DB 7; Length 1758;
Best Local Similarity 77.3%; Pred. No. 56;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTTTCGG 22
Db 288 GTTGAACGTCATGCCCTTTAGG 267

RESULT 14
US-10-505-928-182
; Sequence 182, Application US/10505928
; Publication No. US20060088532A1
```

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; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 182
; LENGTH: 5900
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-182

Query Match      63.6%; Score 14; DB 6; Length 5900;
Best Local Similarity 77.3%; Pred. No. 64;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTTTCGG 22
Db 1001 GTCTACCGGAAGACCTGGCGG 1022

RESULT 15
US-09-949-925-78/c
; Sequence 78, Application US/09949925
; Publication No. US20060099575A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2023P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1212)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-949-925-78

Query Match      62.7%; Score 13.8; DB 1; Length 1931;
Best Local Similarity 88.2%; Pred. No. 71;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TCGAACGGAAGGCCTT 18
||||| ||||||| ||
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```
Db      248 TCGAACGGAAGGCATT 232
RESULT 16
US-09-949-925-12/c
; Sequence 12, Application US/09949925
; Publication No. US20060099575A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1932
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-949-925-12

Query Match      62.7%; Score 13.8; DB 1; Length 1932;
Best Local Similarity 88.2%; Pred. No. 71;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 TCGAACGGAAGGCCTT 18
Db      248 TCGAACGGAAGGCATT 232
RESULT 17
US-11-252-080-11/c
; Sequence 11, Application US/11252080
; Publication No. US20060090217A1
; GENERAL INFORMATION:
; APPLICANT: Texas A&M University
; TITLE OF INVENTION: ISOLATION OF SUGARCANE PROTEINS INVOLVED IN POSTTRANSCRIPTIONAL G
; FILE REFERENCE: 017575.0693 (TAMUS 1743)
; CURRENT APPLICATION NUMBER: US/11/252,080
; CURRENT FILING DATE: 2005-10-17
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: US/10/226,715
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 829
; TYPE: DNA
; ORGANISM: Saccharum hybrid cultivar CP72-1210
US-11-252-080-11

Query Match      61.8%; Score 13.6; DB 7; Length 829;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      3 CGAACGGAAGGCCTTTCGG 22
Db      589 CGAACGGAAGGCCTTTTGG 570
RESULT 18
US-11-217-529-4440
; Sequence 4440, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4440
; LENGTH: 903
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4440

Query Match      61.8%; Score 13.6; DB 7; Length 903;
Best Local Similarity 80.0%; Pred. No. 83;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 TCGAACGGAAGGCCTTTCG 21
Db      268 TCGAACGGAAGGCCTTTGG 287
RESULT 19
US-11-217-529-80747
; Sequence 80747, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80747
; LENGTH: 1326
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-80747

Query Match      61.8%; Score 13.6; DB 7; Length 1326;
Best Local Similarity 80.0%; Pred. No. 87;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 TCGAACGGAAGGCCTTTCG 21
```

Db 269 TCCAAGTGAATGGCCTTCG 288
|| ||| ||| ||| ||| ||| |||

RESULT 20

US-11-217-529-3010/c
; Sequence 3010, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3010
; LENGTH: 1872
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3010

Query Match 61.8%; Score 13.6; DB 7; Length 1872;
Best Local Similarity 80.0%; Pred. No. 90;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TCGAAGGAAAGCCCTTCG 21
||| ||| ||| ||| ||| ||| |||
Db 159 TCGATGTGAATGCCCTTTG 140

RESULT 21

US-11-217-529-4946/c
; Sequence 4946, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4946
; LENGTH: 2952
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4946

Query Match 61.8%; Score 13.6; DB 7; Length 2952;
Best Local Similarity 80.0%; Pred. No. 95;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TCGAAGGAAAGCCCTTCG 21
||| ||| ||| ||| ||| ||| |||
Db 2661 TCGATGTGAAGGCCCTTCG 2642

RESULT 22

US-11-217-529-82302
; Sequence 82302, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82302
; LENGTH: 3102
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82302

Query Match 61.8%; Score 13.6; DB 7; Length 3102;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 CGAACGGAAGCCCTTCGG 22
||| ||| ||| ||| ||| ||| |||
Db 1393 CTAATGGAATGCCATTCGG 1412

RESULT 23

US-10-488-619-2075
; Sequence 2075, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2075
; LENGTH: 497
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2075

Query Match 60.9%; Score 13.4; DB 6; Length 497;
Best Local Similarity 93.3%; Pred. No. 98;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTCGACGGAAGGC 15
||| ||| ||| ||| ||| ||| |||
Db 72 GTCGACGGAAGGC 86

RESULT 24

US-10-488-619-2156
; Sequence 2156, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2156
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2156

Query Match      60.9%; Score 13.4; DB 6; Length 599;
Best Local Similarity 93.3%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GTCGACGGAAGGC 15
      ||||| ||||| |||||
Db      540 GTCGACGGAAGGC 554

RESULT 25
US-11-217-529-5130/c
; Sequence 5130, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5130
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5130

Query Match      60.9%; Score 13.4; DB 7; Length 762;
Best Local Similarity 93.3%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5  AACGGAAGGCCTTT 19
      ||||| ||||| |||||
Db      539 AACGGAAGGCCTTT 525

RESULT 26
US-10-488-619-2155/c
; Sequence 2155, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2155
; LENGTH: 784
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2155

Query Match      60.9%; Score 13.4; DB 6; Length 784;
Best Local Similarity 93.3%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GTCGACGGAAGGC 15
      ||||| ||||| |||||
Db      394 GTCGACGGAAGGC 380

RESULT 27
US-10-525-126-124/c
; Sequence 124, Application US/10525126
; Publication No. US20060093596A1
; GENERAL INFORMATION:
; APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
; TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
; FILE REFERENCE: 6899-6/PAR
; CURRENT APPLICATION NUMBER: US/10/525,126
; CURRENT FILING DATE: 2005-02-18
; PRIOR FILING DATE: 2003-08-22
; PRIOR FILING DATE: 2003-08-22
; PRIOR FILING DATE: 2003-08-22
; PRIOR FILING DATE: 2002-08-22
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 124
; LENGTH: 814
; TYPE: DNA
; ORGANISM: Platichthys stellatus
US-10-525-126-124

Query Match      60.9%; Score 13.4; DB 6; Length 814;
Best Local Similarity 93.3%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5  AACGGAAGGCCTTT 19
      ||||| ||||| |||||
Db      254 AACGGAAGGCCTTT 240

RESULT 28
US-10-541-993-4
; Sequence 4, Application US/10541993
; Publication No. US20060099670A1
; GENERAL INFORMATION:
; APPLICANT: Matuschek, Markus
; APPLICANT: Heinekamp, Thorsten
; APPLICANT: Schmidt, Andre
; APPLICANT: Brakhage, Axel
; TITLE OF INVENTION: Method for the genetic modification of organisms of the genus
; FILE REFERENCE: 13311-00010-US
; CURRENT APPLICATION NUMBER: US/10/541,993
; CURRENT FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: PCT/EP2004/000100
; PRIOR FILING DATE: 2004-01-09
; PRIOR FILING DATE: 2003-01-09
; PRIOR FILING DATE: 2003-01-09
; PRIOR FILING DATE: 2003-09-08
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 11611
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Vector
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (227)..(227)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (318)..(318)
; OTHER INFORMATION: n is a, c, g, or t
```

```
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (526)..(526)
; OTHER INFORMATION: n is a, c, g, or t
;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8946)..(8946)
; OTHER INFORMATION: n is a, c, g, or t
;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10028)..(10028)
; OTHER INFORMATION: n is a, c, g, or t
US-10-541-993-4
```

```
Query Match 60.9%; Score 13.4; DB 6; Length 11611;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 4 GAACGGAAGGCCTT 18
Db 8484 GAACGGAAGGCCTT 8498
```

RESULT 29

```
US-11-217-529-173378
; Sequence 173378, Application US/11217529
; Publication No. US20060095612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 173378
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-173378
```

```
Query Match 60.0%; Score 13.2; DB 7; Length 492;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 4 GAACGGAAGGCCTTTCG 21
Db 439 GAGCGGAAGGCCTATTG 456
```

RESULT 30

```
US-11-217-529-76021/c
; Sequence 76021, Application US/11217529
; Publication No. US20060095612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
```

```
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76021
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76021
```

```
Query Match 60.0%; Score 13.2; DB 7; Length 498;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 5 AACGGAAGGCCTTTCGG 22
Db 145 AACGGAAGGCCTTTTGG 128
```

RESULT 31

```
US-10-488-619-2026
; Sequence 2026, Application US/10488619
; Publication No. US2006009578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations v
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2026
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2026
```

```
Query Match 60.0%; Score 13.2; DB 6; Length 523;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 2 TCGAACGGAAGGCCTTT 19
Db 259 TCAAAAGGAAGGACTTT 276
```

RESULT 32

```
US-10-488-619-2939/c
; Sequence 2939, Application US/10488619
; Publication No. US2006009578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations v
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2939
; LENGTH: 806
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2939
```

```
Query Match 60.0%; Score 13.2; DB 6; Length 806;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 2 TCGAACGGAAGGCCTTT 19
Db 21 TGGGAAGGAAGGCCTTT 4
```

```
RESULT 33
US-11-217-529-75628
; Sequence 75628, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75628
; LENGTH: 1242
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75628

Query Match      60.0%; Score 13.2; DB 7; Length 1242;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 CGAACGGAAGGCCTTTC 20
Db      887 CAACGCAACGCGCTTTC 904

RESULT 34
US-11-217-529-75/c
; Sequence 75, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75

Query Match      60.0%; Score 13.2; DB 7; Length 1269;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      5 AACGGAAGGCCTTCGG 22
Db      507 AAGGGAAGGCCTGTAGG 490

RESULT 35
US-11-217-529-4877/c
; Sequence 4877, Application US/11217529
; Publication No. US20060099612A1
```

```
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4877
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4877

Query Match      60.0%; Score 13.2; DB 7; Length 1377;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GTCGAACGGAAGGCCTT 18
Db      85 GTTTAACGGAAGGCCTT 68

RESULT 36
US-11-217-529-3860
; Sequence 3860, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3860
; LENGTH: 1611
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3860

Query Match      60.0%; Score 13.2; DB 7; Length 1611;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 TCGAACGGAAGGCCTTT 19
Db      712 TCCAAACGGAAGGCCTTT 729

RESULT 37
US-11-312-958-13
; Sequence 13, Application US/11312958
; Publication No. US20060100152A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Rosenfeld, Julie Beth
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
```


;/ TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
;/ TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
;/ TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
;/ TITLE OF INVENTION: 95431, 2245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
;/ TITLE OF INVENTION: 13424 MOLECULES
;/ FILE REFERENCE: MPI02-027P1RNONMIM
;/ CURRENT APPLICATION NUMBER: US/11/312,958
;/ CURRENT FILING DATE: 2005-12-20
;/ PRIOR APPLICATION NUMBER: US/10/369,022
;/ PRIOR FILING DATE: 2003-02-19
;/ PRIOR APPLICATION NUMBER: US 60/360,495
;/ PRIOR FILING DATE: 2002-02-28
;/ PRIOR APPLICATION NUMBER: US 60/370,121
;/ PRIOR FILING DATE: 2002-04-04
;/ PRIOR APPLICATION NUMBER: US 60/373,010
;/ PRIOR FILING DATE: 2002-04-16
;/ PRIOR APPLICATION NUMBER: US 60/373,908
;/ PRIOR FILING DATE: 2002-04-19
;/ PRIOR APPLICATION NUMBER: US 60/377,717
;/ PRIOR FILING DATE: 2002-05-03
;/ PRIOR APPLICATION NUMBER: US 60/379,949
;/ PRIOR FILING DATE: 2002-05-13
;/ PRIOR APPLICATION NUMBER: US 60/382,409
;/ PRIOR FILING DATE: 2002-05-21
;/ PRIOR APPLICATION NUMBER: US 60/385,280
;/ PRIOR FILING DATE: 2002-06-03
;/ PRIOR APPLICATION NUMBER: US 60/386,879
;/ PRIOR FILING DATE: 2002-06-06
;/ Remaining Prior Application data removed - See File Wrapper or PALM.
;/ NUMBER OF SEQ ID NOS: 64
;/ SOFTWARE: FastSEQ for Windows Version 4.0
;/ SEQ ID NO 13
;/ LENGTH: 1968
;/ TYPE: DNA
;/ ORGANISM: Homo sapiens
;/ FEATURE:
;/ NAME/KEY: CDS
;/ LOCATION: (73)...(1176)
US-11-312-958-13

Query Match 60.0%; Score 13.2; DB 7; Length 1968;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCGCTTTC 20
Db 1182 CGAAGGGAAGGCGCTC 1199

RESULT 38
US-10-511-937-440
;/ Sequence 440, Application US/10511937
;/ Publication No. US20060089836A1
;/ GENERAL INFORMATION:
;/ APPLICANT: EXPRESSION DIAGNOSTICS, INC.
;/ APPLICANT: Wohlgemuth, Jay
;/ APPLICANT: Fry, Kirk
;/ APPLICANT: Woodward, Robert
;/ APPLICANT: Ly, Ngoc
;/ APPLICANT: Prentice, James
;/ APPLICANT: Morris, MacDonald
;/ APPLICANT: Rosenberg, Steven
;/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;/ TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
;/ FILE REFERENCE: 506612000104
;/ CURRENT APPLICATION NUMBER: US/10/511,937
;/ CURRENT FILING DATE: 2004-10-19
;/ PRIOR APPLICATION NUMBER: PCT/US2003/012946
;/ PRIOR FILING DATE: 2003-04-24
;/ PRIOR APPLICATION NUMBER: US 10/131,831
;/ PRIOR FILING DATE: 2002-04-24
;/ PRIOR APPLICATION NUMBER: US 10/325,899
;/ PRIOR FILING DATE: 2002-12-20

;/ NUMBER OF SEQ ID NOS: 3117
;/ SOFTWARE: PatentIn version 3.2
;/ SEQ ID NO 440
;/ LENGTH: 2545
;/ TYPE: DNA
;/ ORGANISM: Homo sapiens
US-10-511-937-440

Query Match 60.0%; Score 13.2; DB 6; Length 2545;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCGCTTTC 20
Db 1826 CGAAGGGAAGGCGCTTTC 1843

RESULT 39
US-11-301-554-1900
;/ Sequence 1900, Application US/11301554
;/ Publication No. US20060088527A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Henderson, Robert A.
;/ APPLICANT: Wang, Tongtong
;/ APPLICANT: Watanabe, Yoshihiro
;/ APPLICANT: Kalos, Michael D.
;/ APPLICANT: Sleath, Paul R.
;/ APPLICANT: Johnson, Jeffrey C.
;/ APPLICANT: Retter, Marc W.
;/ APPLICANT: Durham, Margarita
;/ APPLICANT: Carter, Darrick
;/ APPLICANT: Fanger, Gary R.
;/ APPLICANT: Vedvick, Thomas S.
;/ APPLICANT: Bangur, Chaitanya S.
;/ APPLICANT: McNabb, Andria
;/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;/ TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
;/ FILE REFERENCE: 210121.478C21
;/ CURRENT APPLICATION NUMBER: US/11/301,554
;/ CURRENT FILING DATE: 2005-12-13
;/ PRIOR APPLICATION NUMBER: US 10/283,017
;/ PRIOR FILING DATE: 2002-10-28
;/ PRIOR APPLICATION NUMBER: US 10/113,872
;/ PRIOR FILING DATE: 2002-03-28
;/ PRIOR APPLICATION NUMBER: US 10/017,754
;/ PRIOR FILING DATE: 2001-10-29
;/ PRIOR APPLICATION NUMBER: US 09/902,941
;/ PRIOR FILING DATE: 2001-07-10
;/ PRIOR APPLICATION NUMBER: US 09/849,626
;/ PRIOR FILING DATE: 2001-05-03
;/ PRIOR APPLICATION NUMBER: US 09/736,457
;/ PRIOR FILING DATE: 2000-12-13
;/ PRIOR APPLICATION NUMBER: US 09/702,705
;/ PRIOR FILING DATE: 2000-10-30
;/ PRIOR APPLICATION NUMBER: US 09/677,419
;/ PRIOR FILING DATE: 2000-10-06
;/ PRIOR APPLICATION NUMBER: US 09/671,325
;/ PRIOR FILING DATE: 2000-09-26
;/ PRIOR APPLICATION NUMBER: US 09/658,824
;/ PRIOR FILING DATE: 2000-09-08
;/ Remaining Prior Application data removed - See File Wrapper or PALM.
;/ NUMBER OF SEQ ID NOS: 2157
;/ SOFTWARE: FastSEQ for Windows Version 4.0
;/ SEQ ID NO 1500
;/ LENGTH: 2545
;/ TYPE: DNA
;/ ORGANISM: Homo sapiens
US-11-301-554-1900

Query Match 60.0%; Score 13.2; DB 7; Length 2545;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCGCTTTC 20
||||| ||||| |||||
Db 1826 CGAAGGAAGGCGCTTTC 1843

RESULT 40

US-11-217-529-79139/c
; Sequence 79139, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79139
; LENGTH: 2850
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79139

Query Match 60.0%; Score 13.2; DB 7; Length 2850;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTT 19
||||| ||||| |||||
Db 377 TTGAACGTAAGGCATT 360

RESULT 41

US-11-217-529-78066/c
; Sequence 78066, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78066
; LENGTH: 3267
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78066

Query Match 60.0%; Score 13.2; DB 7; Length 3267;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTT 19
||||| ||||| |||||
Db 440 TTGTATGGAAGGCGCTTT 423

RESULT 42

US-11-217-529-3415
; Sequence 3415, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3415
; LENGTH: 3330
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3415

Query Match 60.0%; Score 13.2; DB 7; Length 3330;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTT 19
||||| ||||| |||||
Db 1435 TCTAACAGAAAGGCGCTTT 1452

RESULT 43

US-10-511-937-346
; Sequence 346, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR FILING DATE: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 346
; LENGTH: 3655
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-346

Query Match 60.0%; Score 13.2; DB 6; Length 3655;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCGCTTTC 20
||||| ||||| |||||
Db 3477 CGAAGGGAATGTCTTTC 3494

```
RESULT 44
US-10-489-730-10/c
; GENERAL INFORMATION: Gennaro
; APPLICANT: Melino, Ian
; APPLICANT: Hayes, Ian
; APPLICANT: de Laurenzi, Vincenzo
; APPLICANT: Barcaroli, Daniela
; APPLICANT: Candi, Eleonora
; APPLICANT: Bernasola, Francesca
; APPLICANT: Tobler, Andreas
; APPLICANT: Novak, Urban
; TITLE OF INVENTION: Human Delta-N p73 Molecules and Uses Thereof
; FILE REFERENCE: 19319.002
; CURRENT APPLICATION NUMBER: US/10/489,730
; CURRENT FILING DATE: 2004-03-16
; PRIOR APPLICATION NUMBER: PCT/GB02/04238
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US 60/322,436
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 39
; OTHER INFORMATION: reverse complement of exons 14 through 1 as reported in GenBank A
US-10-489-730-10

Query Match      60.0%; Score 13.2; DB 6; Length 138941;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CGAAGCGGAAAGGCCTTTC 20
Db 106669 CGAATGGAATGCTTTC 106652

RESULT 45
US-11-217-529-91576
; Sequence 91576, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 91576
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-91576

Query Match      59.1%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CGGAAGGCCTTT 19
Db 9 CGGAAGGCCTTT 21

RESULT 46
US-11-217-529-132068
; Sequence 132068, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
```

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; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 132068
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-132068

Query Match      59.1%; Score 13; DB 7; Length 25;
Best Local Similarity 76.2%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCCTTTCG 22
Db 3 TCAGACGAGAGCCCTTTCG 23

RESULT 47
US-11-217-529-152160
; Sequence 152160, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 152160
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-152160

Query Match      59.1%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ACGAAAGGCCTT 18
Db 10 ACGAAAGGCCTT 22

RESULT 48
US-11-264-784-222/c
; Sequence 222, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
```

; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 222
; LENGTH: 95
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer D8-7A
US-11-264-784-222

Query Match 59.1%; Score 13; DB 7; Length 95;
Best Local Similarity 76.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTCGG 22
|||||
Db 43 TGGAACTGAATGAGCTTTCGG 23

RESULT 49

US-11-264-784-223
; Sequence 223, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 223
; LENGTH: 95
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer D8-7B
US-11-264-784-223

Query Match 59.1%; Score 13; DB 7; Length 95;
Best Local Similarity 76.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTCGG 22
|||||
Db 57 TGGAACTGAATGAGCTTTCGG 77

RESULT 50

US-11-217-529-4142/c
; Sequence 4142, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:

; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4142
; LENGTH: 117
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; OTHER INFORMATION: Saccharomyces pastorianus
US-11-217-529-4142

Query Match 59.1%; Score 13; DB 7; Length 117;
Best Local Similarity 76.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTCGG 22
|||||
Db 53 TCGAACGGTATGACATTTCGG 33

RESULT 51

US-11-264-784-246/c
; Sequence 246, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 246
; LENGTH: 264
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 264 bp XhoI/SacI fragment of pT8 (7-9)
US-11-264-784-246

Query Match 59.1%; Score 13; DB 7; Length 264;
Best Local Similarity 76.2%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTCGG 22
|||||
Db 39 TGGAACTGAATGAGCTTTCGG 19

RESULT 52

US-10-488-619-347/c
; Sequence 347, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:

```

; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 347
; LENGTH: 404
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(404)
; OTHER INFORMATION: n is g, c, a or t
US-10-488-619-347

Query Match      59.1%; Score 13; DB 6; Length 404;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8  GGAAGGCGCTTTCG 21
Db      235  GGAAGGCGCTTTCG 222

RESULT 53
US-10-488-619-763/c
; Sequence 763, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 763
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-488-619-763

Query Match      59.1%; Score 13; DB 6; Length 411;
Best Local Similarity 76.2%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2  TCGAACGGAAGGCGCTTTCG 22
Db      286  TCGACTGAAGGCGCGCTTCGG 266

RESULT 54
US-10-488-619-762
; Sequence 762, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 762
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-488-619-762

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```

Query Match      59.1%; Score 13; DB 6; Length 451;
Best Local Similarity 76.2%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2  TCGAACGGAAGGCGCTTTCGG 22
Db      319  TCGCACTGAAGGCGCGCTTCGG 339

RESULT 55
US-11-256-428-55/c
; Sequence 55, Application US/11256428
; Publication No. US20060095987A1
; GENERAL INFORMATION:
; APPLICANT: Niblett, Charles L.
; TITLE OF INVENTION: Methods and Materials for Conferring Resistance to Pests and
; FILE REFERENCE: VEN-100
; CURRENT APPLICATION NUMBER: US/11/256,428
; CURRENT FILING DATE: 2005-10-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 55
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Cercospora zeae-maydis 18s rDNA
US-11-256-428-55

Query Match      59.1%; Score 13; DB 7; Length 536;
Best Local Similarity 76.2%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2  TCGAACGGAAGGCGCTTTCGG 22
Db      324  TCGAACAGGCATGCCCTTCGG 304

RESULT 56
US-11-217-529-79746
; Sequence 79746, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79746
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79746

Query Match      59.1%; Score 13; DB 7; Length 696;
Best Local Similarity 76.2%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2  TCGAACGGAAGGCGCTTTCGG 22
Db      421  TCAGACGAGAGCCCTTCGG 441

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RESULT 57
US-11-217-529-81537
; Sequence 81537, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81537
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-81537
Query Match 59.1%; Score 13; DB 7; Length 702;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ACGGAAAGCCCTT 18
Db 332 ACGGAAAGCCCTT 344

RESULT 58
US-10-975-697-7
; Sequence 7, Application US/10975697
; Publication No. US20060094099A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: Inactivated Enzyme Variants And Associated Process and Reagent
; TITLE OF INVENTION: System
; FILE REFERENCE: 5727-76273
; CURRENT APPLICATION NUMBER: US/10/975,697
; CURRENT FILING DATE: 2004-10-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GlucDH variant RC-21
US-10-975-697-7
Query Match 59.1%; Score 13; DB 6; Length 1080;
Best Local Similarity 76.2%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTTCG 21
Db 1015 GTCGAAGACTGGGCCTTTCG 1035

RESULT 59
US-10-975-697-9
; Sequence 9, Application US/10975697
; Publication No. US20060094099A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: Inactivated Enzyme Variants And Associated Process and Reagent
; TITLE OF INVENTION: System
```

```
; FILE REFERENCE: 5727-76273
; CURRENT APPLICATION NUMBER: US/10/975,697
; CURRENT FILING DATE: 2004-10-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GlucDH variant RC-28
US-10-975-697-9
Query Match 59.1%; Score 13; DB 6; Length 1080;
Best Local Similarity 76.2%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTTCG 21
Db 1015 GTCGAAGACTGGGCCTTTCG 1035

RESULT 60
US-10-975-697-11
; Sequence 11, Application US/10975697
; Publication No. US20060094099A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: Inactivated Enzyme Variants And Associated Process and Reagent
; TITLE OF INVENTION: System
; FILE REFERENCE: 5727-76273
; CURRENT APPLICATION NUMBER: US/10/975,697
; CURRENT FILING DATE: 2004-10-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GlucDH variant RC-35
US-10-975-697-11
Query Match 59.1%; Score 13; DB 6; Length 1080;
Best Local Similarity 76.2%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTTCG 21
Db 1015 GTCGAAGACTGGGCCTTTCG 1035

RESULT 61
US-11-217-529-190860
; Sequence 190860, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 190860
; LENGTH: 1092
```

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; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-190860

```

Query Match 59.1%; Score 13; DB 7; Length 1092;
Best Local Similarity 76.2%; Pred. NO. 1.7e+02;
Matches 16; Conservative 0; Mismatches 5; Indels

Qy 2 TCGAACGGAAAGGCGTTTCGG 22
Db 657 TCCAATGGCTAGGCATTTCGG 677

RESULT 62
 US-11-217-529-494
 ; Sequence 494, Application US/11217529
 ; Publication No. US20060099612A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUNTORY LIMITED
 ; APPLICANT: NAKAO, YOSHIHIRO
 ; APPLICANT: NAKAMURA, NORIHISA
 ; APPLICANT: KODAMA, YUKIO
 ; APPLICANT: FUJIMURA, TOMOKO
 ; APPLICANT: ASHIKARI, TOSHIHIKO
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 ; FILE REFERENCE: S-38-285
 ; CURRENT APPLICATION NUMBER: US/11/217,529
 ; CURRENT FILING DATE: 2005-09-02
 ; PRIOR APPLICATION NUMBER: US 10/932,182
 ; PRIOR FILING DATE: 2004-09-02
 ; NUMBER OF SEQ ID NOS: 197023
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 494
 ; LENGTH: 1098

Query Match 59.1%; Score 13; DB 7; Length 1098;
Best Local Similarity 76.2%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 5. Indels

Qy 2 TCGAACGGAAGCCTTTCGG 22
89 TCGAATTGAAAGTCCTTGGG 109

```

RESULT 63
US-11-217-529-998
; Sequence 998, Application US/11217529
; Publication No. US2006099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 998
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-998

```

Query Match

```
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 GTCGAACGGAAG 13
Db 333 GTCGAACGGAAG 345

```

RESULT 64
US-11-217-529-5416
; Sequence 5416, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5416
; LENGTH: 1254
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5416

```

```
Query Match          59.1%; Score 13; DB 7; Length 1254;
Best Local Similarity 76.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

QY 2 TCGAACGGAAGGCCTTTCGG 22
||| ||| ||| ||| ||| ||| |||
db 72 TCGAGCGGTACGGCATTTCGG 92

```

RESULT 65
US-11-264-784-255/c
; Sequence 255, Application US/11264784
; Publication No. US2006094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRO
; FILE REFERENCE: CLU3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 255
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D8S-3: synthetic delta 8
; OTHER INFORMATION: Yarrowia lipolytica in pl
US-11-264-784-255

```

```
Query Match      59.1%; Score 13; DB 7; Length 1269;
Best Local Similarity 76.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 TCGAACGGAAGGCGCTTTCGG 22
Db      677 TGGAACTGAATGAGCTTTCGG 657

RESULT 66
US-11-264-784-209/c
; Sequence 209, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 209
; LENGTH: 1270
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D8S-1: Synthetic gene codon-optimized for expression in Yarrowia
US-11-264-784-209

Query Match      59.1%; Score 13; DB 7; Length 1270;
Best Local Similarity 76.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 TCGAACGGAAGGCGCTTTCGG 22
Db      670 TGGAACTGAATGAGCTTTCGG 650

RESULT 67
US-11-264-784-48/c
; Sequence 48, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 48
; LENGTH: 1272
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D8SF: synthetic delta-8 desaturase (codon-optimized for Yarrowia
US-11-264-784-48

Query Match      59.1%; Score 13; DB 7; Length 1272;
Best Local Similarity 76.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 TCGAACGGAAGGCGCTTTCGG 22
Db      678 TGGAACTGAATGAGCTTTCGG 658

RESULT 68
US-11-264-784-263/c
; Sequence 263, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 263
; LENGTH: 1272
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chlmeric gene
US-11-264-784-263

Query Match      59.1%; Score 13; DB 7; Length 1272;
Best Local Similarity 76.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 TCGAACGGAAGGCGCTTTCGG 22
Db      678 TGGAACTGAATGAGCTTTCGG 658

RESULT 69
US-11-217-529-75890/c
; Sequence 75890, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
```



```
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75890
; LENGTH: 1473
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-11-217-529-75890

Query Match          59.1%; Score 13; DB 7; Length 1473;
Best Local Similarity 76.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 TCGAACCGGAAAGGCCTTTCCG 22
       ||||| ||||| ||||| |||||
Db      1337 TCGAATGCAAGCCTTAGG 1317

RESULT 70
US-11-324-517-36
; Sequence 36, Application US/11324517
; Publication No. US20060099221A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, MARY
; TITLE OF INVENTION: METHOD OF SCREENING ANTI-MYCOBACTERIAL MOLECULES
; FILE REFERENCE: 03495.0182-01
; CURRENT APPLICATION NUMBER: US/11/324,517
; CURRENT FILING DATE: 2006-01-04
; PRIOR APPLICATION NUMBER: US/10/914,165
; PRIOR FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: US/10/383,675
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 09/429,370
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/113,375
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/111,813
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 09/181,934
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 1600
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (549)..(1562)
; US-11-324-517-36

Query Match          59.1%; Score 13; DB 7; Length 1600;
Best Local Similarity 76.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 TCGAACCGGAAAGGCCTTTCCG 22
       ||||| ||||| ||||| |||||
Db      1480 TCGACCGGAAAGCGGTACGG 1500

RESULT 71
US-11-264-784-250/c
; Sequence 250, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.

; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 251
; LENGTH: 1898
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric D8S-2::XPR gene
; US-11-264-784-251

Query Match          59.1%; Score 13; DB 7; Length 1898;
Best Local Similarity 76.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 TCGAACCGGAAAGGCCTTTCCG 22
       ||||| ||||| ||||| |||||
Db      1082 TCGAACTGAATGAGCTTCCG 1062

RESULT 72
US-11-264-784-251/c
; Sequence 251, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 251
; LENGTH: 1898
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric D8S-2::XPR gene
; US-11-264-784-251

Query Match          59.1%; Score 13; DB 7; Length 1898;
Best Local Similarity 76.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 TCGAACCGGAAAGGCCTTTCCG 22
       ||||| ||||| ||||| |||||
Db      1082 TCGAACTGAATGAGCTTCCG 1062

RESULT 73
US-11-217-529-76130
; Sequence 250, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
```

```
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 250
; LENGTH: 1852
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric D8S-1::XPR gene
; US-11-264-784-250

Query Match          59.1%; Score 13; DB 7; Length 1852;
Best Local Similarity 76.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 TCGAACCGGAAAGGCCTTTCCG 22
       ||||| ||||| ||||| |||||
Db      1082 TCGAACTGAATGAGCTTCCG 1062

RESULT 72
US-11-264-784-251/c
; Sequence 251, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 251
; LENGTH: 1898
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric D8S-2::XPR gene
; US-11-264-784-251

Query Match          59.1%; Score 13; DB 7; Length 1898;
Best Local Similarity 76.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 TCGAACCGGAAAGGCCTTTCCG 22
       ||||| ||||| ||||| |||||
Db      1082 TCGAACTGAATGAGCTTCCG 1062

RESULT 73
US-11-217-529-76130
; Sequence 250, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
```

```
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76130
; LENGTH: 2853
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76130

Query Match          59.1%; Score 13; DB 7; Length 2853;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 CGGAAGGCGCTTT 19
        |||||
Db      2501 CGGAAGGCGCTT 2513

RESULT 74
US-11-217-529-95
; Sequence 95, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 95
; LENGTH: 3078
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-95

Query Match          59.1%; Score 13; DB 7; Length 3078;
Best Local Similarity 76.2%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 TCGAACGGAAGGCGCTTTCCG 22
        |||||
Db      936 TCCAACGGAAGAGATTTTGG 956

RESULT 75
US-11-217-529-1369/c
; Sequence 1369, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
```

```
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1369
; LENGTH: 3663
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1369

Query Match          59.1%; Score 13; DB 7; Length 3663;
Best Local Similarity 76.2%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 TCGAACGGAAGGCGCTTTCCG 22
        |||||
Db      344 TCTAACGTAAGGCTTTTGG 324

RESULT 76
US-11-217-529-80723
; Sequence 80723, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80723
; LENGTH: 3864
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-80723

Query Match          59.1%; Score 13; DB 7; Length 3864;
Best Local Similarity 76.2%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 TCGAACGGAAGGCGCTTTCCG 22
        |||||
Db      2489 TCAACGCGAGAGATTTTCCG 2509

RESULT 77
US-11-217-529-3980/c
; Sequence 3980, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
```

```
; SEQ ID NO 3980
; LENGTH: 4005
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3980

Query Match          59.1%; Score 13; DB 7; Length 4005;
Best Local Similarity 76.2%; Pred. No. 2.e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAAGCCTTTTCG 21
Db 2989 GTTGAAGAGTAAGGATTTTCG 2969

RESULT 78
US-11-217-529-3246
; Sequence 3246, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3246
; LENGTH: 5223
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3246

Query Match          59.1%; Score 13; DB 7; Length 5223;
Best Local Similarity 76.2%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TCGAACGGAAAGCCTTTTCG 22
Db 322 TTGATCGGAATGCGTTTTCG 342

RESULT 79
US-10-520-210-29/c
; Sequence 29, Application US/10520210
; Publication No. US20060099692A1
; GENERAL INFORMATION:
; APPLICANT: Yocum, R. Rogers
; APPLICANT: Patterson, Thomas A.
; APPLICANT: Pero, Janice G.
; APPLICANT: Hermann, Theron
; TITLE OF INVENTION: MICROORGANISMS AND PROCESSES FOR ENHANCED PRODUCTION OF
; FILE REFERENCE: BGI-154US
; CURRENT APPLICATION NUMBER: US/10/520,210
; CURRENT FILING DATE: 2005-01-03
; PRIOR APPLICATION NUMBER: PCT/US2003/021336
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 6805
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid

US-10-520-210-29

Query Match          59.1%; Score 13; DB 6; Length 6805;
Best Local Similarity 76.2%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAAGCCTTTTCG 21
Db 1257 GTCGAAGACTGGGCTTTTCG 1237

RESULT 80
US-10-520-210-31/c
; Sequence 31, Application US/10520210
; Publication No. US20060099692A1
; GENERAL INFORMATION:
; APPLICANT: Yocum, R. Rogers
; APPLICANT: Patterson, Thomas A.
; APPLICANT: Pero, Janice G.
; APPLICANT: Hermann, Theron
; TITLE OF INVENTION: MICROORGANISMS AND PROCESSES FOR ENHANCED PRODUCTION OF
; FILE REFERENCE: BGI-154US
; CURRENT APPLICATION NUMBER: US/10/520,210
; CURRENT FILING DATE: 2005-01-03
; PRIOR APPLICATION NUMBER: PCT/US2003/021336
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 7330
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid

US-10-520-210-31

Query Match          59.1%; Score 13; DB 6; Length 7330;
Best Local Similarity 76.2%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAAGCCTTTTCG 21
Db 1257 GTCGAAGACTGGGCTTTTCG 1237

RESULT 81
US-10-520-210-25/c
; Sequence 25, Application US/10520210
; Publication No. US20060099692A1
; GENERAL INFORMATION:
; APPLICANT: Yocum, R. Rogers
; APPLICANT: Patterson, Thomas A.
; APPLICANT: Pero, Janice G.
; APPLICANT: Hermann, Theron
; TITLE OF INVENTION: MICROORGANISMS AND PROCESSES FOR ENHANCED PRODUCTION OF
; FILE REFERENCE: BGI-154US
; CURRENT APPLICATION NUMBER: US/10/520,210
; CURRENT FILING DATE: 2005-01-03
; PRIOR APPLICATION NUMBER: PCT/US2003/021336
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 7701
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: glyA overexpression

US-10-520-210-25
```

Query Match 59.1%; Score 13; DB 6; Length 7701;
Best Local Similarity 76.2%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTTCG 21
| | | | | | | | | | | | | | | | | | | | | |
Db 1262 GTCGAAGACTGGGCTTTTCG 1242

RESULT 82

US-10-520-210-24/c
; Sequence 24, Application US/10520210
; Publication No. US20060099692A1
; GENERAL INFORMATION:
; APPLICANT: Yocum, R. Rogers
; APPLICANT: Patterson, Thomas A.
; APPLICANT: Pero, Janice G.
; APPLICANT: Hermann, Theron
; TITLE OF INVENTION: MICROORGANISMS AND PROCESSES FOR ENHANCED PRODUCTION OF
; FILE REFERENCE: BGI-154US
; CURRENT APPLICATION NUMBER: US/10/520,210
; CURRENT FILING DATE: 2005-01-03
; PRIOR APPLICATION NUMBER: PCT/US2003/021336
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 7926
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sera overexpression
; FEATURE:
; OTHER INFORMATION: plasmid
US-10-520-210-24

Query Match 59.1%; Score 13; DB 6; Length 7926;
Best Local Similarity 76.2%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTTCG 21
| | | | | | | | | | | | | | | | | | | | | |
Db 1262 GTCGAAGACTGGGCTTTTCG 1242

RESULT 83

US-11-024-544A-129/c
; Sequence 129, Application US/11024544A
; Publication No. US20060094086A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Yadav, Narendra
; APPLICANT: Xue, Zhixiong
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: DIACYLGLYCEROL ACYLTRANSFERASES FOR ALTERATION OF POLYUNSATURATED
; FILE REFERENCE: CL2717
; CURRENT APPLICATION NUMBER: US/11/024,544A
; CURRENT FILING DATE: 2004-12-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 129
; LENGTH: 10448
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pKO2UM26E
US-11-024-544A-129

Query Match 59.1%; Score 13; DB 7; Length 10448;
Best Local Similarity 76.2%; Pred. No. 2.2e+02;

Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCTTTTCGG 22
| | | | | | | | | | | | | | | | | | | | | |
Db 1650 TGGAACTGAATGAGCTTTTCGG 1630

RESULT 84

US-11-190-750-112/c
; Sequence 112, Application US/11190750
; Publication No. US20060094088A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Yadav, Narendra
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: ACYLTRANSFERASE REGULATION TO INCREASE THE PERCENT OF
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN TOTAL LIPIDS AND OILS OF
; TITLE OF INVENTION: OLEAGINOUS ORGANISMS
; FILE REFERENCE: CL2718
; CURRENT APPLICATION NUMBER: US/11/190,750
; CURRENT FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 112
; LENGTH: 10448
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pKO2UM26E
US-11-190-750-112

Query Match 59.1%; Score 13; DB 7; Length 10448;
Best Local Similarity 76.2%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCTTTTCGG 22
| | | | | | | | | | | | | | | | | | | | | |
Db 1650 TGGAACTGAATGAGCTTTTCGG 1630

RESULT 85

US-11-264-784-123/c
; Sequence 123, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 123
; LENGTH: 10448
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pDMW297
US-11-264-784-123

Query Match 59.1%; Score 13; DB 7; Length 10448;
Best Local Similarity 76.2%; Pred. No. 2.2e+02;

```
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 TCGAACGGAAAGGCTTTCGG 22
Db 1650 TGGAACTGAATGAGCTTTCGG 1630

RESULT 86
US-11-264-784-125
; Sequence 125, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 125
; LENGTH: 13295
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pDMW314
; NAME/KEY: misc feature
; LOCATION: (10915)..(10918)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10923)..(10923)
; OTHER INFORMATION: n is a, c, g, or t
US-11-264-784-125

Query Match 59.1%; Score 13; DB 7; Length 13295;
Best Local Similarity 76.2%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 TCGAACGGAAAGGCTTTCGG 22
Db 3608 TGGAACTGAATGAGCTTTCGG 3628

RESULT 87
US-11-264-784-124
; Sequence 124, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
```

```
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 124
; LENGTH: 15543
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pZP2C16M899
US-11-264-784-124

Query Match 59.1%; Score 13; DB 7; Length 15543;
Best Local Similarity 76.2%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 TCGAACGGAAAGGCTTTCGG 22
Db 11262 TGGAACTGAATGAGCTTTCGG 11282

RESULT 88
US-11-264-784-127
; Sequence 127, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 127
; LENGTH: 16325
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pZKSL5598
US-11-264-784-127

Query Match 59.1%; Score 13; DB 7; Length 16325;
Best Local Similarity 76.2%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 TCGAACGGAAAGGCTTTCGG 22
Db 14741 TGGAACTGAATGAGCTTTCGG 14761

RESULT 89
US-10-473-173-32/c
; Sequence 32, Application US/10473173
; Publication No. US20060088823A1
; GENERAL INFORMATION:
; APPLICANT: VAN ANDEL INSTITUTE
; TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
; TITLE OF INVENTION: Carcinoma: Prognosis and Drug Target Identification
; FILE REFERENCE: 38345-170094
; CURRENT APPLICATION NUMBER: US/10/473,173
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/279,411
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 498
```



```
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAACGGAAGGCCTTT 19
    ||| | ||||| |||
Db 18 GAATGCAAGGCCTTT 3

RESULT 94
US-10-488-619-1860/c
; Sequence 1860, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1860
; LENGTH: 617
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1860

Query Match 58.2%; Score 12.8; DB 6; Length 617;
Best Local Similarity 87.5%; Pred. No. 2.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAACGGAAGGCCTTT 19
    ||| | ||||| |||
Db 582 GAAAGGAAGGCCTTT 567

RESULT 95
US-10-488-619-1455/c
; Sequence 1455, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1455
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1455

Query Match 58.2%; Score 12.8; DB 6; Length 630;
Best Local Similarity 87.5%; Pred. No. 2.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCCTT 18
    ||||| ||||| |||
Db 332 CGAACGGAAGGCCTT 317

RESULT 96
US-10-488-619-1859
; Sequence 1859, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
```

```
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1859
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1859

Query Match 58.2%; Score 12.8; DB 6; Length 711;
Best Local Similarity 87.5%; Pred. No. 2.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAACGGAAGGCCTTT 19
    ||| | ||||| |||
Db 647 GAAAGGAAGGCCTTT 662

RESULT 97
US-10-473-173-120
; Sequence 120, Application US/10473173
; Publication No. US20060088823A1
; GENERAL INFORMATION:
; APPLICANT: VAN ANDEL INSTITUTE
; TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
; FILE REFERENCE: 38345-170094
; CURRENT APPLICATION NUMBER: US/10/473,173
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/279,411
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 498
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 120
; LENGTH: 828
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-473-173-120

Query Match 58.2%; Score 12.8; DB 6; Length 828;
Best Local Similarity 87.5%; Pred. No. 2.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16
    ||||| ||||| |||
Db 6 GTCGAACGGAAGGAC 21

RESULT 98
US-11-217-529-490/c
; Sequence 490, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 490
; LENGTH: 996
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-490
```

```

Query Match      58.2%; Score 12.8; DB 7; Length 996;
Best Local Similarity 87.5%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CGAACGGAAAGGCCTT 18
Db 270 CGAAGCGGAAGGCCTT 255

RESULT 99
US-11-217-529-76912/c
; Sequence 76912, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIRO
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76912
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76912

Query Match      58.2%; Score 12.8; DB 7; Length 1074;
Best Local Similarity 87.5%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CGAACGGAAAGGCCTT 18
Db 792 CGTACGCAAGGCCTT 777

RESULT 100
US-11-217-529-5765/c
; Sequence 5765, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIRO
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5765
; LENGTH: 1098
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5765

Query Match      58.2%; Score 12.8; DB 7; Length 1098;
Best Local Similarity 87.5%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAACGGAAAGGCCTT 19

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Query Match      58.2%; Score 12.8; DB 7; Length 996;
Best Local Similarity 87.5%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY   3 CGAACGGAAAGGCCTT 18
Db    270 CGAAGCGGAAGGCCTT 255

RESULT 99
US-11-217-529-76912/c
; Sequence 76912, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIRO
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76912
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76912

Query Match      58.2%; Score 12.8; DB 7; Length 1074;
Best Local Similarity 87.5%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY   3 CGAACGGAAAGGCCTT 18
Db    792 CGTAGCGCAAGGCCTT 777

RESULT 100
US-11-217-529-5765/c
; Sequence 5765, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIRO
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5765
; LENGTH: 1098
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5765

Query Match      58.2%; Score 12.8; DB 7; Length 1098;
Best Local Similarity 87.5%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY   4 GAACGGAAGGCCTTT 19

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 02:22:49 ; Search time 223.994 seconds
(without alignments)
591.412 Million cell updates/sec

Title: US-10-665-708-24

Perfect score: 19

Sequence: 1 gaacggaagccttcgg 19

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

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- 6: geneseqn2002as:*
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- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	19	100.0	22	AD11273	Ad11273 Mycobacte
5	19	100.0	22	ADG88354	Adg88354 Mycobacte
6	19	100.0	22	AEA08229	Aea08229 Mycobacte
7	18	94.7	24	AD11272	Ad11272 Mycobacte
8	18	94.7	24	ADG88353	Adg88353 Mycobacte
9	18	94.7	24	AEA08228	Aea08228 Mycobacte
10	18	94.7	25	AD11271	Ad11271 Mycobacte
11	18	94.7	25	ADG88352	Adg88352 Mycobacte
12	18	94.7	25	AEA08227	Aea08227 Mycobacte
13	17.4	91.6	25	AAS30718	Aas30718 Mycobacte
14	17.4	91.6	25	AD220587	Adz20587 Formaldeh
15	17.4	91.6	500	AD22405	Aea22405 Mycobacte
16	17.4	91.6	1449	AEA22405	Aea22405 Mycobacte
17	17.4	91.6	1455	AEA22412	Aea22412 Mycobacte
18	17.4	91.6	1482	AEA22404	Aea22404 Mycobacte

AAV24413	Human CGD	1137	89.5	17	19	c
AAV24413	Target se	23	86.3	20	20	c
AAV13021	Mycobacte	23	86.3	21	21	c
AAV24418	Target se	25	86.3	22	22	c
AAV13026	Mycobacte	25	86.3	23	23	c
ADA68711	Rice gene	765	85.3	24	24	c
AAA02278	Human col	935	84.2	25	25	c
ADFA9057	Microorga	50	83.2	26	26	c
AA32481	Preferred	166	83.2	27	27	c
AA31293	Plant mic	170	83.2	28	28	c
AA31415	Plant mic	305	83.2	29	29	c
AB276674	Microctr	460	83.2	30	30	c
AEB72673	Streptosp	497	83.2	31	31	c
AED64356	Rhodococc	500	83.2	32	32	c
AED67301	DNA encod	576	83.2	33	33	c
ADO80217	Rhodococc	1343	83.2	34	34	c
ADW16264	DNA copy	1390	83.2	35	35	c
ADJ38609	Micromono	1403	83.2	36	36	c
ADW16290	DNA copy	1427	83.2	37	37	c
ADG61232	Baeyer-Vi	1439	83.2	38	38	c
ADZ35975	Verrucosi	1440	83.2	39	39	c
ADX38843	Microbisp	1443	83.2	40	40	c
AEA22406	Mycobacte	1461	83.2	41	41	c
AED35651	Pseudonoc	1483	83.2	42	42	c
ADR90327	Rhodococc	1511	83.2	43	43	c
ADR90325	Rhodococc	1511	83.2	44	44	c
AED11327	Aliphatic	1511	83.2	45	45	c
ADA1084	Coralli	1584	83.2	46	46	c
AEA1361	Mouse gen	1849	83.2	47	47	c
ACC47372	Human lat	2896	83.2	48	48	c
ADL35344	Murine se	2898	83.2	49	49	c
ACC47371	Rat late	3054	83.2	50	50	c
AA136998	Human mus	6883	83.2	51	51	c
ABX59986	cDNA enco	6883	83.2	52	52	c
ADJ30736	Human mus	6883	83.2	53	53	c
AED48445	M. echino	84222	83.2	54	54	c
AAC55929	Eucalyptu	455	81.1	55	55	c
AAC57218	Eucalyptu	455	81.1	56	56	c
ACL67957	M. xanthu	861	81.1	57	57	c
AB104331	Drosophil	5433	81.1	58	58	c
AB104330	Drosophil	7162	81.1	59	59	c
ACL64755	M. xanthu	23677	81.1	60	60	c
ADB82110	Human CDN	297	78.9	61	61	c
ABQ89167	Human pro	331	78.9	62	62	c
ACH79967	Human gen	592	78.9	63	63	c
ADI31363	Human CDN	1429	78.9	64	64	c
AD83430	Human lym	1429	78.9	65	65	c
AAN9589	Human pro	1453	78.9	66	66	c
ABN59917	Novel hum	2010	78.9	67	67	c
Aaf88159	Human thy	2015	78.9	68	68	c
AAS03044	Human dia	2098	78.9	69	69	c
AAK94562	Human ful	2169	78.9	70	70	c
ADL31436	Full leng	2169	78.9	71	71	c
ABA23974	Human tra	2173	78.9	72	72	c
ADB76868	A. gossyp	2240	78.9	73	73	c
ABL07155	Drosophil	3003	78.9	74	74	c
AAS25944	Human CDN	3293	78.9	75	75	c
ABX73285	Human nov	3293	78.9	76	76	c
AE83945	Human CDN	5165	78.9	77	77	c
AB107154	Drosophil	8544	78.9	78	78	c
AAT70787	Stenotic	40	77.9	79	79	c
AAK85278	Motif I f	87	77.9	80	80	c
ADP20374	Pinus rad	365	77.9	81	81	c
ACH95596	Klebsiell	375	77.9	82	82	c
ABD06974	Pseudomon	543	77.9	83	83	c
AAI43438	Probe #12	591	77.9	84	84	c
ABD07046	Pseudomon	600	77.9	85	85	c
ACA27357	Prokaryot	981	77.9	86	86	c
ADW16249	DNA copy	1158	77.9	87	87	c
AAZ11765	Maize his	1392	77.9	88	88	c
ADA71495	Rice gene	2000	77.9	89	89	c
ACL36116	Rice stre	2000	77.9	90	90	c
ABL14648	Drosophil	7564	77.9	91	91	c

92	14.8	77.9	7564	4	AAS57142	Aas57142 DNA encod	c 165	14.4	75.8	3764	4	ABL22306	AbL22306 Drosophil
93	14.8	77.9	7564	10	ADC35854	Adc35854 Drosophil	c 166	14.4	75.8	3809	6	ABK95303	Abk95303 Human pro
94	14.8	77.9	19183	4	AAK64938	Aak64938 Human imm	c 167	14.4	75.8	5634	4	ABL28614	AbL28614 Drosophi
95	14.8	77.9	19183	8	AAK36434	Aak36434 Human mus	c 168	14.4	75.8	5832	6	ABQ71069	Abq71069 Listeria
96	14.8	77.9	19183	8	ABX59422	Abx59422 cDNA enco	c 169	14.4	75.8	15419	4	ABL20618	AbL20618 Drosophi
97	14.8	77.9	19183	12	ADJ30172	Adj30172 Human mus	c 170	14.4	75.8	15434	4	ABL20620	AbL20620 Drosophi
98	14.8	77.9	30904	4	AAK75071	Aak75071 Human car	c 171	14.4	75.8	17794	4	ABL02220	AbL02220 Drosophi
99	14.8	77.9	32249	4	AAK36814	Aak36814 Human car	c 172	14.4	75.8	22958	13	ADT05537	Adt05537 Haemophil
100	14.8	77.9	32249	13	ADK47508	Adk47508 Human car	c 173	14.4	75.8	23615	14	AEC09537	Aec09537 Human Bli
101	14.8	77.9	32249	13	ADU08926	Adu08926 Human car	c 174	14.4	75.8	24281	13	ABD33480	Abd33480 Murine ca
102	14.8	77.9	42104	11	ACN44606	Acn44606 Human gen	c 175	14.4	75.8	24281	14	ADZ13479	Adz13479 Murine ca
103	14.8	77.9	87731	11	ACN44742	Acn44742 Human gen	c 176	14.4	75.8	41685	11	ACN44330	Acn44330 Human gen
104	14.8	77.9	89328	6	ABL61995	AbL61995 Colon ade	c 177	14.4	75.8	105305	11	ACN44760	Acn44760 Mouse gen
105	14.8	77.9	110000	9	ADB12064_02	AdB12064_02	c 178	14.4	75.8	110000	2	ATA2063_03	Ata2063_03
106	14.8	77.9	110000	9	ADB12064_03	AdB12064_03	c 179	14.4	75.8	110000	6	ABQ69245_03	AbQ69245_03
107	14.8	77.9	110000	12	ADN46845_10	AdN46845_10	c 180	14.4	75.8	110000	6	ABQ67197_02	AbQ67197_02
108	14.8	77.9	110000	12	ADN47591_10	AdN47591_10	c 181	14.4	75.8	110000	6	ABA03041_03	AbA03041_03
109	14.8	77.9	110000	12	ADN46123_10	AdN46123_10	c 182	14.4	75.8	110000	12	ADN46845_13	AdN46845_13
110	14.8	77.9	110000	12	ADN47209_10	AdN47209_10	c 183	14.4	75.8	110000	12	ADN47591_06	AdN47591_06
111	14.8	77.9	110000	12	ADN46464_10	AdN46464_10	c 184	14.4	75.8	110000	12	ADN46123_13	AdN46123_13
112	14.8	77.9	110000	12	ADN47960_10	AdN47960_10	c 185	14.4	75.8	110000	12	ADN47209_06	AdN47209_06
113	14.8	77.9	173115	14	AEB989425_10	Aeb989425_10	c 186	14.4	75.8	110000	12	ADN46464_13	AdN46464_13
114	14.4	75.8	27	2	AAV24410	Aav24410 Target se	c 187	14.4	75.8	110000	12	ADN47960_06	AdN47960_06
115	14.4	75.8	27	2	AAV13018	Aav13018 Mycobacte	c 188	14.4	75.8	138839	14	AED18450	Aed18450 Fibrotic
116	14.4	75.8	28	4	AAD11025	AdA11025 Probe #5	c 189	14.4	75.8	161974	15	AEP80153	Aep80153 Cancer-as
117	14.4	75.8	28	4	AAD11018	AdA11018 PCR prime	c 190	14.4	75.8	198161	6	ABK83564	Abk83564 Human CDN
118	14.4	75.8	32	4	AAD11024	AdA11024 Probe #4	c 191	14.4	75.8	198161	12	ADQ17348	Adq17348 Human sof
119	14.4	75.8	32	4	AAD11017	AdA11017 PCR prime	c 192	14.4	75.8	198161	13	ADR52701	Adr52701 Drug ther
120	14.4	75.8	50	2	AAX99195	Aax99195 M. avium	c 193	14.4	75.8	349980	5	AAH41224	Aah41224 Pyrococcu
121	14.4	75.8	50	2	AAX99196	Aax99196 M. fortui	c 194	14.4	75.8	349980	5	AAH41225	Aah41225 Pyrococcu
122	14.4	75.8	50	12	ADP94050	AdP94050 Microorga	c 195	14.4	75.8	349980	13	ADT05648	Adt05648 Haemophil
123	14.4	75.8	209	14	AEB98762	Aeb98762 Mycobacte	c 196	14.2	74.7	142	6	AAS98571	Aas98571 Human neu
124	14.4	75.8	341	4	AAS36010	Aas36010 Human car	c 197	14.2	74.7	159	10	ABZ39038	Abz39038 N. gonorr
125	14.4	75.8	341	4	AAS36011	Aas36011 Human car	c 198	14.2	74.7	193	2	AAT22735	Aat22735 Human gen
126	14.4	75.8	341	10	ADS46704	AdS46704 Human car	c 199	14.2	74.7	301	3	AAA06480	Aaa06480 Human imm
127	14.4	75.8	341	10	ADE46705	AdE46705 Human car	c 200	14.2	74.7	301	4	AAH93596	Aah93596 Human pro
128	14.4	75.8	341	13	ADJ08123	Adj08123 Human car	c 201	14.2	74.7	301	4	AAS63688	Aas63688 Human pro
129	14.4	75.8	341	13	ADJ08122	Adj08122 Human car	c 202	14.2	74.7	301	4	AAH02661	Aah02661 Prostate
130	14.4	75.8	352	4	AAS35269	Aas35269 Human car	c 203	14.2	74.7	301	4	AAH84910	Aah84910 Human pro
131	14.4	75.8	352	10	ADE45348	AdE45348 Human car	c 204	14.2	74.7	301	5	ACA59497	AcA59497 Prostate
132	14.4	75.8	352	13	ADJ06766	Adj06766 Human car	c 205	14.2	74.7	301	6	ABU95060	AbU95060 Human PTP
133	14.4	75.8	381	5	AAS77874	AdS77874 DNA encod	c 206	14.2	74.7	301	8	ACC95224	Acc95224 Prostate
134	14.4	75.8	560	10	ABT23571	AbT23571 Stabilisi	c 207	14.2	74.7	301	10	ADB13697	AdB13697 Human pro
135	14.4	75.8	649	4	AAH69025	Aah69025 Human cer	c 208	14.2	74.7	301	10	ADG26113	Adg26113 Human pro
136	14.4	75.8	649	4	AAH69025	Aah69025 Human cer	c 209	14.2	74.7	301	15	AEP66394	Aep66394 Human pro
137	14.4	75.8	981	3	AAC54004	Aac54004 Arabidops	c 210	14.2	74.7	341	14	ADV75211	Adv75211 Human col
138	14.4	75.8	983	3	AAC52885	Aac52885 Arabidops	c 211	14.2	74.7	387	14	ACL67607	ACL67607 M. xanthu
139	14.4	75.8	1158	4	ABL23865	AbL23865 Drosophil	c 212	14.2	74.7	411	8	ABX39805	Abx39805 Bovine ES
140	14.4	75.8	1158	13	ADQ89669	Adq89669 Antagonis	c 213	14.2	74.7	424	4	ABA08574	AbA08574 Human enh
141	14.4	75.8	1296	4	ABL22307	AbL22307 Drosophil	c 214	14.2	74.7	426	10	ADC35700	AdC35700 Rhodococc
142	14.4	75.8	1421	14	AEA22411	Aea22411 Mycobacte	c 215	14.2	74.7	427	14	ADY37634	Ady37634 Leishmani
143	14.4	75.8	1431	12	ADM66476	AdM66476 Corynebac	c 216	14.2	74.7	447	14	ADY37632	Ady37632 Leishmani
144	14.4	75.8	1431	12	ADM66445	AdM66445 Corynebac	c 217	14.2	74.7	447	14	ADY37633	Ady37633 Leishmani
145	14.4	75.8	1446	2	AAV38415	Aav38415 DNA encod	c 218	14.2	74.7	447	14	ADY37631	Ady37631 Leishmani
146	14.4	75.8	1449	2	AAQ37639	Aaq37639 Mycobacte	c 219	14.2	74.7	447	14	ADY37630	Ady37630 Leishmani
147	14.4	75.8	1454	14	AEA22401	Aea22401 Mycobacte	c 220	14.2	74.7	456	10	ABZ39039	Abz39039 N. gonorr
148	14.4	75.8	1465	10	ADB61680	AdB61680 16S rRNA	c 221	14.2	74.7	499	9	ACH13049	Ach13049 Human adu
149	14.4	75.8	1472	13	ADR90572	AdR90572 M avium 1	c 222	14.2	74.7	503	12	ADJ39286	Adj39286 Plant CDN
150	14.4	75.8	1906	13	ADQ85867	AdQ85867 Human tum	c 223	14.2	74.7	508	3	AAC59084	AcA59084 Human sec
151	14.4	75.8	1907	4	AAH14960	Aah14960 Human cDN	c 224	14.2	74.7	511	13	AAF08440	Aaf08440 Fusarium
152	14.4	75.8	1907	13	ADX27659	AdX27659 Plant ful	c 225	14.2	74.7	511	13	ADU52481	AdU52481 Fusarium
153	14.4	75.8	1908	13	ADR76376	AdR76376 Novel hum	c 226	14.2	74.7	511	14	ADZ90484	AdZ90484 Fusarium
154	14.4	75.8	1908	13	ADR24740	AdR24740 Breast ca	c 227	14.2	74.7	523	3	AAQ35675	Aaq35675 Arabidops
155	14.4	75.8	1908	13	ADP56021	AdP56021 Human PRO	c 228	14.2	74.7	526	4	AAH11789	Aah11789 Human CDN
156	14.4	75.8	1942	6	ABK34562	AbK34562 Human cDN	c 229	14.2	74.7	529	10	ADC35702	AdC35702 Rhodococc
157	14.4	75.8	1972	10	ADD14695	AdD14695 Human src	c 230	14.2	74.7	535	13	ADS75567	AdS75567 Rhodococc
158	14.4	75.8	1972	14	AED17806	Aed17806 Fibrotic	c 231	14.2	74.7	600	3	AAC79222	AcA79222 Human lun
159	14.4	75.8	1972	15	AEE60944	Aee60944 Human pat	c 232	14.2	74.7	600	4	ADZ32298	AdZ32298 Human lun
160	14.4	75.8	2400	13	AEE31095	Aee31095 Haemophil	c 233	14.2	74.7	600	10	ADD66572	AdD66572 Human lun
161	14.4	75.8	2919	13	ADS59960	AdS59960 Bacterial	c 234	14.2	74.7	600	10	ADB87826	AdB87826 Human lun
162	14.4	75.8	3231	11	ADM03126	AdM03126 Human cDN	c 235	14.2	74.7	610	13	ACN56868	AcN56868 Cotton gy
163	14.4	75.8	3291	14	AEC86056	Aec86056 Human cDN	c 236	14.2	74.7	624	10	ADC72425	AdC72425 DNA Seq I
164	14.4	75.8	3417	4	ABL23864	AbL23864 Drosophil	c 237	14.2	74.7	633	10	ACF70237	AcF70237 Photorehab

238	14.2	74.7	691	2	AAX20463	Aax20463 Human sec
239	14.2	74.7	691	3	AAA72426	Aaa72426 Human nuc
240	14.2	74.7	691	10	ADD90247	Add90247 Novel hum
241	14.2	74.7	691	10	ADG90066	Adg90066 Human cDN
242	14.2	74.7	691	14	ADY25406	Ady25406 Novel hum
243	14.2	74.7	713	10	ABX95074	Abx95074 Human p11
244	14.2	74.7	713	14	AED14036	Aed14036 Human cum
245	14.2	74.7	769	6	ABQ56097	Abq56097 Human ova
246	14.2	74.7	776	4	AAI94564	Aai94564 Human neu
247	14.2	74.7	788	3	AAC33114	Aac33114 Arabidops
248	14.2	74.7	798	5	AAH68033	Aah68033 C glucami
249	14.2	74.7	851	4	AAI94024	Aai94024 Human neu
250	14.2	74.7	861	3	AAAD01331	Aaad01331 Soybean P
251	14.2	74.7	861	6	ABK34319	Abk34319 Human cDN
252	14.2	74.7	861	10	ABZ39185	Abz39185 N. gonorr
253	14.2	74.7	879	4	AAF71819	Aaf71819 Corynebac
254	14.2	74.7	879	4	AAF72312	Aaf72312 Corynebac
255	14.2	74.7	891	4	AAH05515	Aah05515 Human cDN
256	14.2	74.7	898	6	ABS70422	Abs70422 Human bon
257	14.2	74.7	928	10	ADD13548	Add13548 C. glutam
258	14.2	74.7	936	6	ABN74448	Abn74448 Bovine em
259	14.2	74.7	954	6	ABQ20284	Abq20284 Oligonuci
260	14.2	74.7	954	6	ABQ20285	Abq20285 Oligonuci
261	14.2	74.7	996	10	ACF67845	Acf67845 Photorhab
262	14.2	74.7	1024	6	ABX65639	Abx65639 Helicobac
263	14.2	74.7	1024	6	ABX66177	Abx66177 Helicobac
264	14.2	74.7	1035	6	ABS51363	Abs51363 cDNA enco
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266	14.2	74.7	1158	4	ABL23865	AbL23865 Drosophil
267	14.2	74.7	1158	13	ADQ96669	Adq96669 Antagonis
268	14.2	74.7	1161	14	ABE66883	Abe66883 Rice geno
269	14.2	74.7	1194	6	ABQ75110	Abq75110 Anopheles
270	14.2	74.7	1194	10	ACF79723	Acf79723 Mosquito
271	14.2	74.7	1236	3	AAC45925	Aac45925 Arabidops
272	14.2	74.7	1315	6	ABL57729	AbL57729 Human sbg
273	14.2	74.7	1329	13	ADU05441	Adu05441 DNA encod
274	14.2	74.7	1332	8	ACA34802	Aca34802 Prokaryot
275	14.2	74.7	1425	12	ADH71201	Adh71201 Human gen
276	14.2	74.7	1437	12	ADF56670	Adf56670 YS-44442
277	14.2	74.7	1437	12	ADG64519	Adg64519 Saccharot
278	14.2	74.7	1437	14	ADY86147	Ady86147 Saccharot
279	14.2	74.7	1443	10	ADB69806	Adb69806 C. neofor
280	14.2	74.7	1471	12	ADF56671	Adf56671 YS-45494
281	14.2	74.7	1471	12	ADG64520	Adg64520 Saccharot
282	14.2	74.7	1471	14	ADY86148	Ady86148 Saccharot
283	14.2	74.7	1477	14	AED47485	Aed47485 Nocardia
284	14.2	74.7	1484	2	AAV90921	Aav90921 Nucleotid
285	14.2	74.7	1488	13	ADS17289	Ads17289 Lechevali
286	14.2	74.7	1491	4	AAF77686	Aaf77686 Human pro
287	14.2	74.7	1494	6	ABL57728	AbL57728 Human sbg
288	14.2	74.7	1498	13	ADS47642	Ads47642 Bacterial
289	14.2	74.7	1514	14	ADW12667	Adw12667 Rhodococ
290	14.2	74.7	1529	2	AAH14164	Aah14164 H. pylori
291	14.2	74.7	1538	3	AAC36652	Aac36652 Arabidops
292	14.2	74.7	1540	2	AAV90845	Aav90845 Nucleotid
293	14.2	74.7	1540	3	AAC45334	Aac45334 Arabidops
294	14.2	74.7	1555	3	ADAD01326	Adad01326 Soybean P
295	14.2	74.7	1584	6	AAD28460	Aad28460 Bacillus
296	14.2	74.7	1612	12	ADH71205	Adh71205 Human gen
297	14.2	74.7	1675	4	AAH89283	Aah89283 Brassica
298	14.2	74.7	1677	4	AAA89279	Aaa89279 Arabidops
299	14.2	74.7	1691	10	ADB63529	Adb63529 Human cDN
300	14.2	74.7	1695	12	ADO02829	Ado02829 Soybean o

ALIGNMENTS

RESULT 1
RAD11274
ID RAD11274 standard; DNA; 19 BP.
XX
AC RAD11274;

XX	24-SEP-2001	(first entry)	24-SEP-2001	(first entry)
DT	Mycobacterium 16S rRNA amplifying primer #18.	Mycobacterium 16S rRNA amplifying primer #18.	Mycobacterium 16S rRNA amplifying primer #18.	Mycobacterium 16S rRNA amplifying primer #18.
DE	Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;	Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;	Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;	Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
XX	Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.	Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.	Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.	Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
XX	Mycobacterium sp.	Mycobacterium sp.	Mycobacterium sp.	Mycobacterium sp.
OS	WO200144510-A2.	WO200144510-A2.	WO200144510-A2.	WO200144510-A2.
PN	21-JUN-2001.	21-JUN-2001.	21-JUN-2001.	21-JUN-2001.
XX	17-DEC-1999;	99WO-US030346.	17-DEC-1999;	99WO-US030346.
XX	17-DEC-1999;	99WO-US030346.	17-DEC-1999;	99WO-US030346.
XX	(GENP-) GEN-PROBE INC.	(GENP-) GEN-PROBE INC.	(GENP-) GEN-PROBE INC.	(GENP-) GEN-PROBE INC.
PA	(INMR) BIOMERIEUX SA.	(INMR) BIOMERIEUX SA.	(INMR) BIOMERIEUX SA.	(INMR) BIOMERIEUX SA.
XX	Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;	Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;	Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;	Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX	WPI; 2001-398170/42.	WPI; 2001-398170/42.	WPI; 2001-398170/42.	WPI; 2001-398170/42.
DR	Detecting Mycobacterium species, involves in vitro amplification of 16S	Detecting Mycobacterium species, involves in vitro amplification of 16S	Detecting Mycobacterium species, involves in vitro amplification of 16S	Detecting Mycobacterium species, involves in vitro amplification of 16S
XX	rRNA or DNA encoding RNA in nucleic acid amplification mixture using	rRNA or DNA encoding RNA in nucleic acid amplification mixture using	rRNA or DNA encoding RNA in nucleic acid amplification mixture using	rRNA or DNA encoding RNA in nucleic acid amplification mixture using
XX	specific primers, and detecting the amplified nucleic acid.	specific primers, and detecting the amplified nucleic acid.	specific primers, and detecting the amplified nucleic acid.	specific primers, and detecting the amplified nucleic acid.
XX	Claim 1; Page 36; 44pp; English.	Claim 1; Page 36; 44pp; English.	Claim 1; Page 36; 44pp; English.	Claim 1; Page 36; 44pp; English.
XX	The invention relates to a method of detecting Mycobacterium species,	The invention relates to a method of detecting Mycobacterium species,	The invention relates to a method of detecting Mycobacterium species,	The invention relates to a method of detecting Mycobacterium species,
XX	that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA	that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA	that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA	that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
XX	encoding 16S rRNA in an in vitro nucleic acid amplification mixture	encoding 16S rRNA in an in vitro nucleic acid amplification mixture	encoding 16S rRNA in an in vitro nucleic acid amplification mixture	encoding 16S rRNA in an in vitro nucleic acid amplification mixture
XX	comprising a polymerase, and at least two primers, and then detecting the	comprising a polymerase, and at least two primers, and then detecting the	comprising a polymerase, and at least two primers, and then detecting the	comprising a polymerase, and at least two primers, and then detecting the
XX	amplified nucleic acid. The method is relatively simple and useful for	amplified nucleic acid. The method is relatively simple and useful for	amplified nucleic acid. The method is relatively simple and useful for	amplified nucleic acid. The method is relatively simple and useful for
XX	detecting the presence of various Mycobacterium species in a biological	detecting the presence of various Mycobacterium species in a biological	detecting the presence of various Mycobacterium species in a biological	detecting the presence of various Mycobacterium species in a biological
XX	sample, and thus important for diagnosis of infections resulting from	sample, and thus important for diagnosis of infections resulting from	sample, and thus important for diagnosis of infections resulting from	sample, and thus important for diagnosis of infections resulting from
XX	them. The method is especially important for screening opportunistic	them. The method is especially important for screening opportunistic	them. The method is especially important for screening opportunistic	them. The method is especially important for screening opportunistic
XX	infections caused by M. tuberculosis or a Mycobacterium other than	infections caused by M. tuberculosis or a Mycobacterium other than	infections caused by M. tuberculosis or a Mycobacterium other than	infections caused by M. tuberculosis or a Mycobacterium other than
XX	tuberculosis (MOTT). The present sequence is a PCR primer used for	tuberculosis (MOTT). The present sequence is a PCR primer used for	tuberculosis (MOTT). The present sequence is a PCR primer used for	tuberculosis (MOTT). The present sequence is a PCR primer used for
XX	amplifying Mycobacterium 16S rRNA	amplifying Mycobacterium 16S rRNA	amplifying Mycobacterium 16S rRNA	amplifying Mycobacterium 16S rRNA
XX	Sequence 19 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 0 Other;	Sequence 19 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 0 Other;	Sequence 19 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 0 Other;	Sequence 19 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
XX	Query Match 100.0%; Score 19; DB 4; Length 19;	Query Match 100.0%; Score 19; DB 4; Length 19;	Query Match 100.0%; Score 19; DB 4; Length 19;	Query Match 100.0%; Score 19; DB 4; Length 19;
XX	Best Local Similarity 100.0%; Pred. No. 5.5;	Best Local Similarity 100.0%; Pred. No. 5.5;	Best Local Similarity 100.0%; Pred. No. 5.5;	Best Local Similarity 100.0%; Pred. No. 5.5;
XX	Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 GAACGGAAGGCTTCGG 19	1 GAACGGAAGGCTTCGG 19	1 GAACGGAAGGCTTCGG 19	1 GAACGGAAGGCTTCGG 19
Db				
Db	1 GAACGGAAGGCTTCGG 19	1 GAACGGAAGGCTTCGG 19	1 GAACGGAAGGCTTCGG 19	1 GAACGGAAGGCTTCGG 19
RESULT 2				
ADG88355				
ID	ADG88355 standard; DNA; 19 BP.	ADG88355 standard; DNA; 19 BP.	ADG88355 standard; DNA; 19 BP.	ADG88355 standard; DNA; 19 BP.
XX	ADG88355;	ADG88355;	ADG88355;	ADG88355;
AC	11-MAR-2004 (first entry)	11-MAR-2004 (first entry)	11-MAR-2004 (first entry)	11-MAR-2004 (first entry)
XX	Mycobacterium amplifying PCR primer #24.	Mycobacterium amplifying PCR primer #24.	Mycobacterium amplifying PCR primer #24.	Mycobacterium amplifying PCR primer #24.
XX	In vitro amplification; PCR; primer; ss.	In vitro amplification; PCR; primer; ss.	In vitro amplification; PCR; primer; ss.	In vitro amplification; PCR; primer; ss.
XX	Mycobacterium xenopi.	Mycobacterium xenopi.	Mycobacterium xenopi.	Mycobacterium xenopi.
XX	US2003165824-A1.	US2003165824-A1.	US2003165824-A1.	US2003165824-A1.
XX	04-SEP-2003.	04-SEP-2003.	04-SEP-2003.	04-SEP-2003.
XX	15-DEC-2000; 2000US-00738274.	15-DEC-2000; 2000US-00738274.	15-DEC-2000; 2000US-00738274.	15-DEC-2000; 2000US-00738274.


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Best Local Similarity 100.0%; Pred. No. 5.6; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 0;

QY 1 GAACGGAAGGCTTCGG 19
DB 4 GAACGGAAGGCTTCGG 22

RESULT 5
ADG88354
ID ADG88354 standard; DNA; 22 BP.
XX
AC ADG88354;
XX
DT 11-MAR-2004 (first entry)
XX
DE Mycobacterium amplifying PCR primer #23.
XX
KW In vitro amplification; PCR; primer; ss.
XX
OS Mycobacterium celatum.
XX
PN US2003165824-A1.
XX
PD 04-SEP-2003.
XX
PF 15-DEC-2000; 2000US-00738274.
XX
PR 17-DEC-1999; 99US-0172190P.
XX
PS (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAI P.
PA (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
DR WPI; 2003-898044/82.
XX
PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample comprises performing in vitro nucleic acid
PT amplification and detection of amplified products.
XX
PS Claim 1; SEQ ID NO 23; 20pp; English.
XX
CC The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample comprises performing an in vitro
CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
CC detecting the amplified Mycobacterium nucleic acid. The present sequence
CC is Mycobacterium amplifying PCR primer.
XX
SQ Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTCGG 19
DB 4 GAACGGAAGGCTTCGG 22

RESULT 6
AEA08229
ID AEA08229 standard; DNA; 22 BP.
XX
AC AEA08229;
XX
DT 14-JUL-2005 (first entry)
XX
DE Mycobacterium celatum 16SrRNA amplifying non-T7 primer, SEQ ID NO: 23.
XX

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Microorganism detection; DNA amplification; 16s ribosomal RNA; 16s rRNA;
PCR; primer; ss.
XX
OS Mycobacterium celatum.
XX
PN US2005100915-A1.
XX
PD 12-MAY-2005.
XX
PF 18-SEP-2003; 2003US-00665708.
XX
PR 17-DEC-1999; 99US-0172190P.
PR 15-DEC-2000; 2000US-00738274.
XX
(BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAI P.
PA (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
DR WPI; 2005-345392/35.
XX
PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample, comprises using in vitro nucleic acid
PT amplification and detection of amplified products.
XX
PS Claim 8; SEQ ID NO 23; 21pp; English.
XX
CC The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample. The method involves using in
CC vitro nucleic acid amplification and detection of amplified products. The
CC invention is useful for diagnostic detection of pathogenic bacteria such
CC as Mycobacterium species. The present sequence is the Mycobacterium
CC celatum (ATCC 51130 and ATCC 51131) 16S ribosomal RNA (16S-rRNA)
CC amplifying non-r7 PCR primer.
XX
SQ Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTCGG 19
DB 4 GAACGGAAGGCTTCGG 22

RESULT 7
AAD11272
ID AAD11272 standard; DNA; 24 BP.
XX
AC AAD11272;
XX
DT 24-SEP-2001 (first entry)
XX
DE Mycobacterium 16S rRNA amplifying primer #16.
XX
KW Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
KW Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
XX
OS Mycobacterium sp.
XX
PN WO200144510-A2.
XX
PD 21-JUN-2001.
XX
PF 17-DEC-1999; 99WO-US030346.
XX
PR 17-DEC-1999; 99WO-US030346.
XX
PA (GENP-) GEN-PROBE INC.

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PA (INMR ) BIOMERIEUX SA.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
XX WPI; 2001-398170/42.
DR
XX
PT Detecting Mycobacterium species, involves in vitro amplification of 16S
PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using
PT specific primers, and detecting the amplified nucleic acid.
XX
XX Claim 1; Page 36; 44pp; English.
XX
XX The invention relates to a method of detecting Mycobacterium species.
XX that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
XX encoding 16S rRNA in an in vitro nucleic acid amplification mixture
XX comprising a polymerase, and at least two primers, and then detecting the
XX amplified nucleic acid. The method is relatively simple and useful for
XX detecting the presence of various Mycobacterium species in a biological
XX sample, and thus important for diagnosis of infections resulting from
XX them. The method is especially important for screening opportunistic
XX infections caused by M. tuberculosis or a Mycobacterium other than
XX tuberculosis (MOTT). The present sequence is a PCR primer used for
XX amplifying Mycobacterium 16S rRNA
XX
XX Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
SQ
Query Match 94.7%; Score 18; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTCG 18
Db |||||
7 GAACGGAAGGCTTCG 24

RESULT 8
ADG88353
ID ADG88353 standard; DNA; 24 BP.
XX
AC ADG88353;
XX
DT 11-MAR-2004 (first entry)
DE Mycobacterium amplifying PCR primer #22.
XX
DE In vitro amplification; PCR; primer; ss.
XX
OS Mycobacterium celatum.
XX
PN US2003165824-A1.
XX
PD 04-SEP-2003.
XX
PF 15-DEC-2000; 2000US-00738274.
XX
PR 17-DEC-1999; 99US-0172190P.
XX
PS (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAT P.
PA (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
DR WPI; 2003-898044/82.
XX
PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample comprises performing in vitro nucleic acid
PT amplification and detection of amplified products.
XX
PS Claim 1; SEQ ID NO 22; 20pp; English.
XX

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CC The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample comprises performing an in vitro
CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
CC detecting the amplified Mycobacterium nucleic acid. The present sequence
CC is Mycobacterium amplifying PCR primer.
XX
SQ Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 94.7%; Score 18; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTCG 18
Db |||||
7 GAACGGAAGGCTTCG 24

RESULT 9
AEA08228
ID AEA08228 standard; DNA; 24 BP.
XX
AC AEA08228;
XX
DT 14-JUL-2005 (first entry)
DE Mycobacterium celatum 16SrRNA amplifying non-T7 primer, SEQ ID NO: 22.
XX
KW Microorganism detection; DNA amplification; 16s ribosomal RNA; 16s rRNA;
KW PCR; primer; ss.
XX
OS Mycobacterium celatum.
XX
PN US2005100915-A1.
XX
PD 12-MAY-2005.
XX
PF 18-SEP-2003; 2003US-00665708.
XX
PR 17-DEC-1999; 99US-0172190P.
PR 15-DEC-2000; 2000US-00738274.
XX
XX (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAT P.
PA (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
DR WPI; 2005-345392/35.
XX
PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample, comprises using in vitro nucleic acid
PT amplification and detection of amplified products.
XX
PS Claim 8; SEQ ID NO 22; 21pp; English.
XX
XX The present invention relates to a method of detecting Mycobacterium
XX species present in a biological sample. The method involves using in
XX vitro nucleic acid amplification and detection of amplified products. The
XX invention is useful for diagnostic detection of pathogenic bacteria such
XX as Mycobacterium species. The present sequence is the Mycobacterium
XX celatum (ATCC 51130 and ATCC 51131) 16S ribosomal RNA (16SrRNA)
XX amplifying non-T7 PCR primer.
XX
XX Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 94.7%; Score 18; DB 14; Length 24;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTCG 18
|||

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Db          7 GAACGGAAAGCCTTTCG 24

RESULT 10
AAD11271
ID AAD11271 standard; DNA; 25 BP.
XX
AC AAD11271;
XX
DT 24-SEP-2001 (first entry)
XX
DE Mycobacterium 16S rRNA amplifying primer #15.
XX
KW Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
KW Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
XX
OS Mycobacterium sp.
XX
PN WO200144510-A2.
XX
PD 21-JUN-2001.
XX
PF 17-DEC-1999; 99WO-US030346.
XX
PR 17-DEC-1999; 99WO-US030346.
XX
PA (GENP-) GEN-PROBE INC.
PA (INMR ) BIOMERIEUX SA.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
DR WPI; 2001-398170/42.
XX
PT Detecting Mycobacterium species, involves in vitro amplification of 16S
PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using
PT specific primers, and detecting the amplified nucleic acid.
XX
SQ Claim 1; Page 36; 44pp; English.
XX
CC The invention relates to a method of detecting Mycobacterium species,
CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture
CC comprising a polymerase, and at least two primers, and then detecting the
CC amplified nucleic acid. The method is relatively simple and useful for
CC detecting the presence of various Mycobacterium species in a biological
CC sample, and thus important for diagnosis of infections resulting from
CC them. The method is especially important for screening opportunistic
CC infections caused by M. tuberculosis or a Mycobacterium other than
CC tuberculosis (MOTT). The present sequence is a PCR primer used for
CC amplifying Mycobacterium 16S rRNA
XX
SQ Sequence 25 BP; 7 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 94.7%; Score 18; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCCTTTCG 18
Db 8 GAACGGAAAGCCTTTCG 25

RESULT 11
ADG88352
ID ADG88352 standard; DNA; 25 BP.
XX
AC ADG88352;
XX
DT 11-MAR-2004 (first entry)
XX
DE Mycobacterium amplifying PCR primer #21.
XX
KW In vitro amplification; PCR; primer; ss.

Mycobacterium celatum.
US2003165824-A1.
04-SEP-2003.
15-DEC-2000; 2000US-00738274.
17-DEC-1999; 99US-0172190P.
(BREN/) BRENTANO S T.
(JUCK/) JUCKER M T.
(DELG/) DELGADO F D.
(CLEU/) CLEUZIAT P.
(RODR/) RODRIGUE M.
Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
WPI; 2003-898044/82.
Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
in a biological sample comprises performing in vitro nucleic acid
amplification and detection of amplified products.
Claim 1; SEQ ID NO 21; 20pp; English.
The present invention relates to a method of detecting Mycobacterium
species present in a biological sample comprises performing an in vitro
amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
detecting the amplified Mycobacterium nucleic acid. The present sequence
is Mycobacterium amplifying PCR primer.
Sequence 25 BP; 7 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 94.7%; Score 18; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCCTTTCG 18
Db 8 GAACGGAAAGCCTTTCG 25

RESULT 12
AEA08227
ID AEA08227 standard; DNA; 25 BP.
XX
AC AEA08227;
XX
DT 14-JUL-2005 (first entry)
XX
DE Mycobacterium celatum 16SrRNA amplifying non-T7 primer, SEQ ID NO: 21.
XX
KW Microorganism detection; DNA amplification; 16S ribosomal RNA; 16S rRNA;
KW PCR; primer; ss.
XX
OS Mycobacterium celatum.
XX
PN US2005100915-A1.
XX
PD 12-MAY-2005.
XX
PF 18-SEP-2003; 2003US-00665708.
XX
PR 17-DEC-1999; 99US-0172190P.
PR 15-DEC-2000; 2000US-00738274.
(BREN/) BRENTANO S T.
(JUCK/) JUCKER M T.
(DELG/) DELGADO F D.
(CLEU/) CLEUZIAT P.
(RODR/) RODRIGUE M.

```


XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
 PI WPI; 2005-345392/35.
 DR
 XX
 PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
 in a biological sample, comprises using in vitro nucleic acid
 PT amplification and detection of amplified products.
 XX
 PS Claim 8; SEQ ID NO 21; 21pp; English.
 XX
 CC The present invention relates to a method of detecting Mycobacterium
 CC species present in a biological sample. The method involves using in
 CC vitro nucleic acid amplification and detection of amplified products. The
 CC invention is useful for diagnostic detection of pathogenic bacteria such
 CC as Mycobacterium species. The present sequence is the Mycobacterium
 CC celatum (ATCC 51130 and ATCC 51131) 16S ribosomal RNA (16SrRNA)
 CC amplifying non-T7 PCR primer.
 XX
 SQ Sequence 25 BP; 7 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
 Query Match 94.7%; Score 18; DB 14; Length 25;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAACGGAAAGCCCTTCG 18
 |||||
 Db 8 GAACGGAAAGCCCTTCG 25
 |||||
 RESULT 13
 AAS30718
 ID AAS30718 standard; DNA; 25 BP.
 XX
 AC AAS30718;
 XX
 XX 06-AUG-2003 (revised)
 DT 04-DEC-2001 (first entry)
 XX
 DE Mycobacterium species-specific probe #24.
 XX
 KW Mycobacterium; species-specific bacterial identification; primer; ss.
 XX
 OS Mycobacterium chelonae.
 XX
 PN WO200166797-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 01-MAR-2001; 2001WO-US006731.
 XX
 PR 03-MAR-2000; 2000US-0186840P.
 XX
 PA (BECI) BECKMAN COULTER INC.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (USSH) US NAT INST OF HEALTH.
 XX
 PI Fischer SH, Rampal JB, Fahle GA, Conville PS;
 XX
 DR WPI; 2001-514847/56.
 XX
 PT Species-specific bacterial identification, used particularly to identify
 PT Mycobacterium species, involves hybridizing bacterial genus-selective or
 PT specific primers to a sample.
 XX
 PS Claim 28; Page 21; 43pp; English.
 XX
 CC The invention relates to a method of species-specific bacterial
 CC identification, comprising hybridising a bacterial genus-selective or
 CC specific primer to a sample and amplifying nucleic acids. This is
 CC followed by hybridising the amplified nucleic acid to a solid phase array
 CC comprising bacterial species specific probe oligonucleotides chemically
 CC linked to a polymeric support in a predetermined pattern. This method is

CC used for species-specific identification of a bacterium, particularly a
 CC Mycobacterium, especially M. gordonae, M. intracellulare, M. avium, M.
 CC tuberculosis, M. marinum, or M. kansasii. The method provides rapid
 CC identification of multiple species of Mycobacterium. AAS30686-AAS30720
 CC represent Mycobacterium species-specific primers and probes used in the
 CC method of the invention. (Updated on 06-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 25 BP; 5 A; 6 C; 10 G; 4 T; 0 U; 0 Other;
 Query Match 91.6%; Score 17.4; DB 4; Length 25;
 Best Local Similarity 94.7%; Pred. No. 39;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GAACGGAAAGCCCTTCG 19
 |||||
 Db 1 GAACGGAAAGCCCTTCG 19
 |||||
 RESULT 14
 AAS30716
 ID AAS30716 standard; DNA; 25 BP.
 XX
 AC AAS30716;
 XX
 XX 06-AUG-2003 (revised)
 DT 04-DEC-2001 (first entry)
 XX
 DE Mycobacterium species-specific probe #22.
 XX
 KW Mycobacterium; species-specific bacterial identification; primer; ss.
 XX
 OS Mycobacterium chelonae.
 XX
 PN WO200166797-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 01-MAR-2001; 2001WO-US006731.
 XX
 PR 03-MAR-2000; 2000US-0186840P.
 XX
 PA (BECI) BECKMAN COULTER INC.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (USSH) US NAT INST OF HEALTH.
 XX
 PI Fischer SH, Rampal JB, Fahle GA, Conville PS;
 XX
 DR WPI; 2001-514847/56.
 XX
 PT Species-specific bacterial identification, used particularly to identify
 PT Mycobacterium species, involves hybridizing bacterial genus-selective or
 PT specific primers to a sample.
 XX
 PS Claim 28; Page 21; 43pp; English.
 XX
 CC The invention relates to a method of species-specific bacterial
 CC identification, comprising hybridising a bacterial genus-selective or
 CC specific primer to a sample and amplifying nucleic acids. This is
 CC followed by hybridising the amplified nucleic acid to a solid phase array
 CC comprising bacterial species specific probe oligonucleotides chemically
 CC linked to a polymeric support in a predetermined pattern. This method is
 CC used for species-specific identification of a bacterium, particularly a
 CC Mycobacterium, especially M. gordonae, M. intracellulare, M. avium, M.
 CC tuberculosis, M. marinum, or M. kansasii. The method provides rapid
 CC identification of multiple species of Mycobacterium. AAS30686-AAS30720
 CC represent Mycobacterium species-specific primers and probes used in the
 CC method of the invention. (Updated on 06-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 25 BP; 6 A; 6 C; 9 G; 4 T; 0 U; 0 Other;
 Query Match 91.6%; Score 17.4; DB 4; Length 25;
 Best Local Similarity 94.7%; Pred. No. 39;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy      1 GAACGGAAGGCCCTTCGG 19
Db      1 GAACGGAAGGCCCTTCGG 19

RESULT 15
ADZ20587
ID      ADZ20587 standard; DNA; 500 BP.
XX
AC      ADZ20587;
XX
DT      16-JUN-2005 (first entry)
XX
DE      Formaldehyde decomposition related Mycobacterium sp. DNA.
XX
KW      decomposition; formaldehyde; ds.
XX
OS      Mycobacterium sp.
XX
PN      JP2003284548-A.
XX
PD      07-OCT-2003.
XX
PF      27-MAR-2002; 2002JP-00089307.
XX
PR      27-MAR-2002; 2002JP-00089307.
XX
PA      (KUMO-) KUMOMOTO KEN PREFECTURE.
PA      (MITS-) MITSUWA CORP YG.
PA      (MITS-) MITSUWA BIRO KK.
XX
DR      WPI; 2004-172963/17.
XX
PT      Decomposing formaldehyde by Mycobacterium and/or growth medium of the
PT      cells.
XX
PS      Example 1; SEQ ID NO 1; 20pp; Japanese.
XX
CC      The invention relates to a novel method for decomposing formaldehyde by
CC      using microbial cells that belong to Mycobacterium sp. or Fusarium
CC      oxysporum, and/or the growth medium of the microbial cells. The invention
CC      further comprises: microbial cells which belong to Mycobacterium sp.
CC      having the ability to decompose formaldehyde; a formaldehyde
CC      decomposition agent comprising Mycobacterium sp. and/or the growth medium
CC      of the microbial cells; and a formaldehyde decomposition agent comprising
CC      F. oxysporum and/or its growth medium. The method is useful for
CC      decomposing formaldehyde in sea water by Mycobacterium sp. or F.
CC      oxysporum that is deposited under FERM P-S18690 or FERM P-18483,
CC      respectively. This polynucleotide sequence represents the Mycobacterium
CC      sp. DNA of the invention.
XX
SQ      Sequence 500 BP; 108 A; 119 C; 178 G; 95 T; 0 U; 0 Other;
Query Match      91.6%; Score 17.4; DB 13; Length 500;
Best Local Similarity 94.7%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GAACGGAAGGCCCTTCGG 19
Db      60 GAACGGAAGGCCCTTCGG 78

RESULT 16
AEA22405
ID      AEA22405 standard; DNA; 1449 BP.
XX
AC      AEA22405;
XX
DT      25-AUG-2005 (first entry)
XX
DE      Mycobacterium fortuitum 16S rRNA sequence SEQ ID NO:6.
XX

microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
Mycobacterium fortuitum.
US2005130168-A1.
16-JUN-2005.
31-OCT-2003; 2003US-00697802.
31-OCT-2003; 2003US-00697802.
(HANX/) HAN X.
(PHAM/) PHAM A S.
Han X, Pham AS;
WPI; 2005-424597/43.
Determining a bacterium species comprises providing oligonucleotide
primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
Disclosure; SEQ ID NO 6; 74pp; English.
The invention relates to a method (M1) for determining a bacterium
species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
extracting a genomic nucleotide from the bacterium to provide a
nucleotide template; (c) annealing a region of a nucleotide template to a
specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
complimentary fashion, the primer set designed to provide a product
having a predetermined size dictated by a complimentary primer set; (d)
amplifying the region of the nucleotide template to produce the product;
and (e) determining a species of a bacterium in a nucleotide sequence of
the product. Also described is an alternative method (M2) for determining
a bacterium species comprising: (a) providing a specimen or a sample
having a template; (b) providing a pair of primers selected from: (i) a
first forward primer having consecutive bases of an AFB-f comprising any
of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
or variations and a first reverse primer having consecutive bases of an
AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
or their fragments or variations, (ii) a second forward primer having
consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
bp (AEA22489-AEA22516) or their fragments or variations and a second
reverse primer having consecutive bases of an UB-r comprising any of the
28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
variations, or (iii) a first forward primer having consecutive bases of
an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
second reverse primer having consecutive bases of an UB-r of AEA22517-
AEA22544 or their fragments or variations; (c) the specimen; and (d)
comparing the product from the specimen with a nucleotide sequence from a
database to determine the bacterium species present in the specimen. The
methods are useful for determining a bacterium species. The present
sequence represents a Mycobacterium fortuitum 16S rRNA nucleotide
sequence, which is used in the exemplification of the present invention.
SQ      Sequence 1449 BP; 322 A; 342 C; 495 G; 290 T; 0 U; 0 Other;
Query Match      91.6%; Score 17.4; DB 14; Length 1449;
Best Local Similarity 94.7%; Pred. No. 55;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GAACGGAAGGCCCTTCGG 19
Db      27 GAACGGAAGGCCCTTCGG 45

RESULT 17
AEA22412
ID      AEA22412 standard; DNA; 1455 BP.
XX
AC      AEA22412;
XX
DT      25-AUG-2005 (first entry)
XX

```

XX Mycobacterium mucogenicum 16S rRNA sequence SEQ ID NO:13.
 XX microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
 XX Mycobacterium mucogenicum.
 XX US2005130168-A1.
 XX 16-JUN-2005.
 XX 31-OCT-2003; 2003US-00697802.
 XX 31-OCT-2003; 2003US-00697802.
 XX (HANX/) HAN X.
 XX (PHAM/) PHAM A S.
 XX Han X, Pham AS;
 XX WPI; 2005-424597/43.
 XX Determining a bacterium species comprises providing oligonucleotide
 PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
 XX Disclosure; SEQ ID NO 13; 74pp; English.
 XX The invention relates to a method (M1) for determining a bacterium
 CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
 CC extracting a genomic nucleotide from the bacterium to provide a
 CC nucleotide template; (c) annealing a region of a nucleotide template to a
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
 CC complimentary fashion, the primer set designed to provide a product
 CC having a predetermined size dictated by a complimentary primer set; (d)
 CC amplifying the region of the nucleotide template to produce the product;
 CC and (e) determining a species of a bacterium in a nucleotide sequence of
 CC the product. Also described is an alternative method (M2) for determining
 CC a bacterium species comprising: (a) providing a specimen or a sample
 CC having a template; (b) providing a pair of primers selected from: (i) a
 CC first forward primer having consecutive bases of an APB-f comprising any
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
 CC or variations, and a first reverse primer having consecutive bases of an
 CC reverse primer having consecutive bases of an APB-f comprising any of the
 CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
 CC variations, or (iii) a first forward primer having consecutive bases of
 CC an APB-f of AEA22417-AEA22452 or their fragments or variations and a
 CC second reverse primer having consecutive bases of an APB-f of AEA22517-
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)
 CC comparing the product from the specimen with a nucleotide sequence from a
 CC database to determine the bacterium species present in the specimen. The
 CC methods are useful for determining a bacterium species. The present
 CC sequence represents a Mycobacterium mucogenicum 16S rRNA nucleotide
 CC sequence, which is used in the exemplification of the present invention.
 XX
 SQ Sequence 1455 BP; 321 A; 347 C; 500 G; 287 T; 0 U; 0 Other;
 Query Match 91.6%; Score 17.4; DB 14; Length 1455;
 Best Local Similarity 94.7%; Pred. No. 55;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GAACGGAAGGCGCTTCGG 19
 DB 37 GAACGGAAGGCGCTTCGG 55
 RESULT 18
 AEA22404
 ID AEA22404 standard; DNA; 1482 BP.
 XX

AC AEA22404;
 XX
 DT 25-AUG-2005 (first entry)
 XX
 DE Mycobacterium farcinogenes 16S rRNA sequence SEQ ID NO:5.
 XX
 XX microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
 XX
 OS Mycobacterium farcinogenes.
 XX
 PN US2005130168-A1.
 XX
 PD 16-JUN-2005.
 XX
 XX 31-OCT-2003; 2003US-00697802.
 XX
 PF 31-OCT-2003; 2003US-00697802.
 XX
 PR (HANX/) HAN X.
 XX (PHAM/) PHAM A S.
 PA
 PA Han X, Pham AS;
 XX
 PI WPI; 2005-424597/43.
 XX
 DR Determining a bacterium species comprises providing oligonucleotide
 PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
 XX Disclosure; SEQ ID NO 5; 74pp; English.
 XX The invention relates to a method (M1) for determining a bacterium
 CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
 CC extracting a genomic nucleotide from the bacterium to provide a
 CC nucleotide template; (c) annealing a region of a nucleotide template to a
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
 CC complimentary fashion, the primer set designed to provide a product
 CC having a predetermined size dictated by a complimentary primer set; (d)
 CC amplifying the region of the nucleotide template to produce the product;
 CC and (e) determining a species of a bacterium in a nucleotide sequence of
 CC the product. Also described is an alternative method (M2) for determining
 CC a bacterium species comprising: (a) providing a specimen or a sample
 CC having a template; (b) providing a pair of primers selected from: (i) a
 CC first forward primer having consecutive bases of an APB-f comprising any
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
 CC or variations, and a first reverse primer having consecutive bases of an
 CC reverse primer having consecutive bases of an APB-f comprising any of the
 CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
 CC variations, or (iii) a first forward primer having consecutive bases of
 CC an APB-f of AEA22417-AEA22452 or their fragments or variations and a
 CC second reverse primer having consecutive bases of an APB-f of AEA22517-
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)
 CC comparing the product from the specimen with a nucleotide sequence from a
 CC database to determine the bacterium species present in the specimen. The
 CC methods are useful for determining a bacterium species. The present
 CC sequence represents a Mycobacterium farcinogenes 16S rRNA nucleotide
 CC sequence, which is used in the exemplification of the present invention.
 XX
 SQ Sequence 1482 BP; 327 A; 353 C; 507 G; 295 T; 0 U; 0 Other;
 Query Match 91.6%; Score 17.4; DB 14; Length 1482;
 Best Local Similarity 94.7%; Pred. No. 55;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GAACGGAAGGCGCTTCGG 19
 DB 35 GAACGGAAGGCGCTTCGG 53
 RESULT 19

AAD57239/c
 ID AAD57239 standard; cDNA; 1137 BP.
 XX AC AAD57239;
 XX DT 06-NOV-2003 (first entry)
 XX DE Human CGDD-19 cDNA.
 XX KW Human; cell growth, differentiation and death protein; CGDD; leukaemia;
 KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;
 KW muscular disorder; myotonic dystrophy; catatonias; endocrine disorder;
 KW diabetes; Grave's disease; cancer; immunological disorder; scleroderma;
 KW systemic lupus erythematosus; allergy; Crohn's disease; renal disorder;
 KW gastrointestinal disorder; Goodpasture's syndrome; infection; cirrhosis;
 KW cardiovascular disorder; atherosclerosis; hepatic disease; transgenic;
 KW transgenic animal; gene therapy; neuroprotective; relaxant; cytosolic;
 KW dermatological; immunosuppressive; cerebroprotective; anticonvulsant;
 KW antibacterial; antiparasitic; fungicide; virucide; uropathic; cardiant;
 KW protozoacide; nootropic; gene; ss.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT 112..687
 XX FT /*tag= a
 XX FT /product= "Human CGDD-19 protein"
 XX PN WO2003050253-A2.
 XX PD 19-JUN-2003.
 XX PF 04-DEC-2002; 2002WO-US039133.
 XX PR 07-DEC-2001; 2001US-0340747P.
 XX PR 20-DEC-2001; 2001US-0342761P.
 XX PR 15-JAN-2002; 2002US-0349705P.
 XX PR 06-FEB-2002; 2002US-0354764P.
 XX PR 12-FEB-2002; 2002US-0356216P.
 XX PA (INCY-) INCYTE GENOMICS INC.
 XX PI Griffin JA, Ramkumar J, Emerling BM, Kable AE, Elliott VS;
 PI Marquis JP, Baughn MR, Gorvad AE, Yue H, Lee EA, Becha SD, Tang YT;
 PI Tran UK, Swarnakar A, Lee S, Ison CH, Hafalia AJA, Tran B;
 PI Sprague WM, Lee SY, Khare R, Gandhi AR, Gietzen KJ, Bhatia U;
 PI Burrill JD, Blake JJ, Ho A, Zheng W;
 XX WPI; 2003-532903/50.
 XX P-PSDB; AAE37930.
 XX New CGDD polypeptides, useful for diagnosing, preventing, and treating
 XX disorders associated with an abnormal expression or activity of CGDD,
 XX e.g. neuromuscular, immunological, cardiovascular disorders, cancer
 XX and/or infections.
 XX Claim 5; Page 283; 299pp; English.
 XX PS The present invention relates to novel cell growth, differentiation and
 XX death (CGDD) proteins and polynucleotides encoding them. The sequences of
 XX the invention are useful in diagnosing, preventing and treating disorders
 XX associated with an abnormal expression or activity of CGDD such as
 XX neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's
 XX disease), muscular disorders (e.g. myotonic dystrophy, catatonias),
 XX endocrine disorders (e.g. diabetes, Grave's disease), cancers (e.g.
 XX leukaemia, cervical or breast cancer), immunological disorders (e.g.
 XX scleroderma, systemic lupus erythematosus, allergies), gastrointestinal
 XX disorders (e.g. Crohn's disease), renal disorders (e.g. Goodpasture's
 XX syndrome), infections (e.g. viral, bacterial, fungal, parasitic,
 XX protozoal, helminthic), cardiovascular disorders (e.g. atherosclerosis)
 XX and hepatic diseases (e.g. cirrhosis). The polynucleotides can be used to
 XX create humanised animals or transgenic animals to model human diseases.
 XX The invention is also used in gene therapy. The present sequence is human

CC CGDD-19 cDNA
 XX SQ Sequence 1137 BP; 317 A; 274 C; 296 G; 250 T; 0 U; 0 Other;
 Query Match 89.5%; Score 17; DB 9; Length 1137;
 Best Local Similarity 100.0%; Pred. NO. 88;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAACGGAAGGCTTTC 17
 DB 1070 GAACGGAAGGCTTTC 1054
 RESULT 20
 AAV24413
 ID AAV24413 standard; preRNA; 23 BP.
 XX AC AAV24413;
 XX DT 24-AUG-1998 (first entry)
 XX DE Target sequence #2 for M. intracellulare specific probe.
 XX KW Probe; target sequence; hybridisation; mycobacterial cell sensitivity;
 XX KW antimicrobial agent; pre-rRNA detection; ss.
 XX OS Synthetic.
 XX OS Mycobacterium intracellulare.
 XX PN US5770373-A.
 XX PD 23-JUN-1998.
 XX PF 08-NOV-1996; 96US-00745638.
 XX PR 16-JUN-1994; 94US-00261068.
 XX PR 07-JUN-1995; 95US-00485602.
 XX PA (BECT) BECTON DICKINSON & CO.
 XX PI Cangelosi GA, Britschgi TB;
 XX WPI; 1998-376792/32.
 XX Mycobacterial sensitivity and drug screening assays - involving release
 XX of pre-rRNA by lysis.
 XX Example 4; Col 17-18; 50pp; English.
 XX This sequence represents a target sequence for mycobacterial probes. This
 XX sequence represents a precursor RNA fragment that is released during the
 XX method of the invention. The method is for the determination of
 XX mycobacterial cell sensitivity to an antimicrobial agent, and comprises:
 XX (a) culturing the cells in the presence of the antimicrobial agent; (b)
 XX treating the cells by enzymatic or mechanical means to expose the cell
 XX membrane to lysis reagents, and contacting the cells with a lysis reagent
 XX under conditions such that pre-rRNA is released from the cells but not
 XX degraded; and (c) detecting the pre-rRNA with an oligonucleotide probe
 XX capable of hybridising to a region of the pre-rRNA that is not present in
 XX mature mycobacterial rRNA, where sensitivity to the antimicrobial agent
 XX is indicated by an increase or decrease in pre-rRNA levels for cells
 XX exposed to the antimicrobial agent compared with mycobacterial cells not
 XX exposed to the antimicrobial agent. The lysis method, unlike known
 XX methods, results in detectable levels of pre-rRNA
 XX SQ Sequence 23 BP; 6 A; 6 C; 7 G; 0 T; 3 U; 1 Other;
 Query Match 86.3%; Score 16.4; DB 2; Length 23;
 Best Local Similarity 78.9%; Pred. No. 1.3e+02;
 Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GAACGGAAGGCTTTCG 19
 ||||| ||||| |||||

```

Db      1 GAACGGAAGNCCCUCCG 19

RESULT 21
AAV13021
ID      AAV13021 standard; rRNA; 23 BP.
XX      AC
XX      AC AAV13021;
XX      18-MAY-1998 (first entry)
XX      Mycobacterium intracellulare mature rRNA target sequence SEQ ID NO:56.
DE      DE
XX      Mycobacterium; pre-rRNA; precursor ribosomal RNA; target sequence; probe;
KW      hybridisation; antibiotic resistance; cell lysis; ss.
XX      Mycobacterium intracellulare.
XX      US5712095-A.
XX      27-JAN-1998.
XX      PD
XX      07-JUN-1995; 95US-00485602.
XX      PR
XX      16-JUN-1994; 94US-00261068.
XX      PA (BECT ) BECTON DICKINSON CO.
XX      PI Cangelosi GA, Britschgi TB;
XX      WPI; 1998-119975/11.
XX      Assay for pre-ribosomal RNA in mycobacterium cells - by hybridisation
PT      with specific probes after cell lysis.
XX      PS Disclosure; Col 18; 54pp; English.
XX      The present sequence represents a mycobacterial mature ribosomal RNA
CC      target sequence. The present invention describes a method for detecting
CC      pre-rRNA in cells of a mycobacterial sample. The method comprises: (a)
CC      treating the cells to release pre-rRNA by: (i) pretreating the cells by
CC      enzymatic degradation using both lysozyme and protease until their cell
CC      walls are rendered porous to expose their cell membranes, making the
CC      cells susceptible to lysis; (ii) contacting the pretreated cells with a
CC      combination of a magnesium chelator, a nonionic detergent and an anionic
CC      detergent; and (iii) heating the cells to 75-99 degrees Celsius until the
CC      mycobacterial cells are lysed; and (b) detecting the pre-rRNA using at
CC      least one oligonucleotide probe which is capable of selectively
CC      hybridizing to a region of the pre-rRNA that is not present in a mature
CC      mycobacterial rRNA. The probes can be used to identify many Mycobacterium
CC      spp. including M. tuberculosis, M. leprae, M. habana, M. avium, M. bovis,
CC      M. lufu, M. paratuberculosis, M. marinum, M. simiae and/or M.
CC      intracellulare. The probes may also be used to measure mycobacterial
CC      response to inhibitors of RNA and protein synthesis and may therefore be
CC      used to screen new antimycobacterial drugs. Mycobacteria have a slow
CC      growth rate. By using the probes, drug developers can now identify
CC      compounds that are more effective, but less stable than those previously
CC      identified
XX      SQ Sequence 23 BP; 6 A; 6 C; 7 G; 0 T; 3 U; 1 Other;
Query Match 86.3%; Score 16.4; DB 2; Length 23;
Best Local Similarity 78.9%; Pred. No. 1.3e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy      1 GAACGGAAGCCTTCGG 19
        |||||
Db      1 GAACGGAAGNCCCUCCG 19

RESULT 22
AAV24418
ID      AAV24418 standard; preRNA; 25 BP.
XX      AC
XX      AC AAV24418;
XX      24-AUG-1998 (first entry)
XX      Target sequence #2 for M. simiae specific probe.
XX      Probe; target sequence; hybridisation; mycobacterial cell sensitivity;
XX      antimicrobial agent; pre-rRNA detection; ss.
XX      Synthetic.
XX      Mycobacterium simiae.
XX      US5770373-A.
XX      23-JUN-1998.
XX      PF
XX      08-NOV-1996; 96US-00745638.
XX      PR
XX      16-JUN-1994; 94US-00261068.
XX      PR
XX      07-JUN-1995; 95US-00485602.
XX      PA (BECT ) BECTON DICKINSON & CO.
XX      PI Cangelosi GA, Britschgi TB;
XX      WPI; 1998-376792/32.
XX      Mycobacterial sensitivity and drug screening assays - involving release
PT      of pre-rRNA by lysis.
XX      Example 4; Col 17-18; 50pp; English.
XX      This sequence represents a target sequence for mycobacterial probes. This
CC      sequence represents a precursor RNA fragment that is released during the
CC      method of the invention. The method is for the determination of
CC      mycobacterial cell sensitivity to an antimicrobial agent, and comprises:
CC      (a) culturing the cells in the presence of the antimicrobial agent; (b)
CC      treating the cells by enzymatic or mechanical means to expose the cell
CC      membrane to lysis reagents, and contacting the cells with a lysis reagent
CC      under conditions such that pre-rRNA is released from the cells but not
CC      degraded; and (c) detecting the pre-rRNA with an oligonucleotide probe
CC      capable of hybridizing to a region of the pre-rRNA that is not present in
CC      mature mycobacterial rRNA, where sensitivity to the antimicrobial agent
CC      is indicated by an increase or decrease in pre-rRNA levels for cells
CC      exposed to the antimicrobial agent compared with mycobacterial cells not
CC      exposed to the antimicrobial agent. The lysis method, unlike known
CC      methods, results in detectable levels of pre-rRNA
XX      SQ Sequence 25 BP; 6 A; 7 C; 7 G; 0 T; 3 U; 2 Other;
Query Match 86.3%; Score 16.4; DB 2; Length 25;
Best Local Similarity 78.9%; Pred. No. 1.3e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy      1 GAACGGAAGCCTTCGG 19
        |||||
Db      2 GAACGGAAGNCCCUCCG 20

RESULT 23
AAV13026
ID      AAV13026 standard; rRNA; 25 BP.
XX      AC
XX      AC AAV13026;
XX      17-OCT-2003 (revised)
XX      18-MAY-1998 (first entry)
XX      Mycobacterium habana mature rRNA target sequence SEQ ID NO:61.
XX      Mycobacterium; pre-rRNA; precursor ribosomal RNA; target sequence; probe;
KW      hybridisation; antibiotic resistance; cell lysis; ss.

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XX OS Mycobacterium simiae.
XX PN US5712095-A.
XX PD 27-JAN-1998.
XX PF 07-JUN-1995; 95US-00485602.
XX PR 16-JUN-1994; 94US-00261068.
XX PA (BECT ) BECTON DICKINSON CO.
XX PI Cangelosi GA, Britschgi TB;
XX PR WPI; 1998-119975/11.
XX PT Assay for pre-ribosomal RNA in mycobacterium cells - by hybridisation
XX PS with specific probes after cell lysis.
XX PS Disclosure; Col 18; 54pp; English.
XX CC The present sequence represents a mycobacterial mature ribosomal RNA
XX CC target sequence. The present invention describes a method for detecting
XX CC pre-rRNA in cells of a mycobacterial sample. The method comprises: (a)
XX CC treating the cells to release pre-rRNA by: (i) pretreating the cells by
XX CC enzymatic degradation using both lysozyme and protease until their cell
XX CC walls are rendered porous to expose their cell membranes, making the
XX CC cells susceptible to lysis; (ii) contacting the pretreated cells with a
XX CC combination of a magnesium chelator, a nonionic detergent and an anionic
XX CC detergent; and (iii) heating the cells to 75-99 degrees Celsius until the
XX CC mycobacterial cells are lysed; and (b) detecting the pre-rRNA using at
XX CC least one oligonucleotide probe which is capable of selectively
XX CC hybridizing to a region of the pre-rRNA that is not present in a mature
XX CC mycobacterial RNA. The probes can be used to identify many Mycobacterium
XX CC spp. including M. tuberculosis, M. leprae, M. habana, M. avium, M. bovis,
XX CC M. lufu, M. paratuberculosis, M. marinum, M. simiae and/or M.
XX CC intracellulare. The probes may also be used to measure mycobacterial
XX CC response to inhibitors of RNA and protein synthesis and may therefore be
XX CC used to screen new antimycobacterial drugs. Mycobacteria have a slow
XX CC growth rate. By using the probes, drug developers can now identify
XX CC compounds that are more effective, but less stable than those previously
XX CC identified. (Updated on 17-OCT-2003 to standardise OS field)
XX SQ Sequence 25 BP; 6 A; 7 C; 7 G; 0 T; 3 U; 2 Other;

Query Match 86.3%; Score 16.4; DB 2; Length 25;
Best Local Similarity 78.9%; Pred. No. 1.3e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTCGG 19
    |||||
Dy 2 GAACGGAAGGCTTCGG 20
    |||||

RESULT 24
ADA68711/C
ID ADA68711 standard; DNA; 765 BP.
XX AC ADA68711;
XX XX
XX XX 20-NOV-2003 (first entry)
XX DE Rice gene, SEQ ID 2034.
XX PR Plant; bacterial infection; fungal infection; viral infection; rice;
XX KW gene; ds.
XX PR 21-OCT-1998; 98US-0105234P.
XX OS Oryza sativa.
XX XX
XX PN WO2003000898-A1.
XX PD 03-JAN-2003.

XX OS Mycobacterium simiae.
XX PN US5712095-A.
XX PD 27-JAN-1998.
XX PF 07-JUN-1995; 95US-00485602.
XX PR 16-JUN-1994; 94US-00261068.
XX PA (BECT ) BECTON DICKINSON CO.
XX PI Cangelosi GA, Britschgi TB;
XX PR WPI; 1998-119975/11.
XX PT Assay for pre-ribosomal RNA in mycobacterium cells - by hybridisation
XX PS with specific probes after cell lysis.
XX PS Disclosure; Col 18; 54pp; English.
XX CC The present sequence represents a mycobacterial mature ribosomal RNA
XX CC target sequence. The present invention describes a method for detecting
XX CC pre-rRNA in cells of a mycobacterial sample. The method comprises: (a)
XX CC treating the cells to release pre-rRNA by: (i) pretreating the cells by
XX CC enzymatic degradation using both lysozyme and protease until their cell
XX CC walls are rendered porous to expose their cell membranes, making the
XX CC cells susceptible to lysis; (ii) contacting the pretreated cells with a
XX CC combination of a magnesium chelator, a nonionic detergent and an anionic
XX CC detergent; and (iii) heating the cells to 75-99 degrees Celsius until the
XX CC mycobacterial cells are lysed; and (b) detecting the pre-rRNA using at
XX CC least one oligonucleotide probe which is capable of selectively
XX CC hybridizing to a region of the pre-rRNA that is not present in a mature
XX CC mycobacterial RNA. The probes can be used to identify many Mycobacterium
XX CC spp. including M. tuberculosis, M. leprae, M. habana, M. avium, M. bovis,
XX CC M. lufu, M. paratuberculosis, M. marinum, M. simiae and/or M.
XX CC intracellulare. The probes may also be used to measure mycobacterial
XX CC response to inhibitors of RNA and protein synthesis and may therefore be
XX CC used to screen new antimycobacterial drugs. Mycobacteria have a slow
XX CC growth rate. By using the probes, drug developers can now identify
XX CC compounds that are more effective, but less stable than those previously
XX CC identified. (Updated on 17-OCT-2003 to standardise OS field)
XX SQ Sequence 25 BP; 6 A; 7 C; 7 G; 0 T; 3 U; 2 Other;

Query Match 86.3%; Score 16.4; DB 2; Length 25;
Best Local Similarity 78.9%; Pred. No. 1.3e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTCGG 19
    |||||
Dy 2 GAACGGAAGGCTTCGG 20
    |||||

RESULT 24
ADA68711/C
ID ADA68711 standard; DNA; 765 BP.
XX AC ADA68711;
XX XX
XX XX 20-NOV-2003 (first entry)
XX DE Rice gene, SEQ ID 2034.
XX PR Plant; bacterial infection; fungal infection; viral infection; rice;
XX KW gene; ds.
XX PR 21-OCT-1998; 98US-0105234P.
XX OS Oryza sativa.
XX XX
XX PN WO2003000898-A1.
XX PD 03-JAN-2003.

XX XX 22-JUN-2001; 2001WO-IB001105.
XX XX 22-JUN-2001; 2001WO-IB001105.
XX PR (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
XX PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX PR WPI; 2003-175290/17.
XX PT Identifying at least one gene involved in plant resistance or response to
XX PT pathogenic infection for conferring resistance or tolerance to a plant to
XX PT bacterial, fungal or viral infection by determining or detecting plant
XX PT gene expression.
XX PS Claim 6; SEQ ID NO 2034; 899pp; English.
XX CC The present invention relates to a method (M1) for identifying genes
XX CC involved in plant resistance or response to pathogenic infection. M1
XX CC comprises identifying a gene whose expression is significantly altered in
XX CC the incompatible interaction of plant gene expression relative to
XX CC expression of the gene in an uninfected plant, in a mutant plant that
XX CC does not express a gene associated with response to pathogenic infection,
XX CC or in a corresponding incompatible or compatible interaction. (M1) is
XX CC useful for conferring resistance to resistance or tolerance to a plant to
XX CC bacterial, fungal or viral infection. The present sequence was used to
XX CC illustrate the invention.
XX SQ Sequence 765 BP; 207 A; 171 C; 153 G; 216 T; 0 U; 18 Other;

Query Match 85.3%; Score 16.2; DB 8; Length 765;
Best Local Similarity 78.9%; Pred. No. 2.2e+02;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTCGG 19
    |||||
Dy 725 GAAVGAARGCTTCGGR 707
    |||||

RESULT 25
AAA02278
ID AAA02278 standard; cDNA; 935 BP.
XX AC AAA02278;
XX XX
XX XX 19-MAY-2000 (first entry)
XX DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:2269.
XX KW Human; colon cancer; tumour; diagnosis; gene expression product; probe;
XX KW detection; cancerous state; metastasis; identification; breast cancer;
XX KW oestrogen receptor-positive breast cancer; therapy;
XX KW oestrogen receptor-negative breast cancer; lung cancer; ss.
XX OS Homo sapiens.
XX PN WO9958675-A2.
XX PD 18-NOV-1999.
XX PF 13-MAY-1999; 99WO-US010602.
XX PR 14-MAY-1998; 98US-0085426P.
XX PR 15-MAY-1998; 98US-0085537P.
XX PR 15-MAY-1998; 98US-0085696P.
XX PR 21-OCT-1998; 98US-0105234P.
XX PR 27-OCT-1998; 98US-0105877P.
XX PA (CHIR ) CHIRON CORP.
XX PA (HYSE-) HYSEQ INC.
XX XX

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PI Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
PI Reinhard C, Giese K, Randazzo F, Kennedy GC, Pot D, Kassam A;
PI Lamson G, Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
PI Leshkowitz D, Kita D, Garcia V, Jones LW, Stache-Crain B;
XX
DR WPI; 2000-126369/11.
XX
XX Polynucleotide library used to determine cancerous states of mammalian
PT cells.
PT
PT
PS Claim 1; Page 892; 1097pp; English.
XX
XX AAA00010 to AAA02716 represent polynucleotides isolated from cDNA
CC libraries constructed from human colon cancer cell lines. The present
CC invention also describes a method of detecting differentially expressed
CC genes correlated with a cancerous state of a mammalian cell, comprising
CC detecting at least one differentially expressed gene product in a test
CC sample derived from a cell suspected of being cancerous, where detection
CC of the differentially expressed gene product is correlated with a
CC cancerous state of the cell from which the test sample was derived. The
CC polynucleotide sequences can be used in a method for detecting
CC differentially expressed genes correlated with a cancerous state of a
CC mammalian cell. The polynucleotides can also be used as probes for
CC detecting and mapping related genes. They can be used in diagnosis and
CC prognosis of diseases and disorders (e.g. identification of pre-
CC metastatic or metastatic cancerous states, stages of cancer, or
CC responsiveness of cancer to therapy). This is particularly for breast
CC cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
CC negative breast cancer, lung cancer, and colon cancer
XX
SQ Sequence 935 BP; 300 A; 234 C; 227 G; 44 T; 0 U; 130 Other;
Query Match 84.2%; Score 16; DB 3; Length 935;
Best Local Similarity 84.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCCCTTCGG 19
||| |||| |||| |||| ||||
Db 452 GAAGGAAGCCCTTNGG 470

RESULT 26
ADF94057
ID ADF94057 standard; DNA; 50 BP.
XX
XX ADF94057;
AC
XX
XX 11-MAR-2004 (first entry)
DT
XX
XX Microorganism detection probe, SEQ ID 150.
DE
XX
XX Probe; detection; identification; microorganism; food; drug;
KW 16S rRNA V1 region; 16S rRNA V2 region; 16S rRNA V3 region; ss.
XX
XX Mycobacterium gordonae.
OS
XX
XX WO2003106676-A1.
PN
XX
XX 24-DEC-2003.
PD
XX
XX 16-JUN-2003; 2003WO-JP007620.
PF
XX
XX 14-JUN-2002; 2002JP-00174564.
PR
XX
XX (HISF) HITACHI SOFTWARE ENG CO LTD.
PA (MITS-) MITSUBISHI KAGAKU BIO-CLINICAL LAB INC.
XX
XX Hashida J, Ueno S, Muto I, Naruse K, Tamura M, Matsuoka K;
PI Shimadzu M, Kobayashi I, Ishiko H;
XX WPI; 2004-071565/07.
DR
XX
XX 20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a

PT microorganism for specific detection and identification of the
PT microorganism in foods and drug compositions.
XX
PS Claim 2; SEQ ID NO 150; 150pp; Japanese.
XX
XX The present invention relates to probes (ADF93908-ADF94059) for the
CC specific detection and identification of harmful microorganisms in
CC samples of foods and drug compositions. The probe sequences are derived
CC from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism,
CC or its complementary sequence. Detection and identification of the
CC microorganism is by amplification of the complete 16S rRNA gene using
CC primers ADF94060 and ADF94061, labelling the amplification product (a
CC fluorescence label is preferred), and hybridising to the probe or probes
CC of the invention. The probes may be immobilised on a DNA chip. The
CC microorganism is selected from Actinobacillus actinomycetemcomitans,
CC Acinetobacter calcoaceticus, Haemophilus influenzae, Stenotrophomonas
CC maltophilia, Proteus mirabilis, Streptococcus pneumoniae, Pseudomonas
CC aeruginosa, Citrobacter freundii, Veillonella parvula, Providencia
CC stuartii, Neisseria gonorrhoeae, Streptococcus agalactiae, Morganella
CC morganii, Bacteroides fragilis, Staphylococcus hominis, Staphylococcus
CC warneri, Staphylococcus haemolyticus, Enterobacter cloacae, Enterobacter
CC aerogenes, Staphylococcus epidermidis, Streptococcus constellatus,
CC Serratia marcescens, Streptococcus anginosus, Escherichia coli,
CC Klebsiella pneumoniae, Enterococcus faecalis, Enterococcus intermedium,
CC Streptococcus sanguis, Streptococcus mitis, Streptococcus intermedius,
CC Listeria monocytogenes, Clostridium parvum, Corynebacterium
CC aquarium, Streptococcus oralis, Staphylococcus aureus, Neisseria
CC meningitidis, Campylobacter fetus, Enterococcus gallinarum, Enterococcus
CC casseliflavus, Aeromonas hydrophila, Salmonella paratyphi, Salmonella
CC typhi, Streptococcus equisimilis, Streptococcus canis, Klebsiella
CC oxytoca, Staphylococcus saprophyticus, Pasteurella multocida, Legionella
CC corradoensis, Streptococcus pyogenes, Moraxella catarrhalis, Legionella
CC pneumophila, Mycobacterium tuberculosis, Mycobacterium avium,
CC Mycobacterium intracellulare, Mycobacterium kansasii or Mycobacterium
CC gordonae.
XX
SQ Sequence 50 BP; 12 A; 11 C; 19 G; 8 T; 0 U; 0 Other;
Query Match 83.2%; Score 15.8; DB 12; Length 50;
Best Local Similarity 89.5%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCCCTTCGG 19
||||| ||||| ||||| |||||
Db 10 GAACGGTAAGCCCTTCGG 28

RESULT 27
AA32481
ID AA32481 standard; DNA; 166 BP.
XX
XX AA32481;
AC
XX
XX 22-JUN-1999 (first entry)
DT
XX
XX Preferred probe of the invention.
DE
XX
XX 16S rRNA; maduromycetes; hybridisation; streptomycetes; probe; ss.
KW
XX
XX Synthetic.
OS
XX Streptomyces ambofaciens.
XX
XX WO9914361-A1.
PN
XX
XX 25-MAR-1999.
PD
XX
XX 16-SEP-1998; 98WO-EP006038.
PF
XX
XX 18-SEP-1997; 97US-0059295P.
PR
XX 16-DEC-1997; 97US-0069748P.
XX
XX (MERI) MERCK SHARP & DOHME ESPANA SAE.
XX

PI Genilloud O, Mellado RP, Parro V, Rodriguez V;
XX
XX WPI; 1999-229548/19.
XX
XX
PT New probes used for detection of maduromycetes bacteria and to
PT differentiate between maduromycetes and streptomycetes.

PS Disclosure; Fig 1; 22pp; English.

The invention relates to a novel nucleic acid probe hybridises to a nucleic acid encoding a portion of 16S rRNA of maduromyces bacteria under hybridisation conditions, and does not hybridise to nucleic acids encoding a portion of 16S rRNA of streptomycetes under identical hybridisation conditions. The probes can be used for detecting the presence of maduromyces bacteria in a sample and for differentiating between maduromyces and streptomycetes bacteria in a sample. The present sequence represents a preferred probe of the invention

SQ Sequence 166 BP; 39 A; 43 C; 55 G; 29 T; 0 U; 0 Other;

Query Match	83.2%	Score 15.8;	DB 2;	Length 166;
Best Local Similarity	89.5%	Pred. No. 3.2e+02;		
Matches 17;	Conservative	0;	Mismatches 2;	Indels 0;
			Gaps 0;	

Qy 1 GAACGGAAAGGCCCTTTTCGG 19
Db 63 GAGCGGAAAGGCCCTTTCGG 81

RESULT 28

AAA31293
ID AAA31293 standard; DNA; 170 BP.

AC AAA31293;

DT 05-JUL-2000 (first entry)

DE Plant microsatellite marker #254.

plant microsatellite sequence; core repeat sequence; detection; probe;
DNA polymorphism; genome mapping; physical mapping; fingerprinting;
variety identification; genetic variability evaluation; primer; ss.

OS *Eucalyptus grandis*.

PN WO9967421-A1.

PD 29-DEC-1999.

25-JUN-1999; 99WO-NZ0000092.

25-JUN-1998: 98US-00105307-

PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FOREST LTD.
XX

XX
PI Havukkala IJ, Bloksberg LN, Glenn M:

DR WPI; 2000-116958/10.

AA New plant microsatellite markers and associated flanking species for the
PT detection of polymorphic genetic markers.
PT

PS Claim 1; Page 151; 392pp: English.

Sequences AAA31040-A32093 represent novel plant microsatellite sequences and associated flanking species. The sequences comprise a central core repeat sequence, especially selected from the sequences AAA32094-A32096 with left and right flanking sequences. The polynucleotide sequences can be used in the detection of DNA polymorphisms, in genome mapping, in physical mapping, in positional cloning of genes, in variety identification and in evaluation of genetic variability within and between plant tissues, populations, cultivars, species and species.

CC groups. They may also be used to design hybridization probes for
CC oligonucleotide fingerprinting and library screening and to design
CC primers for microsatellite-primed PCR. Microsatellite markers are useful
CC to locate specific economically useful genes in plant genomes
xx
SQ Sequence 170 BP; 44 A; 35 C; 65 G; 22 T; 0 U; 4 Other:

Query Match 83.2%; Score 15.8; DB 3; Length 170;
Best Local Similarity 89.5%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels

Oy

|||||
1 GAACGGAAGCCCTTTCGG 19

Dd

|||||
69 GAAGCGAAGGCCCTTAGG 87

RESULT 29

AAA31415
ID AAA31415 standard: DNA: 305 BP.

AA
AC

XX
DT 05-JUL-2000 (first entry)

XX DE Plant microsatellite marker #376.

Plant microsatellite sequence; core repeat sequence; detection; probe;
KW
DNA polymorphism; genome mapping; physical mapping; fingerprinting;
KW
variety identification; genetic variability evaluation; primer; ss.
KW

OS *Eucalyptus grandis*.

PN WO9967421-A1.

PD 29-DEC-1999.

25-JUN-1999; 99WO-NZ000092.

PR 25-JUN-1998; 98US-00105307.

PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FOREST LTD.

PI Havukkala IJ, Bloksberg LN, Glenn M;

AA
DR WPI; 2000-116958/10.

XX New plant microsatellite markers and associated flanking species for the
PT detection of polymorphic genetic markers.
PT

PS Claim 1; Page 187; 392pp; English.

Sequences AAA1040-A12093 represent novel plant microsatellite sequences and associated flanking species. The sequences comprise a central core repeat sequence, especially selected from the sequences AAA32094-A32096 with left and right flanking sequences. The polynucleotide sequences can be used in the detection of DNA polymorphisms, in genome mapping, in physical mapping, in positional cloning of genes, in variety identification and in evaluation of genetic variability within and between plant tissues, populations, cultivars, species and species groups. They may also be used to design hybridization probes for oligonucleotide fingerprinting and library screening and to design primers for microsatellite-primed PCR. Microsatellite markers are useful to locate specific economically useful genes in plant genomes

Sequence 305 BP: 82 A: 67 C: 121 G: 35 T: 0 U: 0 Other: 0

Query Match . 83.2%; Score 15.8; DB 3; Length 305;
Best Local Similarity 89.5%; Pred. No. 3.3e+02;
Matches 17: Conservative 0: Mismatches 2: Indels

Qy 1 GAACGGAAAGGCCTTTCGG 19


```
Db 70 GAAGGGAAGGCGCTTTAGG 88

RESULT 30
ABZ76674
ID ABZ76674 standard; DNA; 460 BP.
AC ABZ76674;
XX
XX
DT 30-APR-2003 (first entry)
XX
DE Microtetraspora recticatena IFO14525 DNA sequence SEQ ID NO:5.
XX
XX Streptomyces sp. TW-7; pravastatin; compactin; hyperlipidaemia;
KW antilipaemic; microorganism; gene; ds.
XX
OS Nonomuraea recticatena.
XX
PN WO200299109-A1.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-JP005252.
XX
PR 01-JUN-2001; 2001JP-00166412.
XX
PA (SAOC ) MERCIAN CORP.
XX
PI Fujii T, Hirose S, Aritoku Y, Morimiya T, Johdo O, Ishiki K;
XX
XX WPI; 2003-148672/14.
XX
XX Novel Streptomyces sp. produced polypeptide for hydroxylation of
PT compactin at 6beta-position and its encoded DNA, applicable in
PT constructing transformant microbes to synthesize pravastatin for treating
PT hyperlipedemia.
XX
PS Disclosure; Page 50-51; 67pp; Japanese.
XX
CC The present invention describes a DNA sequence which contains a base
CC sequence from bases 544-1758 in the sequence of (I) with 1992 base pairs,
CC or a DNA hybridisable with the DNA under stringent conditions and
CC encoding a polypeptide with hydroxylase activity on compactin at 6beta-
CC position. Also described: (1) DNA containing base sequences from bases
CC 544-1758 and from bases 1782-1970 in the sequence of (I) or a DNA
CC hybridisable with the DNA under stringent conditions and encoding a
CC polypeptide with hydroxylase activity on compactin at the 6beta-position;
CC (2) a polypeptide encoded by any of the DNA or containing an amino acid
CC sequence based on the polypeptide but with some amino acids deleted,
CC substituted or added and having hydroxylase activity on compactin at the
CC 6beta-position; (3) a recombinant DNA obtained by integrating with any of
CC the DNA; (4) a microorganism transferred with the recombinant DNA; (5) a
CC process for producing pravastatin by culturing the transformant
CC microorganism before isolating the culture liquor or cells, and addition
CC of compactin for reaction to give pravastatin for recovery; and (6)
CC Streptomyces sp. TW-6 (FERM BP-8002) or TW-7 (FERM BP-8003). (I) has
CC antilipaemic activity. The polypeptide and its encoded DNA are applicable
CC in constructing transformant microorganisms to synthesise pravastatin for
CC treating hyperlipidaemia. With the recombinant microorganisms,
CC pravastatin can be produced efficiently, with much less galpha
CC hydroxylated epimer formed. The present sequence represents a
CC Microtetraspora recticatena IFO14525 nucleotide sequence, which is given
CC in the exemplification of the present invention
XX
SQ Sequence 460 BP; 97 A; 119 C; 166 G; 78 T; 0 U; 0 Other;
Query Match 83.2%; Score 15.8; DB 8; Length 460;
Best Local Similarity 89.5%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCGCTTTTCGG 19
Db 37 GAGCGGAAGGCGCTTTTCGG 55

RESULT 31
ABZ72673
ID AEB72673 standard; DNA; 497 BP.
AC AEB72673;
XX
XX
DT 06-OCT-2005 (first entry)
XX
DE Streptosporangium sp. AF935 16S rDNA, SEQ ID 2.
XX
XX cyclosporin; cyclosporin A; ds.
KW cyclosporin; cyclosporin A; ds.
XX
OS Streptosporangium sp.
XX
PN JP2005198543-A.
XX
PD 28-JUL-2005.
XX
PF 15-JAN-2004; 2004JP-00007488.
XX
PR 15-JAN-2004; 2004JP-00007488.
XX
PA (SAOC ) MERCIAN CORP.
XX
PI Ota K, Uematsu H, Kaneko K, Tsuchida T;
XX
XX WPI; 2005-537020/55.
XX
XX Producing cyclosporin derivative useful as reference standard for
PT quantitative measurement of cyclosporin A in blood, by incubating
PT cyclosporin A in presence of Dactyosporangium and extracting cyclosporin
PT derivative.
XX
PS Disclosure; SEQ ID NO 2; 12pp; Japanese.
XX
CC The invention relates to a novel method for producing a cyclosporin
CC derivative. The method involves incubating cyclosporin A in the presence
CC of a strain belonging to Dactyosporangium, Streptomyces, Nocardia,
CC Pseudonocardia or Streptosporangium or its cultured microbial cells and
CC extracting the cyclosporin derivative from the incubated liquid. The
CC cyclosporin derivative is used as a reference standard for quantitative
CC measurement of cyclosporin A and its metabolite in blood and urine. This
CC polynucleotide represents a Streptosporangium 16S rDNA sequence used in
CC the cyclosporin production method of the invention.
XX
SQ Sequence 497 BP; 105 A; 121 C; 178 G; 93 T; 0 U; 0 Other;
Query Match 83.2%; Score 15.8; DB 14; Length 497;
Best Local Similarity 89.5%; Pred. No. 3.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCGCTTTTCGG 19
Db 60 GAGCGGAAGGCGCTTTTCGG 78

RESULT 32
AED64356
ID AED64356 standard; DNA; 500 BP.
XX
XX AED64356;
AC AED64356;
XX
XX
DT 12-JAN-2006 (first entry)
XX
DE Rhodococcus sp. 16S rDNA, SEQ ID 1.
XX
KW 16S ribosomal RNA; 16S rRNA; ds.
XX
OS Rhodococcus sp.; Z-35-1 strain.
XX
PN JP2005304498-A.
```


QY 1 GAACGGAAAGCCCTTCGG 19
 || |||||
 Db 32 GAGCGGAAAGCCCTTCGG 50

RESULT 37

ADW16290
 ID ADW16290 standard; DNA; 1427 BP.

XX AC ADW16290;

XX DT 07-APR-2005 (first entry)

XX DE DNA copy of the Actinomycete 16S ribosomal RNA EN47 isolate.

XX KW 16S ribosomal RNA; ds; 16S rRNA; medicinal plant; plant breeding;
 KW disease resistance; insect resistance; crop improvement;
 KW plant growth factor; antibacterial; antimicrobial; fungicide;
 KW insecticide; nematocide.

XX OS Actinomycetales.

XX PN W02005003328-A1.

XX PD 13-JAN-2005.

XX PF 07-JUL-2004; 2004WO-AU000914.

XX PR 07-JUL-2003; 2003US-0485241P.

XX PR 22-SEP-2003; 2003US-0504703P.

XX PA (FLIN-) FLINDERS TECHNOLOGIES PTY LTD.

XX PI Franco CMM, Coombs JT;

XX DR WPI; 2005-091806/10.

XX PT Improving plant productivity comprises introducing into the plant or
 PT propagation material an endophytic actinomycete that facilitates
 PT induction of at least one characteristic related to improved
 PT productivity.

XX PS Example 18; Fig 19; 235pp; English.

XX CC This invention relates to a novel method for improving plant
 CC productivity. Specifically, it refers to introducing into the plant or
 CC propagation material an endophytic actinomycetes or variant thereof,
 CC where the actinomycetes facilitate induction of a characteristic related
 CC to improved productivity. The present invention further describes
 CC metabolites of the actinomycetes microorganism such as auxin, gibberellin
 CC or cytokinin that are able to induce disease resistance in plants i.e.
 CC provide disease bio-control capabilities against pathogen infection.
 CC Accordingly, the method facilitates the improvement of cereal crop
 CC productivity including increasing germination by up-regulating plant
 CC growth promoting activities, as well as improving plant vigor or flower
 CC and fruit yield. Furthermore, the new actinomycete or metabolite is
 CC useful in the manufacture of a medicament for the therapeutic and/or
 CC prophylactic treatment of a mammalian or non-mammalian subject i.e.
 CC plant. As such, this method provides plant protectants and plant growth
 CC stimulants that exhibit antibacterial, antimicrobial, fungicide,
 CC insecticide and nematocide activities. This polynucleotide is the DNA
 CC sequence of an actinomycetes 16S ribosomal RNA sequence of the invention.

XX SQ Sequence 1427 BP; 326 A; 351 C; 471 G; 277 T; 0 U; 2 Other;

Query Match 83.2%; Score 15.8; DB 14; Length 1427;
 Best Local Similarity 89.5%; Pred. No. 3.8e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCCCTTCGG 19
 || |||||
 Db 31 GAGCGGAAAGCCCTTCGG 49

RESULT 38

ADC61232
 ID ADC61232 standard; DNA; 1439 BP.

XX AC ADC61232;

XX DT 18-DEC-2003 (first entry)

XX DE Baeyer-Villiger enzyme 16S rDNA gene from Rhodococcus erythropolis AM12.

XX KW Baeyer-Villiger; BV; monooxygenase; ketone substrate; lactone; ester;
 KW 16S rDNA; ds.

XX OS Rhodococcus erythropolis.

XX PN W02003020890-A2.

XX PD 13-MAR-2003.

XX PF 29-AUG-2002; 2002WO-US027549.

XX PR 29-AUG-2001; 2001US-0315546P.

XX PA (DUPO) DU PONT DE NEMOURS & CO E I.

XX PI Bramucci MG, Brzostowicz PC, Kostichka KN, Nagarajan V;

XX PI Rouviere PE, Thomas SM;

XX DR WPI; 2003-313085/30.

XX PT Novel nucleic acid fragment useful for converting ketone substrates to
 PT the corresponding lactone or ester, is isolated from Rhodococcus,
 PT Arthrobacter or Acidovorax, encoding Baeyer-Villiger monooxygenase
 PT polypeptide.

XX PS Claim 54; SEQ ID NO 6; 225pp; English.

XX CC The invention relates to a novel isolated nucleic acid fragment
 CC comprising a fragment encoding a Baeyer-Villiger (BV) monooxygenase
 CC polypeptide having a sequence of 542, 541, 439, 518, 462, 523, 493, 539,
 CC 649, 494, 499, 545, 532 or 538 amino acids defined in the specification;
 CC a nucleic acid molecule that hybridises with the above sequence under the
 CC hybridisation conditions; or their complements. The BV monooxygenase
 CC fragment is useful for obtaining a nucleic acid fragment encoding a BV
 CC monooxygenase polypeptide, by probing a genomic library with the
 CC fragment, identifying a DNA clone that hybridises with the fragment, and
 CC sequencing the genomic fragment that comprises the above identified
 CC clone, where the sequenced genomic fragment encodes a BV monooxygenase
 CC polypeptide. The genes and their products are useful for converting
 CC suitable ketone substrates to the corresponding lactone or ester. This
 CC polynucleotide sequence represents the 16S rDNA gene from Arthrobacter
 CC sp. BP2 relating to the Baeyer-Villiger enzymes of the invention.

XX SQ Sequence 1439 BP; 333 A; 357 C; 465 G; 283 T; 0 U; 1 Other;

Query Match 83.2%; Score 15.8; DB 10; Length 1439;
 Best Local Similarity 89.5%; Pred. No. 3.8e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCCCTTCGG 19
 || |||||
 Db 38 GAGCGGTAAGCCCTTCGG 56

RESULT 39

ADZ35975
 ID ADZ35975 standard; DNA; 1440 BP.

XX AC ADZ35975;

XX DT 30-JUN-2005 (first entry)

Verrucosisspora sp. AB-18-032 16S rRNA gene.
ds; antibiotic; antimalarial; protozoacide; 16S rRNA;
polycyclic macrolactone; abyssomicin; p-Aminobenzoic acid; folic acid;
vitamin; abyssomicin B; abyssomicin C; abyssomicin D;
Staphylococcus aureus infection; protozoal infection;
plasmodium infection; Leishmania infection; chagas disease;
Gram positive bacteria infection; mrsa infection .
Verrucosisspora sp. AB-18-032.
WO2005033114-A1.
14-APR-2005.
23-SEP-2004; 2004WO-EP010661.
01-OCT-2003; 2003DE-01047472.
11-NOV-2003; 2003DE-01053300.
(UYTU-) UNIV TUEBINGEN.
Fiedler H, Suessmuth R, Zaehner H, Bull A;
WPI; 2005-296122/30.
New abyssomicin polycyclic macrolactone compounds, useful as antibiotics
and antiprotozoal agents effective against multiresistant strains,
PT prepared using bacteria of genus Verrucosisspora.
PS Disclosure; SEQ ID NO 1; 47pp; German.
This invention describes novel polycyclic macrolactones and their
derivatives , prepared using bacteria of genus Verrucosisspora and
designated abyssomicins. The polycyclic macrolactones have at least one
oxa-bicyclo system as a partial structure and at least one Michael system
as double bond system. The polycyclic macrolactones are prepared by
culturing Verrucosisspora strain AB 18-032, recovering a culture
supernatant from the culture, optionally preparing a culture filtrate and
optionally isolating one or more polycyclic macrolactones from the
supernatant and/or filtrate. Alternatively the microorganism is cultured
followed by isolating one or more polycyclic macrolactones from the
microorganism. The Verrucosisspora strain AB 18-032 was isolated from
marine sediment collected at a depth of 1000m in Sagami bay in the
Japanese Sea and is deposited as DSM No. 15899. The polycyclic
macrolactones inhibit the biosynthesis of p-Aminobenzoic acid, (an
essential component in the biosynthesis of folic acid) from chorismic
acid, thus inhibiting folic acid biosynthesis. The vitamin folic acid is
essential to the life of microorganisms, especially prokaryotes and
protozoa. The polycyclic macrolactones do not inhibit the biosynthesis of
folic acid in mammals (including humans), and thus have no adverse
effects on mammalian cells. Three polycyclic macrolactones are
specifically claimed, i.e. abyssomicin B, abyssomicin C and abyssomicin
D. Abyssomicin C strongly inhibited growth of methicillin-resistant
CC Staphylococcus aureus strain N315 and vancomycin-resistant Staphylococcus
CC aureus strain Mu50. The products of the invention are useful as
CC antibiotics (especially effective against Gram positive bacteria) and
CC antiprotozoal agents, specifically effective against bacteria and
CC protozoa resistant (especially multi-resistant) to conventional
CC antibiotics. Typically polycyclic macrolactones are useful for combating
CC tropical protozoal diseases (e.g. malaria, leishmaniasis, sleeping
CC sickness and Chagas disease) and infections caused by resistant Gram
CC positive bacteria such as methicillin- and vancomycin-resistant
CC Staphylococcus aureus strains. Polycyclic macrolactones are also useful
CC as disinfectants (especially in hospitals and other medical
CC establishments) and as lead structures for the development of further
CC active agents. This sequence represents the Verrucosisspora strain AB 18-
CC 032 16S rRNA DNA which is used to phylogenically classify the bacterial
CC strain.
Sequence 1440 BP; 313 A; 363 C; 500 G; 264 T; 0 U; 0 Other;

Query Match 83.2%; Score 15.8; DB 14; Length 1440;
Best Local Similarity 89.5%; Pred. No. 3.8e+02; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 2;
QY 1 GAACGGAAAGGCGCTTCGG 19
Db 7 GAGCGGAAAGGCGCTTCGG 25
RESULT 40
ADX38843
ID ADX38843 standard; DNA; 1443 BP.
XX
AC ADX38843;
XX
DT 05-MAY-2005 (first entry)
XX
DE Microbispora 16S rDNA.
XX
KW antibiotic; bacterial infection; animal growth; 16S rDNA; ds;
KW antibacterial; anabolic.
XX
OS Microbispora sp. ATCC PTA-5024.
XX
PN WO2005014628-A1.
XX
PD 17-FEB-2005.
XX
PF 12-JUL-2004; 2004WO-EP007658.
XX
PR 18-JUL-2003; 2003EP-00016306.
XX
PA (VICU-) VICURON PHARM INC.
XX
PI Lazzarini A, Gastaldo L, Candiani G, Ciciliato I, Losi D;
PI Marinelli F, Selva E, Parenti F;
XX
DR WPI; 2005-173079/18.
XX
PT New antibiotic 107891 complex comprising Factor A1 and Factor A2 and
PT having specified physico-chemical characteristics, used to form
PT medicament for the treatment or prevention of bacterial infections, or
PT used as animal growth promoter.
XX
PS Disclosure; SEQ ID NO 1; 85pp; English.
XX
CC The invention relates to an antibiotic 107891 complex comprising Factor
CC A1 and Factor A2. The antibiotic is used to form a pharmaceutical
CC composition used as medicament for the treatment or prevention of
CC bacterial infections, or as animal growth promoter. The present sequence
CC represents the Microbispora 16S rDNA.
XX
SQ Sequence 1443 BP; 308 A; 352 C; 504 G; 279 T; 0 U; 0 Other;
Query Match 83.2%; Score 15.8; DB 14; Length 1443;
Best Local Similarity 89.5%; Pred. No. 3.8e+02; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 2;
QY 1 GAACGGAAAGGCGCTTCGG 19
Db 37 GAGCGGAAAGGCGCTTCGG 55
RESULT 41
AEA22406
ID AEA22406 standard; DNA; 1461 BP.
XX
AC AEA22406;
XX
DT 25-AUG-2005 (first entry)
XX
DE Mycobacterium gordonae 16S rRNA sequence SEQ ID NO:7.
XX


```
Query Match      83.2%; Score 15.8; DB 14; Length 1483;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTCGG 19
DB 38 GAGCGGTAAGGCTTTCGG 56

RESULT 43
ADR90327
ID ADR90327 standard; DNA; 1511 BP.
XX
AC ADR90327;
XX
DT 16-DEC-2004 (first entry)
XX
DE Rhodococcus sp. M-15 bioremediation-related 16S rDNA.
XX
KW alkane; petroleum; bioremediation; 16S ribosomal RNA; 16S rRNA; ds.
XX
OS Rhodococcus sp.
XX
PN JP2004261126-A.
XX
PD 24-SEP-2004.
XX
PF 03-MAR-2003; 2003JP-00056155.
XX
PR 03-MAR-2003; 2003JP-00056155.
XX
PA (EBAR ) EBARA CORP.
XX
WPI; 2004-665486/65.
XX
Evaluating the ability of an environmental sample to degrade alkanes for
PT providing alkane degrading bacteria, comprises measuring alkane degrading
PT bacteria having high resolving power of alkane present in petroleum.
PS Claim 1; SEQ ID NO 3; 33pp; Japanese.
XX
CC The invention relates to a novel method for evaluating the ability of an
CC environmental sample to degrade alkanes. The method comprises measuring
CC the number of alkane-degrading bacteria present in the sample, where the
CC bacteria have high resolving power of a type of alkane present in
CC petroleum and gyrB (gyrase beta subunit) DNA and 16S rDNA. The method of
CC the invention may be useful for evaluating the ability of an
CC environmental sample to degrade alkanes and thus, for providing alkane-
CC degrading bacteria to be utilised in bioremediation of an environment
CC contaminated with petroleum. The method is rapid and simple. The current
CC sequence is that of the Rhodococcus sp. M-15 bioremediation-related 16S
CC ribosomal RNA gene (rDNA) of the invention.
XX
SQ Sequence 1511 BP; 342 A; 362 C; 510 G; 297 T; 0 U; 0 Other;

Query Match      83.2%; Score 15.8; DB 13; Length 1511;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTCGG 19
DB 57 GAGCGGTAAGGCTTTCGG 75

RESULT 44
ADR90325
ID ADR90325 standard; DNA; 1511 BP.
XX
AC ADR90325;
XX
DT 16-DEC-2004 (first entry)
XX
DE Rhodococcus sp. M-13 bioremediation-related 16S rDNA.
XX
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XX alkane; petroleum; bioremediation; 16S ribosomal RNA; 16S rRNA; ds.
KW Rhodococcus sp.
OS
XX JP2004261126-A.
XX
PD 24-SEP-2004.
XX
PF 03-MAR-2003; 2003JP-00056155.
XX
PR 03-MAR-2003; 2003JP-00056155.
XX
PA (EBAR ) EBARA CORP.
XX
WPI; 2004-665486/65.
XX
Evaluating the ability of an environmental sample to degrade alkanes for
PT providing alkane degrading bacteria, comprises measuring alkane degrading
PT bacteria having high resolving power of alkane present in petroleum.
PS Claim 1; SEQ ID NO 1; 33pp; Japanese.
XX
CC The invention relates to a novel method for evaluating the ability of an
CC environmental sample to degrade alkanes. The method comprises measuring
CC the number of alkane-degrading bacteria present in the sample, where the
CC bacteria have high resolving power of a type of alkane present in
CC petroleum and gyrB (gyrase beta subunit) DNA and 16S rDNA. The method of
CC the invention may be useful for evaluating the ability of an
CC environmental sample to degrade alkanes and thus, for providing alkane-
CC degrading bacteria to be utilised in bioremediation of an environment
CC contaminated with petroleum. The method is rapid and simple. The current
CC sequence is that of the Rhodococcus sp. M-13 bioremediation-related 16S
CC ribosomal RNA gene (rDNA) of the invention.
XX
SQ Sequence 1511 BP; 343 A; 367 C; 507 G; 294 T; 0 U; 0 Other;

Query Match      83.2%; Score 15.8; DB 13; Length 1511;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTCGG 19
DB 57 GAGCGGTAAGGCTTTCGG 75

RESULT 45
AED11327
ID AED11327 standard; DNA; 1511 BP.
XX
AC AED11327;
XX
DT 01-DEC-2005 (first entry)
XX
DE Aliphatic hydrocarbon degrading R. erythropolis strain 16S rRNA gene.
XX
KW degradation; aliphatic hydrocarbon; bioremediation; oil degradation;
KW pollutant; degradation; groundwater decontamination; 16S rRNA;
KW 16S ribosomal RNA; gene; ds.
XX
OS Rhodococcus erythropolis.
XX
PN JP2005261218-A.
XX
PD 29-SEP-2005.
XX
PF 16-MAR-2004; 2004JP-00074370.
XX
PR 16-MAR-2004; 2004JP-00074370.
XX
PA (EBAR ) EBARA CORP.
XX
PI Karube M, Tamatsubo K, Miya A;
```


XX WPI; 2005-678804/70.

XX Novel Rhodococcus erythropolis M-13 strain capable of degrading aliphatic

PT hydrocarbon, useful for bioremediation of oil-polluted environment such

PT as river water, underground water, ocean, sea coast.

PS Claim 1; SEQ ID NO 1; 14pp; Japanese.

XX The invention relates to a novel Rhodococcus erythropolis M-13 strain

CC capable of degrading aliphatic hydrocarbons. The invention further

CC provides the 16S rRNA gene of the novel strain showing 98% or more

CC homology with a nucleotide sequence of a fully defined 1511 nucleotide

CC (AED11327) sequence given in specification. The novel strain is useful

CC for the bioremediation of an oil-polluted environment, such as river

CC water, underground water, ocean, sea coast, etc. The novel strain degrades

CC linear or branched aliphatic hydrocarbons efficiently. This

CC polynucleotide sequence represents the DNA of the novel Rhodococcus

CC erythropolis M-13 strain 16S rRNA gene of the invention.

XX

SQ Sequence 1511 BP; 343 A; 367 C; 507 G; 294 T; 0 U; 0 Other;

Query Match 83.2%; Score 15.8; DB 14; Length 1511;

Best Local Similarity 89.5%; Pred. No. 3.8e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGCCCTTCGG 19

Db 57 GAGCGGTAGGCCCTTCGG 75

RESULT 46

ADE41084

ID ADE41084 standard; rRNA; 1584 BP.

XX

AC ADE41084;

XX

DT 29-JAN-2004 (first entry)

DE . corallina partial 16s rRNA sequence.

XX

KW Antibiotic; ss; 16s rRNA; MF-BA-1768alpal; MF-BA-1768betal;

KW Staphylococcus; Enterococcus; Streptococcus; Haemophilus; Escherichia;

KW bacterial infection.

XX

OS Microbispora corallina; strain NRRL 30420.

XX

PN US6551591-B1.

XX

PD 22-APR-2003.

XX

PF 07-SEP-2001; 2001US-00949230.

XX

PR 07-SEP-2001; 2001US-00949230.

XX

PA (ESSE-) ESSENTIAL THERAPEUTICS INC.

XX

PI Lee MD;

XX

DR WPI; 2003-895156/82.

XX

PT Novel antibiotics isolated from fermentation broth of novel strain of

PT Microbispora corallina, useful for treating a wide range of bacterial

PT infections.

XX

PS Disclosure; SEQ ID NO 1; 20pp; English.

XX

CC The invention relates to antibiotic MF-BA-1768alpal or MF-BA-1768-betal

CC or its pharmaceutically acceptable salt, having physicochemical

CC characteristics in the non-salt form as detailed in the specification.

CC The antibiotics are isolated from a novel strain of Microbispora

CC corallina designated NRRL 30420. Also included are producing the above

CC antibiotic (by cultivating Microbispora corallina NRRL 30420, or an

CC antibiotic MF- BA-1768alpal or MF-BA-1768betal -producing mutant,

CC variant or its recombinant form, in a culture medium containing

CC assimilable sources of carbon, nitrogen and inorganic salts under aerobic

CC fermentation conditions until the antibiotic is produced and then

CC recovering the antibiotic) and a composition comprising the above

CC antibiotic or its salt. The antibiotics are useful for treating a

CC bacterial infection caused by Staphylococcus (e.g. S.aureus , S.epidermis

CC , S.haemolyticus), Enterococcus (e.g. E.faecalis , E.faecium),

CC Streptococcus (e.g. S.pneumoniae , S.pyrogenes), Haemophilus (e.g.

CC H.influenzae) or Escherichia (e.g. E.coli) in a patient. The present

CC sequence is partial 16S rRNA sequence from M. corallina NRRL 30420, which

CC identifies the strain.

XX

SQ Sequence 1584 BP; 339 A; 384 C; 525 G; 320 T; 0 U; 16 Other;

Query Match 83.2%; Score 15.8; DB 10; Length 1584;

Best Local Similarity 89.5%; Pred. No. 3.8e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGCCCTTCGG 19

Db 131 GAGCGGAAGCCCTTCGG 149

RESULT 47

AEA51361/c

ID AEA51361 standard; DNA; 1849 BP.

XX

AC AEA51361;

XX

DT 25-AUG-2005 (first entry)

XX

DE Mouse gene expressed during angiogenesis, NOC8009G23.

XX

KW angiogenesis disorder; antiangiogenic; diagnosis; pharmaceutical; cancer;

KW cytostatic; retinopathy; ophthalmological; macular degeneration;

KW corneal ulcer; antiulcer; cerebrovascular ischemia; cerebroprotective;

KW vasotropic; ischemic heart disease; cardiac; infertility;

KW antiinfertility; ulcer; scleroderma; dermatological; wound healing;

KW vulnarary; ischemia; myocardial infarction; angina; antianginal;

KW unstable angina; coronary arteriosclerosis; antiarteriosclerotic;

KW embolism; thrombolytic; cerebral infarction; chronic inflammation;

KW inflammatory bowel disease; psoriasis; sarcoidosis; rheumatoid arthritis;

KW antiinflammatory; gastrointestinal-gen.; antipsoriatic; antiarthritic;

KW antirheumatic; ds; gene.

XX

OS Mus.

XX

PN WO2005054426-A2.

XX

PD 16-JUN-2005.

XX

PF 06-DEC-2004; 2004WO-SE001814.

XX

PR 05-DEC-2003; 2003SE-00003268.

XX

PR 05-DEC-2003; 2003US-0481741P.

XX

PA (ANGI-) ANGIOGENETICS SWEDEN AB.

XX

PI Hellstroem M, Wallgard E, Kalen M;

XX

DR WPI; 2005-435379/44.

XX

PT New nucleic acid molecule encoding angiogenesis affecting polypeptides,

PT for treating an angiogenesis-related disorder, e.g. cancer, infertility,

PT scleroderma, wound healing, arterial thrombosis, psoriasis, or rheumatoid

PT arthritis.

XX

PS Claim 1; SEQ ID NO 44; 149pp; English.

XX

CC The present invention relates to genes and proteins associated with

CC vasculogenesis and angiogenesis related disorders. Specifically claimed

CC is an isolated nucleic acid encoding an angiogenesis affecting

CC polypeptide. The nucleic acid has the ability to stimulate or inhibit at
 CC least one biological activity, e.g. vasculogenesis, angiogenesis,
 CC vascular permeability, endothelial cell proliferation, endothelial cell
 CC differentiation, endothelial cell migration, or endothelial cell
 CC survival. Also claimed is an isolated siRNA molecule targeted to the
 CC nucleic acid, and an antibody with specific reactivity to the nucleic
 CC acid or peptide, which may further comprise a detectable fluorescent
 CC label. Described is a method of treating an angiogenesis-related
 CC condition, and a method of detecting an angiogenesis-related transcript
 CC in a cell of a patient. The protein or nucleic acid are useful as
 CC pharmaceuticals for affecting vasculogenesis or angiogenesis. The
 CC angiogenesis-related disorder is cancer, retinopathy, macular
 CC degeneration, corneal ulceration, stroke, ischemic heart disease,
 CC infertility, ulcers, scleroderma, wound healing, ischemia, myocardial
 CC infarction, myocardiosis, angina pectoris, unstable angina, coronary
 CC arteriosclerosis, arteriosclerosis obliterans, Berger's disease, arterial
 CC embolism, arterial thrombosis, cerebrovascular occlusion, cerebral
 CC infarction, cerebral thrombosis, cerebral embolism, rubeosis
 CC proliferative vitreoretinopathy, chronic inflammation, inflammatory bowel
 CC disease, psoriasis, sarcoidosis, or rheumatoid arthritis. The present
 CC sequence is mouse gene NOC8009G23, identified as being expressed during
 CC angiogenesis based on microarray data.

SQ Sequence 1849 BP; 528 A; 399 C; 369 G; 553 T; 0 U; 0 Other;
 Query Match 83.2%; Score 15.8; DB 14; Length 1849;
 Best Local Similarity 89.5%; Pred. No. 3.9e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCGCTTCGG 19
 |||||
 DB 54 GAATGGAGAGCGCTTCGG 36

RESULT 48
 ACC47372
 ID ACC47372 standard; cDNA; 2896 BP.

AC ACC47372;
 DT 11-AUG-2003 (first entry)
 DE Human late gestation lung 1 (LGL1) polypeptide encoding cDNA.
 DE LGL1: late gestation lung 1; bronchodilator; respiratory; gene therapy;
 KW antisense therapy; vaccine; human; gene; ss.
 XX Homo sapiens.

XX Key Location/Qualifiers
 FH 32..1525
 FT CDS /*tag= a
 FT /product= "LGL1"
 XX WO2003020766-A1.
 PN 13-MAR-2003.
 PD 04-SEP-2002; 2002WO-CA001350.
 PF 04-SEP-2001; 2001CA-02357746.
 PR 05-DEC-2001; 2001US-0336598P.
 XX (UYMC-) UNIV MCGILL.
 PA (HOSP-) HOSPITAL FOR SICK CHILDREN.

XX Kaplan F, Swezey NB;
 PI WPI: 2003-290169/28.
 DR P-PSDB; ABR39981.
 XX Novel late gestation lung 1 polypeptide and lg1l genes encoding the
 PT polypeptide, useful for preparing a medicament for use in the treatment

PT of a lung disease or disorder e.g. abnormal alveolarization.
 XX Claim 1; Page 128-131; 138pp; English.
 XX The invention relates to late gestation lung (LGL) 1 polypeptides and
 CC encoding polynucleotides. The LGL1 polypeptides can be expressed by
 CC standard recombinant methodology. The LGL1 polypeptides, polynucleotides
 CC and modulators are useful for modulating lung disease, airway branching
 CC and/or abnormal alveolarization. The lung disease is bronchopulmonary
 CC dysplasia (BPD), emphysema, New BPD, chronic obstructive pulmonary
 CC disease (COPD), congenital diaphragmatic hernia (CDH), chronic bronchial
 CC infection, in a human with a deficiency of alpha-1-antitrypsin. The LGL1
 CC polypeptide or polynucleotide is useful for the preparation of a
 CC medicament for use in the treatment of lung disease or disorder. They are
 CC useful in research, diagnostics and the preparation of therapeutics to
 CC treat diseases. The present sequence represents a cDNA encoding a human
 CC LGL1 polypeptide

SQ Sequence 2896 BP; 636 A; 769 C; 825 G; 666 T; 0 U; 0 Other;
 Query Match 83.2%; Score 15.8; DB 10; Length 2896;
 Best Local Similarity 89.5%; Pred. No. 4e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCGCTTCGG 19
 |||||
 DB 1486 GAACGGAAAGCGCTTCGG 1504

RESULT 49
 ADL35344
 ID ADL35344 standard; cDNA; 2898 BP.

AC ADL35344;
 DT 20-MAY-2004 (first entry)
 DE Murine secreted extracellular matrix 33145 cDNA.

XX extracellular matrix; cytostatic; neuroprotective; tissue regeneration;
 KW cancer metastatic inhibition; morphogenesis; cell growth;
 KW differentiation; brain disease; prion; taste bud; murine; mouse; ss;
 XX gene; 33145.

OS Mus musculus.
 XX Key Location/Qualifiers
 FH 171..1658
 FT CDS /*tag= a
 FT /product= "Murine secreted extracellular matrix 33145
 FT protein"

XX JP2004008021-A.
 PN 15-JAN-2004.
 PD 03-JUN-2002; 2002JP-00162211.
 PF 03-JUN-2002; 2002JP-00162211.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 PA (RIKA) RIKAGAKU KENKYUSHO.
 PA (DANA-) DANAFOMU KK.
 XX WPI: 2004-085645/09.
 DR P-PSDB; ADL35345.

XX Novel extra-cellular matrix protein derived from mouse, useful for tissue
 PT regeneration in regenerative medicine.
 XX Claim 3; SEQ ID NO 1; 86pp; Japanese.
 XX The invention relates to a novel extracellular matrix protein. The

CC protein of the invention demonstrates cytostatic and neuroprotective
CC activities and may be useful for tissue regeneration in regenerative
CC medicine and artificial tissue formation in an external, for metastatic
CC inhibition of a cancer cell and for diagnosing a disease accompanying
CC morphogenesis or tissue malformation. Furthermore, the protein may be
CC useful in the research of physiological functions such as human cell
CC growth and differentiation, as well as for diagnosing, treating or
CC relieving a brain disease caused by prion in individual and analysing
CC taste bud-specific protein function in the vertebrate. The current
CC sequence is that of a murine secreted extracellular matrix cDNA of the
CC invention.

XX Sequence 2898 BP; 634 A; 812 C; 807 G; 645 T; 0 U; 0 Other;
SQ

Query Match 83.2%; Score 15.8; DB 12; Length 2898;
Best Local Similarity 89.5%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGCCCTTCGG 19
Db 1619 GAACGGAAAGCCCTTCGG 1637

RESULT 50
ACC47371
ID ACC47371 standard; cDNA; 3054 BP.
XX
AC ACC47371;
XX
DT 11-AUG-2003 (first entry)
XX
DE Rat late gestation lung 1 (LGL1) polypeptide encoding cDNA.
XX
KW LGL1; late gestation lung 1; bronchodilator; respiratory; gene therapy;
KW antisense therapy; vaccine; rat; gene; ss.
XX
OS Rattus norvegicus.
XX
FH Key Location/Qualifiers
FT CDS 86..1579
FT /*tag= a
FT /*product= "LGL1"
XX
W02003020766-A1.
XX
XX 13-MAR-2003.
XX
XX 04-SEP-2002; 2002WO-CA001350.
XX
XX 04-SEP-2001; 2001CA-02357746.
XX
XX 05-DEC-2001; 2001US-0336598P.
XX
XX (UVMC-) UNIV MCGILL.
XX (HOSP-) HOSPITAL FOR SICK CHILDREN.
XX
XX Kaplan F, Swezey NB;
XX
XX WPI; 2003-290169/28.
XX
XX P-PSDB; ABR39980.
XX
XX Novel late gestation lung 1 polypeptide and lg1l genes encoding the
XX polypeptide, useful for preparing a medicament for use in the treatment
XX of a lung disease or disorder e.g. abnormal alveolarization.
XX
XX Claim 1; Page 124-127; 138pp; English.
XX
XX The invention relates to late gestation lung (LGL) 1 polypeptides and
XX encoding polynucleotides. The LGL1 polypeptides can be expressed by
XX standard recombinant methodology. The LGL1 polypeptides, polynucleotides
XX and modulators are useful for modulating lung disease, airway branching
XX and/or abnormal alveolarization. The lung disease is bronchopulmonary
XX dysplasia (BPD), emphysema, New BPD, chronic obstructive pulmonary
XX disease (COPD), congenital diaphragmatic hernia (CDH), chronic bronchial

CC infection, in a human with a deficiency of alpha-1-antitrypsin. The LGL1
CC polypeptide or polynucleotide is useful for the preparation of a
CC medicament for use in the treatment of lung disease or disorder. They are
CC useful in research, diagnostics and the preparation of therapeutics to
CC treat diseases. The present sequence represents a cDNA encoding a rat
CC LGL1 polypeptide
XX
SQ Sequence 3054 BP; 691 A; 817 C; 856 G; 690 T; 0 U; 0 Other;
Query Match 83.2%; Score 15.8; DB 10; Length 3054;
Best Local Similarity 89.5%; Pred. No. 4.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGCCCTTCGG 19
Db 1540 GAACGGAAAGCCCTTCGG 1558

RESULT 51
AAL36998
ID AAL36998 standard; DNA; 6883 BP.
XX
AC AAL36998;
XX
DT 08-JAN-2002 (first entry)
XX
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3363.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein;
KW musculoskeletal system; ds.
XX
OS Homo sapiens.
XX
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XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Barash SC, Ruben SM;	
XX	WPI; 2001-451937/48.	
DR		
XX		
PT	Isolated polypeptide for treating, preventing and/ or prognosing	
PT	disorders related to the musculoskeletal system including musculoskeletal	
XX	cancers and also for testing and detection e.g. diagnosis.	
PS	Example 2; SEQ ID NO 3363; 781pp + Sequence Listing; English.	
XX		
CC	The invention relates to novel genes (AAL34669-AAL37666) and proteins	
CC	(ABB03087-ABB04109) associated with the musculoskeletal system useful for	
CC	preventing, treating or ameliorating medical conditions e.g. by protein	
CC	or gene therapy. The genes are isolated from a range of human tissues	
CC	disclosed in the specification. The nucleic acids, proteins, antibodies	
CC	and (ant)agonists are useful in the diagnosis, treatment and prevention	
CC	of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the	
CC	adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,	
CC	lung, or urogenital; (b) immune disorders e.g. Addison's disease,	
CC	allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,	
CC	diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid	
CC	arthritis and ulcerative colitis; (c) cardiovascular disorders such as	
CC	myocardial ischaemia; (d) wound healing; (e) neurological diseases e.g.	
CC	cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,	
CC	bacterial, fungal and parasitic infections. Note: The sequence data for	
CC	this patent did not form part of the printed specification, but was	
CC	obtained in electronic format directly from WIPO at	
CC	ftp.wipo.int/pub/published_pct_sequences	
XX		
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DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3363.	PR	21-SEP-2000;	2000US-0234223P.
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XX gene therapy; vaccine; human; ds.	PR	25-SEP-2000;	2000US-0234998P.
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 PR 17-JAN-2001; 2001US-00764877.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Ruben SM, Barash SC;
 XX
 XX WPI; 2004-090458/09.
 XX
 XX New nucleic acid molecule, useful for preparing a medicament for
 PT preventing, treating or ameliorating a medical condition e.g., cancer of
 PT musculoskeletal tissues or osteoporosis.
 XX
 XX Disclosure; SEQ ID NO 3363; 289pp; English.
 XX
 XX The invention relates to a novel isolated musculoskeletal system-
 CC associated nucleic acid molecule. The nucleic acid of the invention
 CC demonstrates cytoskeletal and osteopathic activities and may be useful for
 CC preparing a medicament for preventing, treating or ameliorating a medical
 CC condition such as cancer of the musculoskeletal tissues or osteoporosis,
 CC possibly via gene therapy or vaccine production. The current sequence is
 CC that of the human musculoskeletal system-associated genomic DNA of the
 CC invention. The current sequence is not shown within the specification per
 CC se but is available on the USPTO web-site
 CC <http://seqdata.uspto.gov/sequence.html?DocID=20040009488>.
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 XX Sequence 6883 BP; 1921 A; 1341 C; 1311 G; 2310 T; 0 U; 0 Other;
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 Best Local Similarity 89.5%; Pred. No. 4.4e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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 XX AED48445;
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 XX 15-DEC-2005 (first entry)
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 XX
 XX ds, gene; antibiotic; virucide; aminoglycoside; bacterial infection;
 KW viral infection; gentamycin; genP; gmrB; genB1; genQ; genD3; genM1; gmrA;
 KW genS1; genC; genD2; genM2; genD1; genS2; genW; genB4; genJ; genB3; genK;
 KW genB2; genX; genU; genT; genE; genY; genA; genF; genG; genH; genI; genJ;
 KW genL; genN; DNA polymerase beta chain; integral membrane protein;
 KW agglutinin; esterase; Trp-tRNA ligase;
 KW queuine/archaeosine tRNA-ribosyltransferase; ribosomal methyltransferase;
 KW gentamicin (hexosaminyl-6-)aminotransferase I; gentamicin oxidoreductase;
 KW (N-acetyl-) hexosaminyltransferase; ribosomal methyltransferase;
 KW L-glutamine:ketocyclitol; 2-deoxy-scylo-inosose synthase;
 KW gentamicin glycosyltransferase II; gentamicin aminotransferase II;
 KW gentamicin production protein; gentamicin aminotransferase IV;
 KW aminoglycoside 3'-phosphotransferase; gentamicin aminotransferase III;
 KW gentamicin C-methyltransferase; gentamicin aminotransferase II;

KW gentamicin exporter; aminocyclitol 1-dehydrogenase; cation transporter;
 KW gentamicin methyltransferase; two-component system histidine kinase;
 KW two-component system response regulator; serine protease;
 KW DNA polymerase III epsilon subunit; RNA polymerase sigma factor;
 KW subtilase; transcriptional regulator; acetyltransferase;
 KW ATP-binding protein; ABC-transporter; permease component.
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 XX Micromonospora echinospora.
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 XX Location/Qualifiers
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FT /product= "biosynthetic aminoglycoside 3'-  
FT phosphotransferase"  
FT complement(36981. .38453)  
FT /*tag= ab  
FT /product= "putative gentamicin aminotransferase III"  
FT /gene= "genB3"  
FT complement(38969. .40885)  
FT /*tag= ac  
FT /gene= "genK"  
FT /product= "putative gentamicin C-methyltransferase"  
FT 41135. .42379  
FT /*tag= ad  
FT /product= "putative gentamicin aminotransferase II"  
FT /gene= "genB2"  
FT complement(42465. .42977)  
FT /*tag= ae  
FT /gene= "genX"  
FT /product= "putative gentamicin production protein"  
FT complement(43032. .43967)  
FT /*tag= af  
FT /product= "putative gentamicin production protein"  
FT /gene= "genU"  
FT complement(44162. .45568)  
FT /*tag= ag  
FT /gene= "genT"  
FT /product= "putative gentamicin exporter"  
FT complement(45861. .46883)  
FT /*tag= ah  
FT /product= "putative aminocyclitol 1-dehydrogenase"
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```
FT /gene= "genE"  
FT 47364. .48878  
FT /*tag= ai  
FT /gene= "genY"  
FT /product= "putative cation antiporter"  
FT 49000. .49737  
FT /*tag= aj  
FT /product= "putative gentamicin production protein"  
FT /gene= "genA"  
FT 49734. .50381  
FT /*tag= ak  
FT /gene= "genF"  
FT /product= "putative gentamicin production protein"  
FT 50381. .50734  
FT /*tag= al  
FT /product= "putative gentamicin production protein"  
FT /gene= "genG"  
FT complement(50813. .54229)  
FT /*tag= am  
FT /product= "putative gentamicin exporter "  
FT /gene= "genH"  
FT complement(54226. .56163)  
FT /*tag= an  
FT /gene= "genI"  
FT /product= "putative gentamicin exporter "  
FT complement(56689. .57627)  
FT /*tag= ao  
FT /gene= "genJ"  
FT /product= "putative gentamicin production protein"  
FT 58121. .58741  
FT /*tag= ap  
FT /product= "putative gentamicin production protein"  
FT
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Query Match 83.2%; Score 15.8; DB 14; Length 84222;
Best Local Similarity 89.5%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCTTTCGG 19

Db 15389 GAGCGAAAGGCCCTTCGG 15371

RESULT 55

AAC55929

ID AAC55929 standard; DNA; 455 BP.

XX AAC55929;

AC AAC55929;

XX 25-JAN-2001 (first entry)

DT 25-JAN-2001 (first entry)

DE Eucalyptus grandis transcription factor DNA sequence #60.

XX Plant; transcription factor; gene expression; eucalyptus; pine; acacia;

KW poplar; sweetgum; teak; mahogany; bz1P; G-box binding factor;

KW basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;

KW homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain;

KW type 2 Cys2His2; CCAAT box element; MYB; ss.

XX Eucalyptus grandis.

OS Eucalyptus grandis.

PN WO200053724-A2.

XX 14-SEP-2000.

PD 09-MAR-2000; 2000WO-US006112.

XX 11-MAR-1999; 99US-00266513.

PR 18-AUG-1999; 99US-0149485P.

XX (GENE-) GENESIS RES & DEV CORP LTD.

PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.

XX Wood M, McGrath A, Shenk MA, Glenn M;

PI

The present invention relates to novel plant transcription factors from *Eucalyptus grandis* or *Pinus radiata*. The present sequence is the coding sequence for one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic helix-loop-helix zipper, LIM domain, AP2 homeotic/homeodomain/homeobox/MADS, homeodomain zipper, CCAAT box elements and ERBs, zinc finger domains of type 2 CysHis2, CCAAT box elements and MYB.

Sequence 455 BP; 156 A; 75 C; 113 G; 111 T; 0 U; 0 Other;

Query Match 81.1%; Score 15.4; DB 3; Length 455;
Best Local Similarity 94.1%; Pred. No. 5.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCGCTTTC 17
||| |||||||
Db 27 GACCGGAAGGCCTTTC 43

RESULT 57
ACL67957
ID ACL67957 standard; DNA; 861 BP.
XX
AC ACL67957;
XX
DT 02-JUN-2005 (first entry)
XX
DE M. xanthus gene sequence, seq id 4420.
XX
KW Transgenic plant; DNA replication; gene regulation; gene expression;
KW gene; ds.
XX
OS Myxococcus xanthus.
XX
US US6833447-B1.
XX
PN 21-DEC-2004.
XX
PD 10-JUL-2001; 2001US-00902540.
XX
PF 10-JUL-2000; 2000US-0217883P.
XX
PR (MONS) MONSANTO TECHNOLOGY LLC.
XX
PA Goldman BS, Hinkle GU, Slater SC, Wiegand RC;
XX
PI WPI; 2005-028716/03.
XX
DR New substantially purified Myxococcus xanthus nucleic acid molecule
XX encoding a nitrite reductase, useful for determining gene expression,
PT identifying mutations in a gene of interest, and for constructing
PT mutations in a gene of interest.
XX
XX Example 2; SEQ ID NO 4420; 25pp; English.
XX
XX The invention relates to a substantially purified nucleic acid molecule
CC encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a
CC recombinant DNA construct for expression of a nitrite reductase gene in a
CC plant cell, and a plant cell comprising the recombinant DNA construct.
CC The nucleic acid is useful for determining gene expression, identifying
CC mutations in a gene of interest, and for constructing mutations in a gene
CC of interest. Sequences given in records for SEQ IDs 1850-9691 represent a
CC set of about 7842 genes or partial genes from the genome of the bacterium
CC Myxococcus xanthus. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from USPTO
XX
XX Sequence 861 BP; 155 A; 316 C; 283 G; 107 T; 0 U; 0 Other;


```
Query Match      81.1%; Score 15.4; DB 14; Length 861;
Best Local Similarity 94.1%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTTC 17
   |||||
Db 3 GAACGGAAGGCTTTC 19

RESULT 58
ABL04331
ID ABL04331 standard; cDNA; 5433 BP.
XX
AC ABL04331;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 7475.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
XX
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE ) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR P-PSDB; ABB60228.
XX
DR
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Claim 1; SEQ ID NO 7475; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 5433 BP; 1554 A; 1471 C; 1434 G; 974 T; 0 U; 0 Other;

Query Match      81.1%; Score 15.4; DB 4; Length 5433;
Best Local Similarity 94.1%; Pred. No. 6.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AACGGAAGGCTTTC 18
   |||||
Db 1687 AACGTAAGGCTTTC 1703

RESULT 59
ABL04330/c
ID ABL04330 standard; cDNA; 7162 BP.
XX
XX
```

PF 10-JUL-2001; 2001US-00902540.
 PR 10-JUL-2000; 2000US-0217883P.
 XX (MONS) MONSANTO TECHNOLOGY LLC.
 XX Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;
 XX WPI; 2005-028716/03.
 XX New substantially purified Myxococcus xanthus nucleic acid molecule
 PT encoding a nitrite reductase, useful for determining gene expression,
 PT identifying mutations in a gene of interest, and for constructing
 PT mutations in a gene of interest.
 XX Example 1; SEQ ID NO 1218; 25pp; English.
 PS
 CC The invention relates to a substantially purified nucleic acid molecule
 CC encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a
 CC recombinant DNA construct for expression of a nitrite reductase gene in a
 CC plant cell, and a plant cell comprising the recombinant DNA construct.
 CC The nucleic acid is useful for determining gene expression, identifying
 CC mutations in a gene of interest, and for constructing mutations in a gene
 CC of interest. Sequences given in records for SEQ IDs 1-1849 represent a
 CC set of 1849 contig and singleton sequences comprising coding sequences,
 CC DNA replication elements, promoters and other regulatory elements from
 CC the genome of the bacterium Myxococcus xanthus. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO
 XX
 SQ Sequence 23677 BP; 3557 A; 7986 C; 8412 G; 3722 T; 0 U; 0 Other;
 Query Match 81.1%; Score 15.4; DB 14; Length 23677;
 Best Local Similarity 94.1%; Pred. No. 7.8e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GAACGGAAGGCTTTC 17
 DB 23339 GAACGGAAGGCTTTC 23323
 RESULT 61
 AD882110/c
 ID ADB82110 standard; cDNA; 297 BP.
 XX
 AC ADB82110;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Human cDNA sequence useful for the treatment of cancer (SeqID 422).
 XX
 DE human; prostate; cancer; cytostatic; gene therapy; vaccine;
 XX immune response; gene; ss.
 XX Homo sapiens.
 OS
 XX WO2003050236-A2.
 PN
 XX 19-JUN-2003.
 PD
 XX
 PF 04-SEP-2002; 2002WO-US028214.
 XX
 XX 07-DEC-2001; 2001US-00012697.
 PR
 XX (CHIR) CHIRON CORP.
 PA (HYSE-) HYSEQ INC.
 XX
 XX Escobedo J, Garcia PD, Kassam A, Lamson G, Drmanac R;
 PI Crkvenjakov R, Dickson M, Drmanac S, Labat I, Leshkowitz D, Kita D;
 PI Garcia V, Jones LW, Stache-Crain B, Scott EM;
 XX WPI; 2003-513972/48.
 DR
 XX
 PT New genes and gene products isolated from human prostate, useful for
 PT treating or diagnosing tumor or cancer (e.g. prostate cancer or breast
 PT cancer), or as vaccines for treating or preventing these diseases.
 XX
 XX Claim 1; SEQ ID NO 423; 186pp + Sequence Listing; English.
 XX The invention relates to an isolated polynucleotide comprising any of

PT New polynucleotides derived from human prostate, useful for modulating
 XX immune response to prevent or treat cancer.
 PS Claim 1; SEQ ID NO 422; 188pp; English.
 XX
 CC This invention relates to novel isolated polynucleotides of human origin,
 CC particularly isolated from the human prostate. Specifically, it refers to
 CC the diagnostics and therapeutics comprising these novel human
 CC polynucleotides, and includes the derived probes, antisense
 CC oligonucleotides and antibodies thereof. The identification of these
 CC human prostate genes that can inhibit tumour growth is useful for
 CC understanding the progression and nature of complex diseases such as
 CC cancer, and hence they are important in the drug discovery process. The
 CC present invention describes these polynucleotides and encoded
 CC polypeptides as exhibiting cytostatic activity, and through gene therapy
 CC and/or vaccines they can be used to modulate the immune response for the
 CC prevention or treatment of cancers, particularly of the prostate, but
 CC also for breast, lung and colon cancer. This polynucleotide sequence is a
 CC human cDNA sequence useful for the treatment of cancer, used in an
 CC exemplification of the invention. NOTE: These sequences are not given in
 CC the specification but are provided on the WIPO website.
 XX
 SQ Sequence 297 BP; 56 A; 72 C; 76 G; 72 T; 0 U; 21 Other;
 Query Match 78.9%; Score 15; DB 9; Length 297;
 Best Local Similarity 100.0%; Pred. No. 8.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 GGAAGGCGCTTTCGG 19
 DB 75 GGAAGGCGCTTTCGG 61
 RESULT 62
 ABQ89167/c
 ID ABQ89167 standard; cDNA; 331 BP.
 XX
 AC ABQ89167;
 XX
 DT 27-SEP-2002 (first entry)
 XX
 DE Human prostate expressed polynucleotide SEQ ID NO 423.
 XX
 DE Human; prostate; cytostatic; tumour; cancer; vaccine; gene therapy; gene;
 XX ss.
 XX Homo sapiens.
 OS
 XX WO200255700-A2.
 PN
 XX 18-JUL-2002.
 PD
 XX
 PF 07-DEC-2001; 2001WO-US047349.
 XX
 XX 07-DEC-2000; 2000US-0254648P.
 PR
 PR 13-MAR-2001; 2001US-0275668P.
 XX
 XX (CHIR) CHIRON CORP.
 PA (HYSE-) HYSEQ INC.
 XX
 XX Escobedo J, Garcia PD, Kassam A, Lamson G, Drmanac R;
 PI Crkvenjakov R, Dickson M, Drmanac S, Labat I, Leshkowitz D, Kita D;
 PI Garcia V, Jones WL, Stache-Crain B, Scott EM;
 XX WPI; 2002-557824/59.
 DR
 XX
 XX New genes and gene products isolated from human prostate, useful for
 PT treating or diagnosing tumor or cancer (e.g. prostate cancer or breast
 PT cancer), or as vaccines for treating or preventing these diseases.
 XX
 XX Claim 1; SEQ ID NO 423; 186pp + Sequence Listing; English.
 XX The invention relates to an isolated polynucleotide comprising any of

CC	1477 sequences or its fragment, degenerate variant, antisense or complement. The polynucleotides and gene products are useful for treating or diagnosing tumour or cancer (e.g. prostate cancer, breast cancer, lung cancer or medullary carcinoma) in a subject (e.g. cattle, dogs, cats, rabbits, horse or human). The polynucleotides and polypeptides are also useful as vaccines for treating or preventing these diseases. The polynucleotides are useful for gene therapy. The present sequence is that of one of a group of polynucleotides (ABQ88745-ABQ90015) disclosed electronically as sequences of the invention. However only 1271 polynucleotide sequences are given, whereas 1477 polynucleotides and 91 proteins are claimed. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequence	CC	and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a vector comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above-mentioned amino acid sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising alternative splicing events, in detecting and characterising gross alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030194704
XX	Sequence 331 BP; 74 A; 77 C; 85 G; 74 T; 0 U; 21 Other;	XX	Sequence 592 BP; 201 A; 114 C; 140 G; 137 T; 0 U; 0 Other;
SQ		SQ	
Query Match	78.9%; Score 15; DB 6; Length 331;	Query Match	78.9%; Score 15; DB 12; Length 592;
Best Local Similarity	100.0%; Pred. No. 8.8e+02;	Best Local Similarity	100.0%; Pred. No. 9.2e+02;
Matches 15; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	Matches 15; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	5 GGAAGGCCCTTCGG 19 	QY	5 GGAAGGCCCTTCGG 19
Db	100 GGAAGGCCCTTCGG 86	Db	532 GGAAGGCCCTTCGG 546
RESULT 63		RESULT 64	
ACH79967		AD131363	
ID	ACH79967 standard; DNA; 592 BP.	ID	AD131363 standard; cDNA; 1429 BP.
AC	ACH79967;	AC	AD131363;
XX		XX	
DT	29-JUL-2004 (first entry)	DT	17-JUN-2004 (first entry)
XX		XX	
DE	Human genome derived single exon probe #13162.	DE	Human cDNA #689.
XX		XX	
KW	Human; probe; ss; gene expression; single exon probe; microarray;	KW	Human; gene; ss; immunological response; immunopathological condition; Crohn's disease; asthma; ulcerative colitis; hyperesinophilia;
KW	alternative splicing event; genomic alteration.	KW	irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
OS	Homo sapiens.	KW	acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;
XX		KW	osteopathic; antiarthritic; antirheumatic; cyostatic.
PN	US2003194704-A1.	OS	Homo sapiens.
XX		XX	
PD	16-OCT-2003.	XX	
XX		XX	
PF	03-APR-2002; 2002US-00029386.	XX	US6607879-B1.
XX		XX	
PR	03-APR-2002; 2002US-00029386.	PD	19-AUG-2003.
PA	(PENN/) PENN S G.	XX	
PA	(RANK/) RANK D R.	XX	09-FEB-1998; 98US-00023655.
PA	(HANZ/) HANZEL D K.	XX	09-FEB-1998; 98US-00023655.
XX		XX	
PI	Penn SG, Rank DR, Hanzel DK;	XX	(INCY-) INCYTE CORP.
XX		XX	
XX	WPI; 2004-119264/12.	XX	Cocks BG, Stuart SG, Seilhamer JJ;
XX		XX	
PT	New human genome-derived single exon nucleic acid probe useful for human	XX	WPI; 2003-895307/82.
PT	gene expression analysis, for identifying or characterizing alternative	XX	
PT	splicing events, for assessing genomic alterations or as tools for	XX	
PT	surveying tissues.	XX	
PS	Claim 15; SEQ ID NO 13162; 80pp; English.	XX	
XX		XX	
CC	The invention relates to a nucleic acid probe for measuring human gene	XX	
CC	expression, comprising any of the 27,400 fully defined nucleotide	XX	
CC	sequences in the specification, or their complements or fragments, and	XX	
CC	encoding at least 8 amino acids of any of the 6888 amino acid sequences	XX	
CC	fully defined in the specification. The probe is a single exon probe that	XX	
CC	hybridises under high stringency conditions to a nucleic acid molecule	XX	
CC	expressed in human cells or tissues. Also included are a spatially-	XX	
CC	addressable set of single exon nucleic acid probes for measuring human	XX	
CC	gene expression (comprising a plurality of single exon nucleic acid	XX	
CC	probes cited above, where each of the plurality of probes is separately	XX	

XX PS Claim 1; SEQ ID NO 689; 50pp; English.

XX CC The invention relates to a composition comprising a plurality of cDNAs

CC for detecting the altered expression of genes in an immunological

CC response. The invention also relates to a method of diagnosing or

CC monitoring the treatment of an immunopathological condition in a sample,

CC comprising obtaining nucleic acids from a sample, contacting the nucleic

CC acids of the sample with an array comprising the plurality of cDNAs under

CC conditions to form one or more hybridisation complexes, detecting the

CC hybridisation complexes and comparing the levels of the detected

CC hybridisation complexes with the level of hybridisation complexes

CC detected in a non-diseased sample, where an altered level of the detected

CC hybridisation complexes correlates with the presence of an

CC immunopathological condition. Also disclosed are an expression profile

CC comprising a microarray and a plurality of detectable complexes and a

CC method for identifying a plurality of polynucleotide probes. The cDNAs

CC are useful as hybridisable array elements in a microarray for monitoring

CC the expression of target polynucleotides. The microarray can be used in

CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,

CC ulcerative colitis, hypersensitivity, irritable bowel syndrome,

CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in

CC identifying agents for the treatment of the diseases. The microarray may

CC also be used in drug discovery and development, toxicological and

CC carcinogenicity studies, forensics or pharmacogenomics. The composition

CC may also be used in purification of a subpopulation of mRNAs, cDNAs or

CC genomic fragments. This sequence represents a human cDNA of the

CC invention. Note: The sequence data for this patent did not form part of

CC the printed specification but was obtained in electronic format directly

CC from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 1429 BP; 424 A; 311 C; 360 G; 329 T; 0 U; 5 Other;

Query Match 78.9%; Score 15; DB 11; Length 1429;

Best Local Similarity 100.0%; Pred. No. 1e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGAAAGCGCTTTCGG 19

Db 264 GGAAAGCGCTTTCGG 278

RESULT 65

ADS83430

ID ADS83430 standard; cDNA; 1429 BP.

AC ADS83430;

XX 11-AUG-2005 (first entry)

DE Human lymph node cDNA #689.

XX ss; gene; human; immunological response; blood cell; cancer;

XX immunopathological; AIDS; allergy; anaemia; asthma; atherosclerosis;

XX bronchitis; ulcerative colitis; diabetes; multiple sclerosis;

XX osteoporosis; pancreatitis; infection; arthritis; lymph node.

OS Homo sapiens.

XX US2004077003-A1.

XX 22-APR-2004.

XX 14-AUG-2003; 2003US-00641643.

XX 09-FEB-1998; 98US-00023655.

XX (INCY-) INCYTE CORP.

XX Cocks BG, Stuart SG, Seilhamer JJ;

XX WPI; 2004-387937/36.

XX

PT New compositions having a number of first, second and third

PT polynucleotide probes, useful in research and diagnostic applications in

PT cancer and immunological conditions e.g. AIDS, diabetes, osteoporosis and

PT infections.

XX Claim 15; SEQ ID NO 689; 16pp; English.

XX The invention relates to polynucleotides which are used as probes to

CC detect genes differentially expressed in an immunological response,

CC abundantly expressed in an immunological response and/or coding for a

CC polypeptide known to regulate blood cell biology. The polynucleotides are

CC useful in research and diagnostic applications particularly in cancer and

CC immunopathological conditions, such as AIDS, allergies, anaemia, asthma,

CC atherosclerosis, bronchitis, ulcerative colitis, diabetes, multiple

CC sclerosis, osteoporosis, pancreatitis, infections and arthritis. The

CC present sequence represents a human lymph node cDNA used to detect blood

CC cell and immunological response gene expression. Note: The present

CC sequence does not appear in the printed specification but was obtained in

CC electronic format from the USPTO web site

CC (seqdata.uspto.gov/sequence.html?DocID=20040077003).

XX SQ Sequence 1429 BP; 424 A; 311 C; 360 G; 329 T; 0 U; 5 Other;

Query Match 78.9%; Score 15; DB 13; Length 1429;

Best Local Similarity 100.0%; Pred. No. 1e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGAAAGCGCTTTCGG 19

Db 264 GGAAAGCGCTTTCGG 278

RESULT 66

AAH99589/c

ID AAH99589 standard; cDNA; 1453 BP.

XX AAH99589;

XX 16-OCT-2001 (first entry)

DE Human protein encoding cDNA sequence SEQ ID NO:424.

XX Human; cancer; ulcer; HIV infection; human immunodeficiency virus;

XX antiinflammatory; antirheumatic; antiarthritis; immunosuppressive;

XX antibacterial; endocrine; cardiac; central nervous system; virucide;

XX anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;

XX antiaggregant; haemostatic; vulnery; antiulcer; osteopathic; eczema;

XX dermatological; antiallergic; antidiabetic; antidiabetic; cystostatic;

XX neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;

XX immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;

XX antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;

XX cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;

XX genetic disease; haematopoietic disorder; platelet disorder; asthma;

XX thrombocytopaenia; osteoporosis; severe combined immunodeficiency;

XX allergic rhinitis; diabetes; multiple sclerosis; depression;

XX Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;

XX neurological disorder; ss.

XX Homo sapiens.

XX WO200153455-A2.

XX 26-JUL-2001.

XX 22-DEC-2000; 2000WO-US035017.

XX 23-DEC-1999; 99US-00471275.

XX 21-JAN-2000; 2000US-00488725.

XX 25-APR-2000; 2000US-00552317.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX

```
XX
DR WPI; 2001-457603/49.
DR P-PSDB; AAM25648.
XX
PT Isolated human polynucleotides encoding polypeptides, useful for the
PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection.
XX
PS Claim 1; Page 516-517; 1217pp; English.
XX
CC AAH99166 to AAH99904 encode the human proteins given in AM25225 to
CC AM25963. The proteins can have activities based on the tissues and cells
CC they are expressed in, such as: antiinflammatory; antirheumatic;
CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
CC cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary;
CC antitumor; osteopathic; dermatological; antiallergic; antiasthmatic;
CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC encoding them can be used in gene therapy, antisense therapy and vaccine
CC production. The proteins and polynucleotides are useful for screening for
CC agonists or antagonists of a protein and for the treatment and diagnosis
CC of disorders associated with the activity of a protein e.g. inflammation,
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
CC osteoporosis, severe combined immunodeficiency, eczema, allergic
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC neurological disorders
XX
SQ Sequence 1453 BP; 340 A; 366 C; 312 G; 435 T; 0 U; 0 Other;
Query Match 78.9%; Score 15; DB 4; Length 1453;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GGAAGGCGCTTTTCGG 19
Db 1173 GGAAGGCGCTTTTCGG 1159
RESULT 67
ABN59917
ID ABN59917 standard; cDNA; 2010 BP.
XX
AC ABN59917;
XX
DT 28-JUN-2002 (first entry)
XX
DE Novel human coding sequence SEQ ID NO: 328.
XX
KW Human; antianaemic; vulnerary; antiinflammatory; immunomodulatory;
KW antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
KW neuroprotective; antiparkinsonian; protein therapy; EST;
KW expressed sequence tag; gene; ss.
XX
OS Homo sapiens.
XX
FN WO200222660-A2.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US026015.
XX
PR 11-SEP-2000; 2000US-00659671.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX
DR WPI; 2002-292408/33.
XX
P-PSDB; ABB97504.
XX
PT An isolated polynucleotide for treating diseases associated with its
PT encoded polypeptide such as cancer and multiple sclerosis.
XX
PS Claim 1; SEQ ID NO 328; 509pp; English.
XX
CC The present invention provides the protein and coding sequences of 444
CC novel human proteins. These were isolated from expressed sequences tags
CC (ESTs). They can be used to stimulate cell growth, to regulate
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
CC e.g. in burn treatment, to regulate the immune system e.g. to treat
CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke
CC and cancer, to screen for drugs, to treat inflammatory conditions e.g.
CC rheumatoid arthritis, and to treat nervous system disorders e.g.
CC Parkinson's disease. The present sequence is a coding sequence of the
CC invention
XX
SQ Sequence 2010 BP; 585 A; 446 C; 527 G; 452 T; 0 U; 0 Other;
Query Match 78.9%; Score 15; DB 6; Length 2010;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GGAAGGCGCTTTTCGG 19
Db 1043 GGAAGGCGCTTTTCGG 1057
RESULT 68
AAF88159
ID AAF88159 standard; cDNA; 2015 BP.
XX
AC AAF88159;
XX
DT 17-JUL-2001 (first entry)
XX
DE Human thyroid malfunction-associated protein RITA encoding cDNA.
XX
KW KRAB domain; hyperplasia; thyroid; tumor; zinc finger motif; cytostatic;
KW antithyroid; gene therapy; chromosome 19; 19q13; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 187..1578
FT /tag= a
FT /product= "RITA"
XX
PN WO200127265-A1.
XX
PD 19-APR-2001.
XX
PF 11-OCT-2000; 2000WO-DE003600.
XX
PR 12-OCT-1999; 99DE-01049179.
XX
PA (UYBR-) UNIV BREMEN.
XX
PI Bullerdiek J, Rippe V, Meiboom M, Belge G;
XX
DR WPI; 2001-290723/30.
DR P-PSDB; AAB86115.
XX
PT New nucleic acid useful for the diagnosis and treatment of thyroid
PT disorders, e.g. tumors.
XX
PS Claim 2; Page 52-54; 59pp; German.
XX
CC This invention describes a novel nucleic acid (N1) encoding a polypeptide
CC which comprises a KRAB-domain and/or at least one zinc finger motif. The
CC products of the invention have cytostatic and antithyroid activity and
```

CC can be used in gene therapy. Nucleic acids, polypeptides, and antibodies
 CC of the invention may be used in the diagnosis and/or the therapy of the
 CC malfunction of the thyroid and/or hyperplasias of the thyroid and/or
 CC thyroid tumors. They may also be used in the production of medicaments.
 CC (NI) can also be used to diagnose thyroid tumors which are located on
 CC chromosome 19 at band 19q13. This sequence encodes the thyroid
 CC malfunction-associated protein, RITA which is described in the method of
 CC the invention
 XX

SQ Sequence 2015 BP; 601 A; 444 C; 503 G; 467 T; 0 U; 0 Other;

Query Match 78.9%; Score 15; DB 5; Length 2015;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGAAGGCGCTTCGG 19
 Db 847 GGAAGGCGCTTCGG 861

RESULT 69
 AAS03044
 ID AAS03044 standard; cDNA; 2098 BP.

AC AAS03044;

XX 29-AUG-2001 (first entry)

XX Human diagnostic and therapeutic (dithp) cDNA sequence #33.

XX Human diagnostic and therapeutic molecule; dithp; gene therapy;
 KW thalassemia; cardiovascular disorder; cell proliferative disorder;
 KW cancer; neurodegenerative disorder; autoimmune disorder;
 KW infectious disorder; inflammatory disorder; developmental disorder;
 KW Incyte ID number 9027913dec; transcription factor molecule; ss.

XX Homo sapiens.

XX WO200121836-A2.

XX 29-MAR-2001.

XX 19-SEP-2000; 2000WO-US025643.

XX 23-SEP-1999; 99US-0155760P.

XX 24-SEP-1999; 99US-0155939P.

XX 24-SEP-1999; 99US-0156294P.

XX 28-SEP-1999; 99US-0156565P.

XX 28-SEP-1999; 99US-0156624P.

XX 28-SEP-1999; 99US-0156625P.

XX 24-NOV-1999; 99US-0167410P.

XX 24-NOV-1999; 99US-0167517P.

XX 24-NOV-1999; 99US-0167520P.

XX 24-NOV-1999; 99US-0167521P.

XX 24-NOV-1999; 99US-0167522P.

XX 24-NOV-1999; 99US-0167542P.

XX 24-NOV-1999; 99US-0167543P.

XX 29-NOV-1999; 99US-0167943P.

XX 29-NOV-1999; 99US-0167945P.

XX 30-NOV-1999; 99US-0168197P.

XX 30-NOV-1999; 99US-0168265P.

XX 30-NOV-1999; 99US-0168432P.

XX 30-NOV-1999; 99US-0168432P.
 XX 01-DEC-1999; 99US-0168468P.
 XX 01-DEC-1999; 99US-0168599P.
 XX 02-DEC-1999; 99US-0168611P.
 XX 02-DEC-1999; 99US-0168613P.
 XX 02-DEC-1999; 99US-0168857P.
 XX (INCY-) INCYTE GENOMICS INC.
 XX Hodgson DW, Lincoln SE, Russo FD, Spiro PA, Banville SC;
 XX Bratcher SR, Dufour GE, Cohen HJ, Rosen BH, Shah P, Chalup MS;

PI Hillman JL, Jones AL, Yu JY, Greenawalt LB, Panzer SR, Roseberry AM;
 PI Wright RJ, Chen W, Liu TF, Yap PE, Stockdreher TK, Ameshey S;
 PI Fong WT;
 XX
 XX WPI; 2001-281607/29.
 XX Novel diagnostic and therapeutic polynucleotides, used in disease
 PT diagnosis and for gene therapy of conditions such as cancer and
 PT thalassemia.
 XX
 XX Claim 1; Page 271; 299pp; English.

XX The present sequence for human diagnostic and therapeutic (dithp) cDNA
 CC sequence #33 is 1 of 71 (AAS03012-AAS03082) novel sequences described in
 CC the invention. The present sequence (Incyte ID No: 9027913dec) encodes a
 CC transcription factor molecule. The dithp polynucleotides may be used to
 CC diagnose a condition disease or disorder associated with human molecules.
 CC They can be used to identify the presence of similar nucleic acids. Dithp
 CC polynucleotides may be used to generate hybridisation probes for use in
 CC chromosomal mapping. Polypeptides (DITHP) encoded by dithp are used to
 CC screen for molecules which bind to them and modulate their activity.
 CC Dithp polynucleotides can be used for gene therapy of disorders such as
 CC severe combined immunodeficiency syndrome (SCID), cystic fibrosis,
 CC thalassemia, haemophilia resulting from Factor VIII or IX deficiencies,
 CC cardiovascular disorders e.g familial hypercholesterolaemia (FH), cell
 CC proliferative disorders e.g. cancers, neurodegenerative disorders,
 CC autoimmune/inflammatory disorders, infectious disorders and developmental
 CC disorders. The antibodies can be used to analyse protein expression
 CC levels

XX SQ Sequence 2098 BP; 610 A; 467 C; 537 G; 484 T; 0 U; 0 Other;

Query Match 78.9%; Score 15; DB 4; Length 2098;

Best Local Similarity 100.0%; Pred. No. 1e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGAAGGCGCTTCGG 19

Db 933 GGAAGGCGCTTCGG 947

RESULT 70

AAK94562

ID AAK94562 standard; cDNA; 2169 BP.

AC AAK94562;

XX 06-NOV-2001 (first entry)

XX Human full-length cDNA, SEQ ID NO: 3469.

XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

XX Homo sapiens.

XX EPI130094-A2.

XX 05-SEP-2001.

XX 07-JUL-2000; 2000EP-00114089.

XX 08-JUL-1999; 99JP-00194486.

XX 11-JAN-2000; 2000JP-00118774.

XX 02-MAY-2000; 2000JP-00183765.

XX (HELI-) HELIX RES INST.

XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 XX Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX WPI; 2001-524255/58.

XX P-PSDB; AAM93629.

PT 830 Primers useful for synthesizing full length cDNA clones and their use
PT in genetic manipulation.

XX PS Claim 8; SEQ ID NO 3469; 1380pp + Sequence Listing; English.

XX CC The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC been determined. Primers for synthesizing the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesised by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is a full length human cDNA of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in CD-ROM format directly
CC from EPO

XX SQ Sequence 2169 BP; 633 A; 485 C; 560 G; 491 T; 0 U; 0 Other;

Query Match 78.9%; Score 15; DB 4; Length 2169;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 GGAAGGCGCTTCGG 19

|||||

Db 1004 GGAAGGCGCTTCGG 1018

RESULT 71

ADL31436

ID ADL31436 standard; cDNA; 2169 BP.

XX AC ADL31436;

XX DT 20-MAY-2004 (first entry)

XX DE Full length human cDNA clone SegID 3469.

XX KW human; medicine; signal transduction; glycoprotein; transcription;
KW oligo-capping method; ss; gene.

XX OS Homo sapiens.

XX PN EP1396543-A2.

XX PD 10-MAR-2004.

XX PF 07-JUL-2000; 2003EP-00025638.

XX PR 08-JUL-1999; 99JP-00194486.

XX PR 11-JAN-2000; 2000JP-00118774.

XX PR 02-MAY-2000; 2000JP-00183865.

XX PR 07-JUL-2000; 2000EP-00114089.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakanatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX WIPI; 2004-204755/20.

XX P-PSDB; ADL31437.

XX PT New oligonucleotide primers (830 cDNAs) useful for synthesizing full
PT length human cDNAs.

XX Example 1; SEQ ID NO 3469; 1340pp; English.

XX PS This invention relates to a novel primers useful for synthesizing full
XX length cDNA molecules that encode human proteins. Specifically, it refers
XX to secretory or membrane proteins that are potential therapeutic agents/
XX target molecules in the field of medicine, and in particular genes
XX encoding proteins that are associated with signal transduction,

CC glycoproteins and transcription. The present invention describes a method
CC for efficiently cloning a full length human cDNA from both the 5' and 3',
CC ends using the oligo-capping method. This polynucleotide sequence is a
CC full length human cDNA clone of the invention.

XX SQ Sequence 2169 BP; 633 A; 485 C; 560 G; 491 T; 0 U; 0 Other;

Query Match 78.9%; Score 15; DB 12; Length 2169;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 GGAAGGCGCTTCGG 19

|||||

Db 1004 GGAAGGCGCTTCGG 1018

RESULT 72

ABA82974

ID ABA82974 standard; DNA; 2173 BP.

XX AC ABA82974;

XX DT 05-FEB-2002 (first entry)

XX DE Human transcription factor TRFX-1 coding sequence.

XX KW Human; transcription factor; TRFX; cell proliferative disease;
KW autoimmune disease; inflammation; neurological disease;

XX KW developmental disorder; cancer; AIDS; infection; cytostatic; anti-HIV;
KW neuroprotective; antiinflammatory; gene therapy; ds.

XX OS Homo sapiens.

XX PN WO200172777-A2.

XX PD 04-OCT-2001.

XX PF 13-MAR-2001; 2001WO-US008117.

XX PR 13-MAR-2000; 2000US-0188986P.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Hillman JL, Baughn MR, Yue H, Lal P, Lu DAM, Patterson C;
PI Azimzai Y, Bandman O, Tang YT, Mathur P, Shah P, Au-Young J;
PI Reddy R;

XX WIPI; 2001-570896/64.

XX P-PSDB; ABB50150.

XX PT Novel transcription factor polypeptides, used to treat diseases
PT associated with altered activity and expression of TRFX, and to screen
PT for agents capable of modulating its activity.

XX Claim 11; Page 252; 327pp; English.

XX CC The present sequence is the coding sequence for a human transcription
XX factor. The transcription factor and its coding sequence are useful in
XX the diagnosis, treatment and prevention of diseases associated with
XX altered expression of the transcription factor e.g. cell proliferative,
XX autoimmune/inflammatory, neurological and developmental disorders. A
XX number of specific disorders/diseases are given in the specification,
XX including: arteriosclerosis, cirrhosis, hepatitis, cancers, AIDS,
XX allergies, anaemia, asthma, autoimmune thyroiditis, bronchitis, atopic
XX dermatitis, diabetes mellitus, emphysema, Goodpasture's syndrome, gout,
XX Grave's disease, multiple sclerosis, osteoarthritis, pancreatitis,
XX psoriasis, rheumatoid arthritis, systemic lupus erythematosus, ulcerative
XX colitis, uveitis, Alzheimer's disease, Huntington's disease, Parkinson's
XX disease, stroke, and viral, bacterial, fungal and protozoal infections

XX SQ Sequence 2173 BP; 648 A; 482 C; 555 G; 488 T; 0 U; 0 Other;

Query Match 78.9%; Score 15; DB 5; Length 2173;

Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGAAGGCGCTTCGG 19
|||||
Db 989 GGAAGGCGCTTCGG 1003
|||||

RESULT 73
ADB76868/c
ID ADB76868 standard; DNA; 2240 BP.
XX AC ADB76868;
XX XX
XX 04-DEC-2003 (first entry)
XX XX
XX A. gossypii metabolism associated oligo 178 DNA SEQ ID 22.
XX XX
XX metabolism; Vitamin B2 production; food supplement; oligo 178; gene; ds.
XX XX
XX Erethothecium gossypii.
XX XX
XX Key Location/Qualifiers
XX CDS 394..2019
FT /*tag= a
FT /product= "oligo 178 derived protein SEQ ID 23"
XX XX
XX WO2003018813-A2.
XX XX
XX 06-MAR-2003.
XX XX
XX 23-AUG-2002; 2002WO-EP009454.
XX XX
XX 23-AUG-2001; 2001DE-01041267.
XX 23-AUG-2001; 2001DE-01041268.
XX 23-AUG-2001; 2001DE-01041280.
XX 23-AUG-2001; 2001DE-01041281.
XX 23-AUG-2001; 2001DE-01041282.
XX 23-AUG-2001; 2001DE-01041283.
XX 23-AUG-2001; 2001DE-01041284.
XX 23-AUG-2001; 2001DE-01041288.
XX 23-AUG-2001; 2001DE-01041289.
XX 23-AUG-2001; 2001DE-01041290.
XX 23-AUG-2001; 2001DE-01041291.
XX 06-MAR-2002; 2002DE-01009829.
XX 11-APR-2002; 2002DE-01016027.
XX 11-APR-2002; 2002DE-01016031.
XX 11-APR-2002; 2002DE-01016032.
XX 16-MAY-2002; 2002DE-01021912.
XX 16-MAY-2002; 2002DE-01021914.
XX 16-MAY-2002; 2002DE-01021917.
XX 16-MAY-2002; 2002DE-01021920.
XX 16-MAY-2002; 2002DE-01021927.
XX 21-JUN-2002; 2002DE-01027797.
XX 21-JUN-2002; 2002DE-01027798.
XX XX
XX (BADI) BASF AG.
XX XX
XX Karos M, Althoefer H, Kroeger B, Revuelta Doval JL;
XX WPI; 2003-332833/31.
XX P-PSDB; ADB76869.
XX XX
XX New polynucleotide from Ashbya gossypii, useful for increasing microbial
XX production of Vitamin B2, encodes protein involved in metabolism.
XX XX
XX Claim 4; Page 100-102; 141pp; German.
XX XX
XX This invention describes novel Ashbya gossypii (also called Erethothecium
XX gossypii) metabolism associated proteins and their encoding nucleic
XX acids. Modulating the metabolism of cells improves microbial production
XX of Vitamin B2, a human and animal food supplement. This sequence
XX represents Oligo 178 which encodes an A. gossypii metabolism associated

CC protein. Oligo 178 encodes a homologue of a Saccharomyces cerevisiae
CC phosphoenolpyruvate carboxykinase.
XX XX
SQ Sequence 2240 BP; 520 A; 597 C; 645 G; 478 T; 0 U; 0 Other;
Query Match 78.9%; Score 15; DB 10; Length 2240;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGAAGGCGCTTCGG 19
|||||
Db 76 GGAAGGCGCTTCGG 62
|||||

RESULT 74
ABL07155
ID ABL07155 standard; cDNA; 3003 BP.
XX XX
XX ABL07155;
XX XX
XX 26-MAR-2002 (first entry)
XX XX
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 15947.
XX DE Drosophila; developmental biology; cell signalling; insecticide;
XX KW Drosophila; pharmaceutical; gene; ss.
XX KW pharmaceutical; gene; ss.
XX OS Drosophila melanogaster.
XX XX
XX WO200171042-A2.
XX XX
XX 27-SEP-2001.
XX XX
XX 23-MAR-2001; 2001WO-US009231.
XX XX
XX 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX XX
XX (PEKE) PE CORP NY.
XX XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX DR P-PSDB; ABB63052.
XX XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signaling and cell-cell
XX interactions.
XX XX
XX Claim 1; SEQ ID NO 15947; 21pp + Sequence Listing; English.
XX PS
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
XX ABB72072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX XX
XX Sequence 3003 BP; 698 A; 798 C; 889 G; 618 T; 0 U; 0 Other;
Query Match 78.9%; Score 15; DB 4; Length 3003;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGGAAGGCCTT 15
|||||
Db 2424 GAACGGGAAGGCCTT 2438
|||||

Accession	Gene	Protein	Function	RefSeq ID
AA025944	AA025944 standard; cDNA; 3293 BP.			08-SEP-2000; 2000US-0231243P
XX	AA025944			PR 08-SEP-2000; 2000US-0231244P
XX	AA025944			PR 08-SEP-2000; 2000US-0231413P
XX	AA025944			PR 08-SEP-2000; 2000US-0231414P
XX	AA025944			PR 08-SEP-2000; 2000US-0231415P
XX	AA025944			PR 08-SEP-2000; 2000US-0232080P
XX	AA025944			PR 08-SEP-2000; 2000US-0232081P
XX	AA025944			PR 08-SEP-2000; 2000US-0232082P
XX	AA025944			PR 08-SEP-2000; 2000US-0232083P
XX	AA025944			PR 08-SEP-2000; 2000US-0232084P
XX	AA025944			PR 08-SEP-2000; 2000US-0232085P
XX	AA025944			PR 08-SEP-2000; 2000US-0232086P
XX	AA025944			PR 08-SEP-2000; 2000US-0232087P
XX	AA025944			PR 08-SEP-2000; 2000US-0232088P
XX	AA025944			PR 08-SEP-2000; 2000US-0232089P
XX	AA025944			PR 08-SEP-2000; 2000US-0232090P
XX	AA025944			PR 08-SEP-2000; 2000US-0232091P
XX	AA025944			PR 08-SEP-2000; 2000US-0232092P
XX	AA025944			PR 08-SEP-2000; 2000US-0232093P
XX	AA025944			PR 08-SEP-2000; 2000US-0232094P
XX	AA025944			PR 08-SEP-2000; 2000US-0232095P
XX	AA025944			PR 08-SEP-2000; 2000US-0232096P
XX	AA025944			PR 08-SEP-2000; 2000US-0232097P
XX	AA025944			PR 08-SEP-2000; 2000US-0232098P
XX	AA025944			PR 08-SEP-2000; 2000US-0232099P
XX	AA025944			PR 08-SEP-2000; 2000US-0232100P
XX	AA025944			PR 08-SEP-2000; 2000US-0232101P
XX	AA025944			PR 08-SEP-2000; 2000US-0232102P
XX	AA025944			PR 08-SEP-2000; 2000US-0232103P
XX	AA025944			PR 08-SEP-2000; 2000US-0232104P
XX	AA025944			PR 08-SEP-2000; 2000US-0232105P
XX	AA025944			PR 08-SEP-2000; 2000US-0232106P
XX	AA025944			PR 08-SEP-2000; 2000US-0232107P
XX	AA025944			PR 08-SEP-2000; 2000US-0232108P
XX	AA025944			PR 08-SEP-2000; 2000US-0232109P
XX	AA025944			PR 08-SEP-2000; 2000US-0232110P
XX	AA025944			PR 08-SEP-2000; 2000US-0232111P
XX	AA025944			PR 08-SEP-2000; 2000US-0232112P
XX	AA025944			PR 08-SEP-2000; 2000US-0232113P
XX	AA025944			PR 08-SEP-2000; 2000US-0232114P
XX	AA025944			PR 08-SEP-2000; 2000US-0232115P
XX	AA025944			PR 08-SEP-2000; 2000US-0232116P
XX	AA025944			PR 08-SEP-2000; 2000US-0232117P
XX	AA025944			PR 08-SEP-2000; 2000US-0232118P
XX	AA025944			PR 08-SEP-2000; 2000US-0232119P
XX	AA025944			PR 08-SEP-2000; 2000US-0232120P
XX	AA025944			PR 08-SEP-2000; 2000US-0232121P
XX	AA025944			PR 08-SEP-2000; 2000US-0232122P
XX	AA025944			PR 08-SEP-2000; 2000US-0232123P
XX	AA025944			PR 08-SEP-2000; 2000US-0232124P
XX	AA025944			PR 08-SEP-2000; 2000US-0232125P
XX	AA025944			PR 08-SEP-2000; 2000US-0232126P
XX	AA025944			PR 08-SEP-2000; 2000US-0232127P
XX	AA025944			PR 08-SEP-2000; 2000US-0232128P
XX	AA025944			PR 08-SEP-2000; 2000US-0232129P
XX	AA025944			PR 08-SEP-2000; 2000US-0232130P
XX	AA025944			PR 08-SEP-2000; 2000US-0232131P
XX	AA025944			


```

XX PI Rosen CA, Ruben SM, Barash SC;
XX PT WPI; 2003-147444/14.
XX DR P-PSDB; ABUS5025.
XX XX
XX PT New polypeptides and nucleic acids, useful in gene therapy for treating,
XX PT inhibiting or preventing e.g. neural, immune system, muscular,
XX PT respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
XX PT renal disorders.
XX PS Claim 1; SEQ ID NO 123; 402pp; English.
XX CC The invention relates to human novel polypeptides and their associated
XX CC polynucleotides. The polypeptides and polynucleotides are useful in gene
XX CC therapy for treating, inhibiting or preventing neural disorders, immune
XX CC system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis
XX CC and multiple sclerosis), muscular disorders, respiratory diseases (e.g.
XX CC nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders,
XX CC gastrointestinal disorders, pulmonary disorders, cardiovascular disorders,
XX CC congenital heart defects, Ebstein's anomaly and hypoplastic left
XX CC heart syndrome), renal disorders (e.g. acute kidney failure and end-stage
XX CC renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and
XX CC leukemia), inflammatory diseases (e.g. septic shock, bursitis and
XX CC appendicitis), allergic reactions and conditions (e.g. asthma), blood
XX CC related disorders (e.g. thrombosis, atherosclerosis and myocardial
XX CC infarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent
XX CC human novel polynucleotides of the invention
XX SQ Sequence 3293 BP; 974 A; 717 C; 750 G; 852 T; 0 U; 0 Other;

Query Match 78.9%; Score 15; DB 8; Length 3293;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGAAGGCGCTTTCGG 19
Db 892 GGAAGGCGCTTTCGG 906

RESULT 77
AEE83945
ID AEE83945 standard; cDNA; 5165 BP.
AC AEE83945;
XX XX
XX DT 23-FEB-2006 (first entry)
XX DE Human cDNA differentially expressed in asthma, SEQ ID NO:353.
XX KW Genetic marker; ss; gene; DNA microarray; asthma; antiasthmatic;
XX KW diagnosis; prognosis; blood; cardiovascular disease; cardiovascular-gen.;
XX KW immune disorder; immunomodulator; musculoskeletal disease; muscular-gen.;
XX KW osteopathic; mood disorder; neuroprotective; autoimmune disease;
XX KW immunosuppressive; respiratory disease; respiratory-gen.;
XX KW endocrine disease; endocrine-gen.; neurological disease; metabolic;
XX KW metabolic disorder; hyperproliferation; cytostatic.
XX XX
XX OS Homo sapiens.
XX DE WO2005118403-A2.
XX PN 15-DEC-2005.
XX XX
XX XX 05-JUN-2005; 2005WO-IL000590.
XX XX
XX PR 04-JUN-2004; 2004US-0576599P.
XX PA (LINK-) LINKGENE LTD.
XX XX
XX PI Kachalsky SG, Horev G;
XX XX WPI; 2006-047464/05.
XX DR

Identifying biomarker, useful for diagnosing, monitoring or prognosing a
disease, e.g. asthma, comprises determining the level of gene transcript
in blood cells.

Claim 38; SEQ ID NO 353; 74pp; English.

The invention relates to identifying at least one biomarker for a
disease, comprising determining the level of at least one gene transcript
in a subpopulation of blood cells obtained from at least one subject
having the disease. The at least one subject having the disease is a
member of a closed population (e.g. Cochin Jews). Also included are
diagnosing/monitoring/prognosing a disease in a subject, nucleic acid
molecules corresponding to one or more biomarkers (or their complement,
the biomarkers having been determined by using the method above), and an
array comprising the nucleic acid molecules. The biomarkers are selected
from AEE83593-AEE84375 or their complements. Determining the level of at
least one gene transcript comprises microarray hybridization, where the
microarray hybridization comprises hybridizing isolated nucleic acid
molecules to an array comprising second nucleic acid molecules. The first
isolated nucleic acid molecules are selected from RNA, DNA, cDNA, or PCR
products. The second isolated nucleic acid molecules is selected from
RNA, DNA, cDNA, PCR products, oligonucleotides, or ESTs. Diagnosing,
monitoring or prognosing a disease in a subject comprises determining the
level of at least one gene transcript in a subpopulation of blood cells
obtained from the subject (where the at least one gene transcript
corresponds to a biomarker, the biomarker having been determined using
the method above); and comparing the level of the at least one gene
transcript of step (a) with the level of the at least one gene transcript
in a reference gene transcript profile, thus determining the status of
the disease in the subject. The method is useful for identifying at least
one biomarker for a disease. The biomarker, array, and method are useful
for diagnosing, monitoring or prognosing a disease, e.g. cardiovascular,
immune, muscular, mood, autoimmune, respiratory, endocrine, neurological,
metabolic, or cellular proliferative diseases, where the respiratory
disease is asthma (a long list of diseases is included in the
specification). The present sequence is a human full-length cDNA that is
differentially expressed in subjects suffering from asthma (the subjects
were from the closed population of Cochin Jews).

XX SQ Sequence 5165 BP; 1542 A; 1069 C; 1267 G; 1287 T; 0 U; 0 Other;

Query Match 78.9%; Score 15; DB 15; Length 5165;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGAAGGCGCTTTCGG 19
Db 2005 GGAAGGCGCTTTCGG 2019

RESULT 78
ABL07154
ID ABL07154 standard; cDNA; 8544 BP.
XX ABL07154;
XX XX
XX DT 26-MAR-2002 (first entry)
XX XX
XX DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 15944.
XX PN Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical; gene; ss.
XX XX
XX OS Drosophila melanogaster.
XX XX
XX PN WO200171042-A2.
XX XX
XX PD 27-SEP-2001.
XX XX
XX PF 23-MAR-2001; 2001WO-US009231.
XX XX 23-MAR-2000; 2000US-0191637P.
XX PR

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PR 11-JUL-2000; 2000US-00614150.
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
DR P-PSDB; ABB63051.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
XX Claim 1; SEQ ID NO 15944; 21bp + Sequence Listing; English.
PS
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 8544 BP; 2263 A; 2022 C; 2092 G; 2167 T; 0 U; 0 Other;
Query Match 78.9%; Score 15; DB 4; Length 8544;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAACGGAAAGGCCTT 15
DB 6899 GAACGGAAAGGCCTT 6913
RESULT 79
AAT70787/c
ID AAT70787 standard; RNA; 40 BP.
AC AAT70787;
XX
XX 30-JUL-1997 (first entry)
XX
XX Stenotic carotid artery binding ligand Civ19.
XX
XX Ligand; peripheral blood mononuclear cell; fibrin clot; carotid artery;
XX systematic evolution of ligands by exponential enrichment method; PBMC;
XX epitope; macromolecule; tissue SELEX method; cancer screening; therapy;
XX AIDS monitoring; localisation of thrombi; atherosclerosis; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1..40
FT /*tag= a
FT /mod_base= all C's are 2-fluorine-C
FT modified_base 1..40
FT /*tag= b
FT /mod_base= all U's are 2-fluorine-U
XX
XX WO9634874-A1.
XX
XX 07-NOV-1996.
XX
XX 01-MAY-1996; 96WO-US006059.
XX
XX 03-MAY-1995; 95US-00433124.
XX
XX 03-MAY-1995; 95US-00433126.
XX
XX (NEXS-) NEXSTAR PHARM INC.
XX
XX (SCHD ) SCHERING AG.
XX
XX Stephens A, Gold L, Speck U;
XX PI
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XX Stephens A, Schneider DJ, Gold L, Speck U;
XX WPI; 1996-506091/50.
XX
XX Nucleic acid ligands used in cancer screening, AIDS monitoring etc. -
XX bind to peripheral blood mononuclear cells, fibrin clots or carotid
XX arteries.
XX
XX Claim 23; Page 58; 138pp; English.
XX
XX AAT70705-T70803 represent the random regions from a degenerate ssDNA
XX library based on the sequence represented by AAT42819. These sequences
XX are all ligands specific for fibrin clots identified using the method of
XX the invention. The method of the invention is for identifying nucleic
XX acid (NA) ligands and NA ligand sequences to a tissue target selected
XX from peripheral blood mononuclear cells (PBMC's) (such as the ligands
XX represented by AAT70584-T70616), fibrin clots (such as the ligands
XX represented by AAT70617-T70704), and carotid arteries (such as these
XX ligands). The method comprises preparing a candidate mixture of NA
XX sequences, and contacting these with the tissue, whereby NAs having an
XX increased affinity to the tissue relative to the candidate mixture may be
XX partitioned from the remainder of the candidate mixture. The increased
XX affinity NAs are then partitioned from the remainder of the candidate
XX mixture, and are amplified to yield a mixture of NAs enriched for NA
XX sequences with a relatively higher affinity and specificity for binding
XX to the tissue, whereby NA ligands of the tissue may be identified. The
XX method represents a tissue SELEX (systematic evolution of ligands by
XX exponential enrichment) method. The NA ligands and epitopes and
XX macromolecules identified using the ligands can be used in diagnostic and
XX therapeutic applications. In particular, they can be used for e.g. cancer
XX screening, AIDS monitoring, detection and localisation of thrombi or
XX atherosclerosis diagnosis and therapy
XX
XX Sequence 40 BP; 9 A; 13 C; 8 G; 0 T; 10 U; 0 Other;
Query Match 77.9%; Score 14.8; DB 2; Length 40;
Best Local Similarity 88.9%; Pred. No. 9.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 AACGGAAGGCCTTCGG 19
DB 27 ATCGGAAGGCCTTCGG 10
RESULT 80
AAX85278/c
ID AAX85278 standard; RNA; 87 BP.
XX
XX AAX85278;
XX
XX 06-AUG-1999 (first entry)
XX
XX Motif I final cluster oligonucleotide SEQ ID NO:221.
XX
XX Nucleic acid ligand; high-affinity; tissue target; blood vessel;
XX atherosclerotic plaque; carotid artery; WHHL; diagnosis; therapy;
XX watanabe heritable hyperlipidaemia; ss.
XX
XX Synthetic.
XX
XX WO9927138-A1.
XX
XX 03-JUN-1999.
XX
XX 19-NOV-1998; 98WO-US025006.
XX
XX 21-NOV-1997; 97US-00976413.
XX
XX (NEXS-) NEXSTAR PHARM INC.
XX
XX (SCHD ) SCHERING AG.
XX
XX Stephens A, Gold L, Speck U;
XX PI
```


CC against Klebsiella pneumoniae. This sequence encodes a Klebsiella
CC pneumoniae polypeptide of the invention
XX
SQ Sequence 375 BP; 71 A; 82 C; 113 G; 109 T; 0 U; 0 Other;

Query Match 77.9%; Score 14.8; DB 11; Length 375;
Best Local Similarity 88.9%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTTCG 18
|||||
DB 333 GAACGGAAGGCTTTTCG 350

RESULT 83
ABD06974

ID ABD06974 standard; DNA; 543 BP.

XX

AC ABD06974;

DT 29-JUL-2004 (first entry)

DE Pseudomonas aeruginosa polynucleotide #5578.

XX Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW antibacterial.

XX Pseudomonas aeruginosa.

XX US6551795-B1.

XX 22-APR-2003.

XX 18-FEB-1999; 99US-00252991.

XX 18-FEB-1998; 98US-0074788P.

XX 27-JUL-1998; 98US-0094190P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;

XX WPI; 2003-615309/58.

DR P-PSDB; ABO73403.

XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.

XX Disclosure; SEQ ID NO 5578; 455pp; English.

XX The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABD01397-
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html

XX Sequence 543 BP; 125 A; 174 C; 147 G; 97 T; 0 U; 0 Other;

Query Match 77.9%; Score 14.8; DB 11; Length 543;
Best Local Similarity 88.9%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTTCG 18
|||||
DB 145 GAACGATAGGCTGTTCG 162

RESULT 84

AAI43438/C

ID AAI43438 standard; DNA; 591 BP.

XX

AC AAI43438;

DT 17-OCT-2001 (first entry)

XX Probe #12124 used to measure gene expression in human placenta sample.

XX Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder; ss.

XX Homo sapiens.

XX WO200157272-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000663.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.

XX Claim 25; SEQ ID NO 12124; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENP).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders

XX Sequence 591 BP; 122 A; 171 C; 156 G; 142 T; 0 U; 0 Other;

Query Match 77.9%; Score 14.8; DB 4; Length 591;
Best Local Similarity 88.9%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTTCG 18
|||||
DB 266 GATGGGAAGGCTTTTCG 249

RESULT 85

ABD07046/C

ID ABD07046 standard; DNA; 600 BP.

XX

AC ABD07046;

DT 29-JUL-2004 (first entry)

XX Pseudomonas aeruginosa polynucleotide #5650.

KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
 KW antibacterial.
 XX
 OS Pseudomonas aeruginosa.
 XX
 PN US6551795-B1.
 XX
 XX 22-APR-2003.
 XX
 XX 18-FEB-1999; 99US-00252991.
 XX
 PR 18-FEB-1998; 98US-0074788P.
 PR 27-JUL-1998; 98US-0094190P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 DR WPI; 2003-615309/58.
 DR P-PSDB; ABO73475.
 XX
 PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.
 XX
 PS Disclosure; SEQ ID NO 5650; 455pp; English.
 XX
 CC The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences ABD01397-
 CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 600 BP; 108 A; 167 C; 189 G; 136 T; 0 U; 0 Other;

Query Match 77.9%; Score 14.8; DB 11; Length 600;
 Best Local Similarity 88.9%; Pred. No. 1.2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTCG 18
 DB 468 GAACGGATAGGCTGTCTG 451

RESULT 86
 ACA27357
 ID ACA27357 standard; DNA; 981 BP.
 XX
 AC ACA27357;
 XX

DT 19-JUN-2003 (first entry)
 DE Prokaryotic essential gene #9014.
 XX

KW Antisense; ds; prokaryotic essential gene; cell proliferation;
 KW drug design; gene.
 XX
 OS Bordetella pertussis.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 XX WPI; 2003-029926/02.
 DR P-PSDB; ABU23487.
 DR

XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 14; SEQ ID NO 15227; 1765pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than S. aureus, S. typhimurium,
 CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 981 BP; 189 A; 306 C; 353 G; 133 T; 0 U; 0 Other;

Query Match 77.9%; Score 14.8; DB 8; Length 981;
 Best Local Similarity 88.9%; Pred. No. 1.2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTCG 18
 DB 169 GAACGGAAGGCTATGCG 186

RESULT 87
 ADW16249
 ID ADW16249 standard; DNA; 1158 BP.
 XX
 AC ADW16249;
 XX
 DT 07-APR-2005 (first entry)

XX DE DNA copy of the Microbispora 16s ribosomal RNA EN2 isolate Seq 1.
 XX KW 16s ribosomal RNA; ds; 16s rRNA; medicinal plant; plant breeding;
 KW disease resistance; insect resistance; crop improvement;
 KW plant growth factor; antibacterial; antimicrobial; fungicide;
 KW insecticide; nematocide.
 XX OS Microbispora.
 XX PN WO2005003328-A1.
 XX PD 13-JAN-2005.
 XX PF 07-JUL-2004; 2004WO-AU000914.
 XX PR 07-JUL-2003; 2003US-0485241P.
 XX PR 22-SEP-2003; 2003US-0504703P.
 XX PA (FLIN-) FLINDERS TECHNOLOGIES PTY LTD.
 XX PI Franco CMW, Coombs JT;
 XX PI WPI; 2005-091806/10.
 XX DR Improving plant productivity comprises introducing into the plant or
 PT propagation material an endophytic actinomycete that facilitates
 PT induction of at least one characteristic related to improved
 PT productivity.
 XX PS Claim 1; SEQ ID NO 1; 235pp; English.
 XX CC This invention relates to a novel method for improving plant
 CC productivity. Specifically, it refers to introducing into the plant or
 CC propagation material an endophytic actinomycetes or variant thereof,
 CC where the actinomycetes facilitate induction of a characteristic related
 CC to improved productivity. The present invention further describes
 CC metabolites of the actinomycetes microorganism such as auxin, gibberellin
 CC or cytokinin that are able to induce disease resistance in plants i.e.
 CC provide disease bio-control capabilities against pathogen infection.
 CC Accordingly, the method facilitates the improvement of cereal crop
 CC productivity including increasing germination by up-regulating plant
 CC growth promoting activities, as well as improving plant vigor or flower
 CC and fruit yield. Furthermore, the new actinomycete or metabolite is
 CC useful in the manufacture of a medicament for the therapeutic and/or
 CC prophylactic treatment of a mammalian or non-mammalian subject i.e.
 CC plant. As such, this method provides plant protectants and plant growth
 CC stimulants that exhibit antibacterial, antimicrobial, fungicide,
 CC insecticide and nematocide activities. This polynucleotide is the DNA
 CC sequence of an actinomycetes 16s ribosomal RNA sequence of the invention.
 XX SQ Sequence 1158 BP; 247 A; 265 C; 379 G; 234 T; 0 U; 33 Other;
 Query Match 77.9%; Score 14.8; DB 14; Length 1158;
 Best Local Similarity 88.9%; Pred. No. 1.2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 AACGGAAGGCGCTTCGG 19
 Db 19 AGCGGAAGGCGCTTCGG 36
 RESULT 88
 AAZ11765
 ID AAZ11765 standard; DNA; 1392 BP.
 XX AC AAZ11765;
 XX AC
 XX DT 15-NOV-1999 (first entry)
 XX DE Maize histone H2B promoter.
 XX KW Promoter; constitutive expression; transgenic plant; maize;

KW genetic modification; ds.
 XX Zea mays.
 XX PH Location/Qualifiers
 FT Key 871..876
 FT TATA_signal /+tag= a
 FT /standard_name= "TATA box"
 FT /notes= "Approximately 25 bases upstream of
 FT transcriptional start site"
 XX PN WO9943797-A2.
 XX PD 02-SEP-1999.
 XX PF 25-FEB-1999; 99WO-US004203.
 XX PR 26-FEB-1998; 98US-0076075P.
 XX PA (PION-) PIONEER HI-BRED INT INC.
 XX PI Rice DA;
 XX PI WPI; 1999-518954/43.
 XX DR New constitutive promoter sequences from maize, useful in genetic
 PT manipulation of plants.
 XX PS Claim 1; Page 39; 53pp; English.
 XX CC This sequence represents a maize histone H2B constitutive promoter. Maize
 CC H2B histones are constitutively expressed at a high level in meristematic
 CC tissue. This promoter was isolated and amplified from a maize seedling
 CC genomic library using an APL primer (AAZ11775) and a gene-specific
 CC primer, histone H2B gsp-1 (AAZ11776). The DNA from this first round of
 CC PCR was diluted and used as a template for a second round of PCR, this
 CC time using an AP2 primer (AAZ06802) and a second gene-specific primer,
 CC histone H2B gsp-2 (AAZ06803). The amplified DNA was sequenced for
 CC verification, cloned into the TA vector pCR2.1, minipreped and subjected
 CC to a third round of PCR using the AP2 primer and a third gene-specific
 CC primer, histone H2B gsp-3 (AAZ06810). This sequence, and other
 CC constitutive plant promoters (AAZ11766-Z11774), are capable of initiating
 CC constitutive expression in plant cells and have potential for use in
 CC vectors used to introduce and express heterologous DNA sequences in
 CC plants. Such a vector would comprise the heterologous DNA sequence
 CC operably linked to the promoter. The vector could then be used to
 CC transform a plant cell. A stably transformed plant could then be
 CC regenerated from the transformed plant cell. The heterologous sequences
 CC that could be linked to these constitutive promoters might include a
 CC pathogen-resistance gene, enabling pathogen-resistance proteins to be
 CC continuously expressed throughout the plant's tissues. Alternatively,
 CC antisense DNA could be used to inhibit the expression of a native gene to
 CC produce a desired phenotype. The antisense RNA transcript would bind to
 CC native mRNA and interfere with translation
 XX SQ Sequence 1392 BP; 394 A; 280 C; 259 G; 459 T; 0 U; 0 Other;
 Query Match 77.9%; Score 14.8; DB 2; Length 1392;
 Best Local Similarity 88.9%; Pred. No. 1.3e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 AACGGAAGGCGCTTCGG 19
 Db 1143 AAAGGAAGGCGCTTCGG 1160
 RESULT 89
 ADA71495
 ID ADA71495 standard; DNA; 2000 BP.
 XX AC ADA71495;
 XX AC
 XX DT 20-NOV-2003 (first entry)

XX Rice gene, SEQ ID 4818.
 XX
 DE Plant; bacterial infection; fungal infection; viral infection; rice;
 KW gene; ds.
 KW
 XX
 OS Oryza sativa.
 XX
 XX WO2003000898-A1.
 PN
 XX
 XX 03-JAN-2003.
 PD
 XX
 XX 22-JUN-2001; 2001WO-IB001105.
 PF
 XX
 XX 22-JUN-2001; 2001WO-IB001105.
 PR
 XX
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA
 XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
 PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
 XX
 XX WPI; 2003-175290/17.
 DR
 XX Identifying at least one gene involved in plant resistance or response to
 PT pathogenic infection for conferring resistance or tolerance to a plant to
 PT bacterial, fungal or viral infection by determining or detecting plant
 PT gene expression.
 XX
 XX Claim 27; SEQ ID NO 4818; 899pp; English.
 PS
 XX The present invention relates to a method (M1) for identifying genes
 CC involved in plant resistance or response to pathogenic infection. M1
 CC comprises identifying a gene whose expression is significantly altered in
 CC the incompatible interaction of plant gene expression relative to
 CC expression of the gene in an uninfected plant, in a mutant plant that
 CC does not express a gene associated with response to pathogenic infection,
 CC or in a corresponding incompatible or compatible interaction. (M1) is
 CC useful for conferring resistance to resistance or tolerance to a plant to
 CC bacterial, fungal or viral infection. The present sequence was used to
 CC illustrate the invention.
 XX
 XX Sequence 2000 BP; 684 A; 323 C; 365 G; 627 T; 0 U; 1 Other;
 SQ

Query Match 77.9%; Score 14.8; DB 8; Length 2000;
 Best Local Similarity 88.9%; Pred. No. 1.3e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AACGGAAGGCGCTTCGG 19
 ||||| ||||| |||||
 Db 949 AACGGAAGGCGCTTCGG 966

RESULT 90
 ACL36116/c
 ID ACL36116 standard; cDNA; 2000 BP.
 XX
 AC ACL36116;
 XX
 XX 02-JUN-2005 (first entry)
 DT
 XX
 DE Rice stress-regulated promoter SEQ ID NO:14679.
 DE
 XX ss; abiotic stress tolerance; transgenic plant; plant; cereal;
 KW agriculture.
 KW
 XX Oryza sativa.
 OS
 XX WO2003008540-A2.
 PN
 XX
 XX 30-JAN-2003.
 PD
 XX
 XX 21-JUN-2002; 2002WO-US019668.
 PF
 XX

PR 22-JUN-2001; 2001US-0300112P.
 PR 24-AUG-2001; 2001US-0314662P.
 PR 26-SEP-2001; 2001US-0325277P.
 PR 21-NOV-2001; 2001US-0332132P.
 XX
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA
 XX Kreps J Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F,
 PI Moughamer T, Provart N, Ricke D, Zhu T;
 XX
 XX WPI; 2003-248011/24.
 DR
 XX
 XX New stress-responsive nucleic acid, useful for altering the
 PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
 PT stress, salt stress or osmotic stress.
 PT
 XX
 XX Claim 48; SEQ ID NO 14679; 89pp; English.
 PS
 XX The invention relates to novel abiotic stress responsive polynucleotides
 CC and polypeptides. Also disclosed are vectors, expression cassettes, host
 CC cells, and plants containing such polynucleotides. Also disclosed are
 CC methods for using the polynucleotides and polypeptides to alter the
 CC responsiveness of a plant to abiotic stress. The invention is useful in
 CC agriculture. The nucleic acid is useful for determining whether a test
 CC plant has been exposed to an abiotic stress condition. It is also useful
 CC for selecting an agent that alters abiotic stress regulated
 CC polynucleotide expression in a plant cell, and to identify a homolog or
 CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
 CC molecule and the polypeptide encoded by it are useful in altering the
 CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
 CC stress, osmotic stress or any of their combinations. The present sequence
 CC is used in the exemplification of the invention
 XX
 XX Sequence 2000 BP; 626 A; 426 C; 367 G; 581 T; 0 U; 0 Other;
 SQ

Query Match 77.9%; Score 14.8; DB 11; Length 2000;
 Best Local Similarity 88.9%; Pred. No. 1.3e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTCG 18
 ||||| ||||| |||||
 Db 1299 GAACGGAAGGCGCTTCG 1282

RESULT 91
 ABL14648
 ID ABL14648 standard; cDNA; 7564 BP.
 XX
 AC ABL14648;
 XX
 XX 26-MAR-2002 (first entry)
 DT
 XX
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 38426.
 XX
 XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.
 KW
 XX Drosophila melanogaster.
 OS
 XX WO200171042-A2.
 PN
 XX
 XX 27-SEP-2001.
 PD
 XX
 XX 23-MAR-2001; 2001WO-US009231.
 PF
 XX
 XX 23-MAR-2000; 2000US-0191637P.
 PR
 XX 11-JUL-2000; 2000US-00614150.
 XX
 XX (PEKE) PE CORP NY.
 PA
 XX Venter JC, Adams M, Li PWD, Myers EW;
 PI
 XX WPI; 2001-656860/75.
 DR

DR P-PSDB; ABB70545.

PT New isolated nucleic acid detection reagent for detecting 1000 or more

PT genes from Drosophila and for elucidating cell signaling and cell-cell

PT interactions.

XX

XX Claim 1; SEQ ID NO 38426; 2lpp + Sequence Listing; English.

PS

CC The invention relates to an isolated nucleic acid detection reagent

CC capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and

CC cell-cell interactions in higher eukaryotes for the development of

CC insecticides, therapeutics and pharmaceutical drugs. The invention

CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-

CC ABB72072). The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX

XX Sequence 7564 BP; 2230 A; 1694 C; 1619 G; 2021 T; 0 U; 0 Other;

XX

Query Match 77.9%; Score 14.8; DB 4; Length 7564;

Best Local Similarity 88.9%; Pred. No. 1.5e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AACGGAAGGCTTTCGG 19

Db 4458 AACGGAAGGCTTTCGG 4475

RESULT 92

AAS57142

ID AAS57142 standard; DNA; 7564 BP.

XX

AC AAS57142;

XX

DT 16-JAN-2002 (first entry)

XX

DE DNA encoding Drosophila G-protein coupled receptor, GPCR #36.

XX

XX Drosophila; G-protein coupled receptor; GPCR; insecticide; diagnostic;

KW mutation detection; ds.

KW Drosophila melanogaster.

OS

XX

XX WO200170980-A2.

PN

XX

XX 27-SEP-2001.

PD

XX

XX 23-MAR-2001; 2001WO-US009341.

PF

XX

XX 23-MAR-2000; 2000US-0191638P.

PR

XX

XX 18-JUL-2000; 2000US-00618893.

PR

XX

XX (PEKE) PE CORP NY.

PA

XX

XX Cravchik A;

PI

XX

XX WPI; 2001-616405/71.

DR

XX

XX P-PSDB; AAU38958.

DR

XX

XX Sixty six Drosophila Melanogaster G-protein coupled receptors (GPCR),

PT useful in the treatment and diagnosis of GPCR-related conditions and for

PT identifying GPCR modulators for use as insecticides.

PT

XX

XX Claim 4; Page 182-184; 392pp; English.

PS

XX

XX The invention relates to sixty six novel isolated Drosophila melanogaster

CC G-protein coupled receptors (GPCR). The GPCR proteins and nucleic acids

CC are useful in the treatment and diagnosis of GPCR-related conditions. The

CC GPCR proteins and nucleic acids are also useful for identifying

CC modulators of GPCR proteins for use as insecticides. The nucleic acid can

CC also be used to detect mutations in GPCR genes and gene expression

CC

CC products such as mRNA. AAS57072-AAS57203 represent D. melanogaster G-

CC coupled protein receptor genomic and coding sequences of the invention

XX

XX Sequence 7564 BP; 2230 A; 1694 C; 1619 G; 2021 T; 0 U; 0 Other;

XX

Query Match 77.9%; Score 14.8; DB 4; Length 7564;

Best Local Similarity 88.9%; Pred. No. 1.5e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AACGGAAGGCTTTCGG 19

Db 4458 AACGGAAGGCTTTCGG 4475

RESULT 93

ADC35854

ID ADC35854 standard; DNA; 7564 BP.

XX

AC ADC35854;

XX

XX 18-DEC-2003 (first entry)

DT

XX

XX Drosophila G protein coupled receptor genomic DNA seq id 36.

DE

XX

XX G-protein coupled receptor; GPCR; insecticide; drug screening;

KW insecticide screening; insecticidal activity; insecticidal tolerance;

KW fruit fly; gene; ds.

KW

XX

XX Drosophila melanogaster.

OS

XX

XX US2003092124-A1.

PN

XX

XX 15-MAY-2003.

PD

XX

XX 15-OCT-2002; 2002US-00270333.

PF

XX

XX 03-DEC-1999; 99US-0168677P.

PR

XX

XX 12-JAN-2000; 2000US-0175691P.

PR

XX

XX 23-MAR-2000; 2000US-0191638P.

PR

XX

XX 18-JUL-2000; 2000US-00618893.

PR

XX

XX (APPL-) APPLERA CORP.

PA

XX

XX Cravchik A;

PI

XX

XX WPI; 2003-765480/72.

DR

XX

XX P-PSDB; ADC35856.

DR

XX

XX New isolated G-protein coupled receptor useful for identifying modulators

PT as potential insecticides, to determine the biological activity of the

PT protein and for identifying compounds that modulate receptor activity.

PT

XX

XX Claim 4; SEQ ID NO 106; 130pp; English.

PS

XX

XX The invention describes an isolated protein (I) consisting or comprising

CC an amino acid sequence selected from fully defined 66 G-protein coupled

CC receptor amino acid sequences (S1), as given in the specification, an

CC allelic variant of (S1), an orthologue of (S1) or fragment of (S1). (I)

CC is useful for identifying an agent that binds to (I) which comprises

CC contacting the protein with an agent and assaying the contacted mixture

CC to determine whether a complex is formed with the agent bound to the

CC protein. (I) is useful for identifying modulators as potential

CC insecticides, to determine the biological activity of the protein (a

CC panel of multiple proteins for high-throughput screening), as targets for

CC identifying agents for use in human drugs and for identifying compounds

CC that modulate receptor activity. An antibody (II) that selectively binds

CC to (I) is useful for assessing normal and aberrant subcellular

CC localisation of cells and monitoring a treatment modality. A nucleic acid

CC (III) encoding (I) is useful for drug/insecticide screening to identify

CC compounds that modulate G-protein coupled receptor (GPCR) nucleic acid

CC expression, diagnostic assays for qualitative changes in GPCR nucleic

CC acid that lead to insecticidal activity/tolerance, to detect mutations in

CC GPCR genes and gene expression products such as mRNA, and as

CC hybridisation probes for determining the presence, level, form and
CC distribution of nucleic acid expression. A host cell comprising a vector
CC containing (III) is useful for conducting cell-based assays involving the
CC GPCR protein or its fragments, and identifying GPCR protein mutants. This
CC sequence encodes a fruit fly G-protein coupled receptor (GPCR).

XX
SQ Sequence 7564 BP; 2230 A; 1694 C; 1619 G; 2021 T; 0 U; 0 Other;

Query Match 77.9%; Score 14.8; DB 10; Length 7564;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AACGGAAGGCCTTCGG 19
||||| |
Db 4458 AACGGAATGCTTCGG 4475

RESULT 94
AAK64938
ID AAK64938 standard; DNA; 19183 BP.

XX AC AAK64938;

DT 06-NOV-2001 (first entry)

XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:19750.

DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; db.

XX Homo sapiens.

XX WC200157182-A2.

XX 09-AUG-2001.

PF 17-JAN-2001; 2001WO-US0001354.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 02-FEB-2000; 2000US-0184664P.

PR 16-MAR-2000; 2000US-0186350P.

PR 17-MAR-2000; 2000US-0189874P.

PR 18-APR-2000; 2000US-0190076P.

PR 19-MAY-2000; 2000US-0198123P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.

PR 18-AUG-2000; 2000US-0226279P.

PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226868P.

PR 23-AUG-2000; 2000US-0227182P.

PR 23-AUG-2000; 2000US-0227009P.

PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234224P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 27-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
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PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
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PR 20-OCT-2000; 2000US-0241785P.
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PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
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PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
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PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
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PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
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PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.

PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249219P.
PR 17-NOV-2000; 2000US-0249220P.
PR 17-NOV-2000; 2000US-0249221P.
PR 17-NOV-2000; 2000US-0249222P.
PR 17-NOV-2000; 2000US-0249223P.
PR 17-NOV-2000; 2000US-0249224P.
PR 17-NOV-2000; 2000US-0249225P.
PR 17-NOV-2000; 2000US-0249226P.
PR 17-NOV-2000; 2000US-0249227P.
PR 17-NOV-2000; 2000US-0249228P.
PR 17-NOV-2000; 2000US-0249229P.
PR 17-NOV-2000; 2000US-0249230P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 03-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251858P.
PR 08-DEC-2000; 2000US-0251859P.
PR 08-DEC-2000; 2000US-0251899P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254037P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX Disclosure; SEQ ID NO 19750; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 19183 BP; 5489 A; 3882 C; 4034 G; 5778 T; 0 U; 0 Other;
Query Match 77.9%; Score 14.8; DB 4; Length 19183;
Best Local Similarity 88.9%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GACGGAAGCCCTTCG 18
Db 3573 GTACGGAAGCCCTTTG 3590
RESULT 95
AAL36434
ID AAL36434 standard; DNA; 19183 BP.
XX

AC AAL36434;
XX
DT 08-JAN-2002 (first entry)
XX
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2799.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer;
KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein;
KW musculoskeletal system; ds.
XX
OS Homo sapiens.
XX
PN WO200155367-A1.
XX
PD 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001338.
XX
XX 31-JAN-2000; 2000US-0179065P.
XX 04-FEB-2000; 2000US-0180628P.
XX 24-FEB-2000; 2000US-0184664P.
XX 02-MAR-2000; 2000US-0186350P.
XX 16-MAR-2000; 2000US-0189874P.
XX 17-MAR-2000; 2000US-0190076P.
XX 18-APR-2000; 2000US-0198123P.
XX 19-MAY-2000; 2000US-0205515P.
XX 07-JUN-2000; 2000US-0209467P.
XX 28-JUN-2000; 2000US-0214886P.
XX 30-JUN-2000; 2000US-0215135P.
XX 07-JUL-2000; 2000US-0216647P.
XX 07-JUL-2000; 2000US-0216880P.
XX 11-JUL-2000; 2000US-0217487P.
XX 11-JUL-2000; 2000US-0217496P.
XX 14-JUL-2000; 2000US-0218290P.
XX 26-JUL-2000; 2000US-0220964P.
XX 14-AUG-2000; 2000US-0224518P.
XX 14-AUG-2000; 2000US-0224519P.
XX 14-AUG-2000; 2000US-0225213P.
XX 14-AUG-2000; 2000US-0225214P.
XX 14-AUG-2000; 2000US-0225266P.
XX 14-AUG-2000; 2000US-0225267P.
XX 14-AUG-2000; 2000US-0225268P.
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XX 14-AUG-2000; 2000US-0225477P.
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XX 18-AUG-2000; 2000US-0226279P.
XX 22-AUG-2000; 2000US-0226681P.
XX 22-AUG-2000; 2000US-0227182P.
XX 23-AUG-2000; 2000US-0227009P.
XX 30-AUG-2000; 2000US-0228924P.
XX 01-SEP-2000; 2000US-0229287P.
XX 01-SEP-2000; 2000US-0229343P.
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XX 05-SEP-2000; 2000US-0229509P.
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XX 06-SEP-2000; 2000US-0230438P.
XX 08-SEP-2000; 2000US-0231422P.
XX 08-SEP-2000; 2000US-0231433P.
XX 08-SEP-2000; 2000US-0231443P.
XX 08-SEP-2000; 2000US-0231413P.
XX 08-SEP-2000; 2000US-0231414P.
XX 08-SEP-2000; 2000US-0232080P.
XX 08-SEP-2000; 2000US-0232081P.
XX 12-SEP-2000; 2000US-0231968P.

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PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0232403P.
PR 14-SEP-2000; 2000US-0232406P.
PR 14-SEP-2000; 2000US-0232423P.
PR 21-SEP-2000; 2000US-0234274P.
PR 21-SEP-2000; 2000US-0234277P.
PR 25-SEP-2000; 2000US-0234957P.
PR 25-SEP-2000; 2000US-0234958P.
PR 25-SEP-2000; 2000US-0234959P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 13-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239335P.
PR 13-OCT-2000; 2000US-0239337P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0241826P.
PR 08-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
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PR 01-DEC-2000; 2000US-0250391P.

PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 06-DEC-2000; 2000US-0256719P.
PR 08-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX PA Rosen CA, Barash SC, Ruben SM;
XX PI WPI; 2001-451937/48.
XX DR
XX PT Isolated polypeptide for treating, preventing and/ or prognosing
XX PT disorders related to the musculoskeletal system including musculoskeletal
XX PS cancers and also for testing and detection e.g. diagnosis.
XX
XX Example 2; SEQ ID NO 2799; 78lpp + Sequence Listing; English.
XX
XX The invention relates to novel genes (AAL34669-AAL37666) and proteins
XX (ABB03087-ABB04109) associated with the musculoskeletal system useful for
XX preventing, treating or ameliorating medical conditions e.g. by protein
XX or gene therapy. The genes are isolated from a range of human tissues
XX disclosed in the specification. The nucleic acids, proteins, antibodies
XX and (ant)agonists are useful in the diagnosis, treatment and prevention
XX of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the
XX adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,
XX lung, or urogenital; (b) immune disorders e.g. Addison's disease,
XX allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
XX diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
XX arthritis and ulcerative colitis; (c) cardiovascular disorders such as
XX myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g.
XX cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,
XX bacterial, fungal and parasitic infections. Note: The sequence data for
XX this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 19183 BP; 5489 A; 3882 C; 4034 G; 5778 T; 0 U; 0 Other;
Query Match 77.9%; Score 14.8; DB 4; Length 19183;
Best Local Similarity 88.9%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GAACGGGAAAGGCTTTCG 18
Db 3573 GTACGGGAAAGGCTTTTG 3590
RESULT 96
ABX59422
ID ABX59422 standard; cDNA; 19183 BP.
XX
XX AC ABX59422;
XX
XX 26-FEB-2003 (first entry)
XX
XX cDNA encoding novel human musculoskeletal system antigen #1766.
XX
XX Gene; ss; musculoskeletal system antigen; cancer; metastasis;
XX re-vascularisation; thrombosis; arteriosclerosis; mineral content;
XX cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;
XX post-operative tissue repair; limb regeneration; neuronal growth;
XX neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
XX AIDS-related complex; chondrocyte growth; bone regeneration;
XX periodontal regeneration; tissue transport; bone graft; skin aging;
XX keratinocyte growth; hair loss; melanocyte growth; cell proliferation;
XX cell growth; organ transplant; cell differentiation; body height; weight;
```

KW hair colour; eye colour; skin; percentage of adipose tissue;
KW pigmentation; cosmetic surgery; metabolism; biorhythm; cardiac rhythm;
KW depression; tendency for violence; pain; reproductive capability;
KW hormone level; endocrine level; appetite; libido; memory; stress;
KW storage capability; fat content; lipid content; protein content;
KW carbohydrate content; vitamin content; cofactor content;
KW nutritional component.

XX Homo sapiens.

XX US2002147140-A1.

XX 10-OCT-2002.

XX 17-JAN-2001; 2001US-00764877.

XX 31-JAN-2000; 2000US-0179065P.

XX 04-FEB-2000; 2000US-0180628P.

XX 28-JUN-2000; 2000US-0214886P.

XX 07-JUL-2000; 2000US-0216647P.

XX 07-JUL-2000; 2000US-0216880P.

XX 11-JUL-2000; 2000US-0217487P.

XX 11-JUL-2000; 2000US-0217496P.

XX 26-JUL-2000; 2000US-0220963P.

XX 26-JUL-2000; 2000US-0220964P.

XX 14-AUG-2000; 2000US-0224518P.

XX 14-AUG-2000; 2000US-0224519P.

XX 14-AUG-2000; 2000US-0225267P.

XX 14-AUG-2000; 2000US-0225268P.

XX 14-AUG-2000; 2000US-0225270P.

XX 14-AUG-2000; 2000US-0225447P.

XX 14-AUG-2000; 2000US-0225477P.

XX 14-AUG-2000; 2000US-0225757P.

XX 22-AUG-2000; 2000US-0225758P.

XX 30-AUG-2000; 2000US-0226868P.

XX 01-SEP-2000; 2000US-0228924P.

XX 01-SEP-2000; 2000US-0229287P.

XX 01-SEP-2000; 2000US-0229343P.

XX 01-SEP-2000; 2000US-0229344P.

XX 01-SEP-2000; 2000US-0229345P.

XX 05-SEP-2000; 2000US-0229509P.

XX 05-SEP-2000; 2000US-0229513P.

XX 08-SEP-2000; 2000US-0231413P.

XX 21-SEP-2000; 2000US-0234223P.

XX 21-SEP-2000; 2000US-0234274P.

XX 25-SEP-2000; 2000US-0234997P.

XX 27-SEP-2000; 2000US-0235834P.

XX 29-SEP-2000; 2000US-0236327P.

XX 29-SEP-2000; 2000US-0236367P.

XX 29-SEP-2000; 2000US-0236368P.

XX 29-SEP-2000; 2000US-0236369P.

XX 29-SEP-2000; 2000US-0236370P.

XX 02-OCT-2000; 2000US-0236802P.

XX 02-OCT-2000; 2000US-0237037P.

XX 02-OCT-2000; 2000US-0237038P.

XX 02-OCT-2000; 2000US-0237039P.

XX 02-OCT-2000; 2000US-0237040P.

XX 13-OCT-2000; 2000US-0239935P.

XX 20-OCT-2000; 2000US-0240960P.

XX 20-OCT-2000; 2000US-0241785P.

XX 20-OCT-2000; 2000US-0241809P.

XX 01-NOV-2000; 2000US-0244617P.

XX 17-NOV-2000; 2000US-0249299P.

XX 08-DEC-2000; 2000US-0251856P.

XX 08-DEC-2000; 2000US-0251868P.

XX 08-DEC-2000; 2000US-0251869P.

XX (ROSE/) ROSEN C A.

PA (RUBE/) RUBEN S M.

PA (BARA/) BARASH S C.

XX Rosen CA, Ruben SM, Barash SC;

XX

DR WPI; 2003-128199/12.

XX Isolated nucleic acid molecules encoding musculoskeletal system

PT associated polypeptides, useful for detecting disorders, e.g. cancer.

XX Disclosure; SEQ ID NO 2799; 321pp; English.

XX The invention describes an isolated nucleic acid molecule comprising a

CC sequence encoding musculoskeletal system associated polypeptides useful

CC for detecting disorders, e.g., cancer or cancer metastases, in animals or

CC humans. The nucleic acid stimulates re-vascularisation of ischaemic

CC tissues associated with conditions such as thrombosis, arteriosclerosis,

CC and other cardiovascular conditions; treats wounds due to injuries,

CC burns, post-operative tissue repair, and ulcers; stimulates angiogenesis

CC and limb regeneration; stimulates neuronal growth; can treat and prevent

CC neuronal damage occurring in certain disorders or neurodegenerative

CC conditions, such as, Alzheimer's disease, Parkinson's disease, and AIDS-

CC related complex; stimulates chondrocyte growth, thus they can be used to

CC enhance bone and periodontal regeneration and aid in tissue transports or

CC bone grafts; prevents skin aging due to sunburn by stimulating

CC keratinocyte growth; prevents hair loss, since FGF family members

CC activate hair-forming cells and promotes melanocyte growth; stimulates

CC growth and differentiation of hematopoietic cells and bone marrow cells

CC when used in combination with other cytokines; maintains organs before

CC transplantation or for supporting cell culture of primary tissues;

CC induces tissue of mesodermal origin to differentiate in early embryos;

CC increases or decreases the differentiation or proliferation of embryonic

CC stem cells, besides, hematopoietic lineage; modulates mammalian

CC characteristics, such as, body height, weight, hair colour, eye colour,

CC skin, percentage of adipose tissue, pigmentation, size, and shape (e.g.,

CC cosmetic surgery); modulates mammalian metabolism; changes mammal's metal

CC state or physical state by influencing biorhythms, cardiac rhythms,

CC depression, tendency for violence, tolerance for pain, reproductive

CC capabilities, hormonal or endocrine levels, appetite, libido, memory, or

CC stress; increases or decreases storage capabilities, fat content, lipid,

CC protein, carbohydrate, vitamins, minerals, cofactors or other nutritional

CC components. This sequence encodes a novel human musculoskeletal system

CC antigen. Note: The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly

CC from the US patent office at

CC ftp.seqdata.uspto.gov/sequence.html?DocID=20020147140

XX SQ Sequence 19183 BP; 5489 A; 3882 C; 4034 G; 5778 T; 0 U; 0 Other;

Query Match 77.9%; Score 14.8; DB 8; Length 19183;

Best Local Similarity 88.9%; Pred. No. 1.6e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGGCTTTCG 18

Db 3573 GTACGGAAAGGCTTTCG 3590

RESULT 97

ADJ30172

ID ADJ30172 standard; DNA; 19183 BP.

XX ADJ30172;

XX 20-MAY-2004 (first entry)

DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2799.

XX musculoskeletal system; cytostatic; osteopathic; cancer; osteoporosis;

XX gene therapy; vaccine; human; ds.

OS Homo sapiens.

XX US2004009488-A1.

XX 15-JAN-2004.

XX 13-SEP-2002; 2002US-00242515.

XX 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
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 PR 17-NOV-2000; 2000US-0249211P.
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 PR 17-NOV-2000; 2000US-0249214P.
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 PR 17-NOV-2000; 2000US-0249297P.
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 PR 17-NOV-2000; 2000US-0249300P.
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 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 11-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 PR 17-JAN-2001; 2001US-00764877.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Ruben SM, Barash SC;
 PI WPI; 2004-090458/09.
 XX New nucleic acid molecule, useful for preparing a medicament for

PT preventing, treating or ameliorating a medical condition e.g., cancer of
PT musculoskeletal tissues or osteoporosis.
XX Disclosure; SEQ ID NO 2799; 289pp; English.
PS
XX
CC The invention relates to a novel isolated musculoskeletal system-
CC associated nucleic acid molecule. The nucleic acid of the invention
CC demonstrates cytostatic and osteopathic activities and may be useful for
CC preparing a medicament for preventing, treating or ameliorating a medical
CC condition such as cancer of the musculoskeletal tissues or osteoporosis,
CC possibly via gene therapy or vaccine production. The current sequence is
CC that of the human musculoskeletal system-associated genomic DNA of the
CC invention. The current sequence is not shown within the specification per
CC se but is available on the USPTO web-site
CC <http://seqdata.uspto.gov/sequence.html?DocID=20040009488>.
XX
SQ Sequence 19183 BP; 5489 A; 3882 C; 4034 G; 5778 T; 0 U; 0 Other;

Query Match 77.9%; Score 14.8; DB 12; Length 19183;
Best Local Similarity 88.9%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCTTCG 18
Db 3573 GTACGGAAGCCTTTG 3590

RESULT 98
AAK75071/c
ID AAK75071 standard; DNA; 30904 BP.
XX AC
XX AAK75071;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29883.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PP 17-JAN-2001; 2001WO-US001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
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PR 28-JUN-2000; 2000US-0214886P.
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PR 11-JUL-2000; 2000US-0217487P.
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29-SEP-2000; 2000US-0236327P.
29-SEP-2000; 2000US-0236367P.
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 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Barash SC, Ruben SM;
 XX MPI; 2001-451930/48.
 DR New cardiovascular system related polynucleotides and polypeptides,
 XX useful for diagnosing, treating and/or preventing disorders of the
 PT cardiovascular system.
 XX
 PS Claim 1; SEQ ID NO 2314; 674pp; English.
 SS Sequences AAS35741-AAS35942 represent genomic DNA molecules, which encode
 CC the cardiovascular system antigen polypeptides of the invention.
 CC Cardiovascular system antigens and their associated polynucleotides are
 CC useful in the diagnosis, treatment and prevention of various types of
 CC disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs,
 CC chickens or sheep. A pathological condition can be determined by
 CC detecting the presence or absence of a mutation in a cardiovascular
 CC system antigen polynucleotide. The treatable disorders include autoimmune
 CC diseases such as rheumatoid arthritis, hyperproliferative disorders such
 CC as neoplasms of the breast or liver, cardiovascular disorders such as
 CC cardiac arrest, cerebrovascular disorders such as cerebral ischaemia,
 CC nervous system disorders such as Alzheimer's disease, infections caused
 CC by bacteria, viruses and fungi, ocular disorders such as corneal
 CC infection, endocrine disorders such as premature labour and infertility,
 CC gastrointestinal disorders such as Crohn's disease, renal disorders such
 CC as glomerulonephritis and respiratory disorders such as asthma and
 CC pleurisy. The polypeptides can also be used to aid wound healing, to
 CC prevent skin aging due to sunburn, to maintain organs before
 CC transplantation, to regenerate tissues and in chemotaxis. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

Query Match 77.9%; Score 14.8; DB 4; Length 32249;
 Best Local Similarity 88.9%; Pred. No. 1.7e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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 Db 13291 AAAGGAAGGCCATTTCGG 13274
 RESULT 100

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PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
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PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
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PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PR 17-JAN-2001; 2001US-00764869.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Barash SC;
XX
XX WPI; 2003-743766/70.
XX
XX New cardiovascular system related polynucleotides and polypeptides,
PT useful for preventing, treating, or ameliorating a medical condition,
FT such as cancer of cardiovascular tissues and cancer metastases.
PT
XX
XX Claim 1; SEQ ID NO 2314; 262pp; English.
XX
XX The invention relates to human cardiovascular system related polypeptides
CC and the polynucleotides encoding them. The polypeptides, polynucleotides
CC and antibodies to the polypeptides are useful for diagnosing a
CC pathological condition or a susceptibility to a pathological condition,
CC for preventing, treating, or ameliorating a medical condition, such as,
CC cancer of cardiovascular system tissues, proliferative disorders, foetal
CC and developmental abnormalities, haematopoietic disorders, diseases of
CC the immune system, AIDS, autoimmune diseases (e.g., rheumatoid
CC arthritis), inflammation, allergies, neurological disorders (e.g.,
CC Alzheimer's disease, Parkinson's disease), cognitive disorders,
CC schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis,
CC diabetes, atherosclerosis, cardiovascular disorders, angiogenic
CC disorders, kidney disorders, gastrointestinal disorders, pregnancy-
CC related disorders, endocrine disorders and infections. The nucleic acids
CC are also useful for chromosome identification, radiation hybrid mapping
CC or long-range restriction mapping. The polypeptides and polynucleotides
CC may also be used as food additives or preservatives to increase or
CC decrease storage capabilities, fat content or other nutritional
CC components. This sequence represents human cardiovascular system related
CC genomic DNA of the invention.
XX
SQ Sequence 32249 BP; 8876 A; 6723 C; 7066 G; 9584 T; 0 U; 0 Other;

Query Match 77.9%; Score 14.8; DB 10; Length 32249;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AACGGAAGGCCTTCGG 19
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Job time : 230.994 secs

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 02:24:46 ; Search time 1270.71 Seconds
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Title: US-10-665-708-24

Perfect score: 19
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 300 summaries

Database :

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6: gb_est7:*

7: gb_est8:*

8: gb_est9:*

9: gb_est10:*

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12: gb_est13:*

13: gb_est14:*

14: gb_est15:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	17.4	91.6	828	7	BF240426 BF240426
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5	16.4	86.3	412	3	BP863510 BP863510
C 6	16.4	86.3	603	3	BU398878 BU398878
8	16.4	86.3	614	14	LBAP055F03
9	16.4	86.3	625	3	BU306528 BU306528
10	16.4	86.3	643	3	BU283959 BU283959
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14	16.4	86.3	847	3	BU409605 BU409605
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C 16	16.4	86.3	910	9	DN561788 DN561788
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	96	15.8	83.2	15.8	83.2	C 169	15.8	83.2	735	3	BU449350	BU449350 603765523
	97	15.8	83.2	15.8	83.2	C 170	15.8	83.2	750	2	CG916273	CG916273 602814995
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	112	15.8	83.2	15.8	83.2	C 185	15.8	83.2	833	10	DR735212	DR735212 FGA08088
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	134	15.8	83.2	15.8	83.2	C 207	15.8	83.2	954	7	BE727405	BE727405 601563071
	135	15.8	83.2	15.8	83.2	C 208	15.8	83.2	954	14	DU777015	DU777015 ASXB1433
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	137	15.8	83.2	15.8	83.2	C 210	15.8	83.2	963	13	DU004026	DU004026 286921>To
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	140	15.8	83.2	15.8	83.2	C 213	15.8	83.2	978	12	CC222241	CC222241 CH261-71C
	141	15.8	83.2	15.8	83.2	C 214	15.8	83.2	988	12	CL114538	CL114538 ISB1-60F2
	142	15.8	83.2	15.8	83.2	C 215	15.8	83.2	1003	4	BY708841	BY708841 BY708841
	143	15.8	83.2	15.8	83.2	C 216	15.8	83.2	1006	9	DR139593	DR139593 49338969
	144	15.8	83.2	15.8	83.2	C 217	15.8	83.2	1039	7	BE036789	BE036789 MF05G07 M
	145	15.8	83.2	15.8	83.2	C 218	15.8	83.2	1040	2	BI555200	BI555200 603236145
	146	15.8	83.2	15.8	83.2	C 219	15.8	83.2	1051	12	CL083385	CL083385 ISB1-1M19
	147	15.8	83.2	15.8	83.2	C 220	15.8	83.2	1120	2	BM460938	BM460938 AGENCYCOURT
	148	15.8	83.2	15.8	83.2	C 221	15.8	83.2	1120	14	CNS06T85	AL414219 T3 end of
	149	15.8	83.2	15.8	83.2	C 222	15.8	83.2	1185	9	DN705397	DN705397 CLJ759-C02
	150	15.8	83.2	15.8	83.2	C 223	15.8	83.2	1198	12	CC260948	CC260948 CH261-166
	151	15.8	83.2	15.8	83.2	C 224	15.8	83.2	1205	11	BZ552660	BZ552660 pacs1-60
	152	15.8	83.2	15.8	83.2	C 225	15.8	83.2	1231	9	DN694833	DN694833 CXG96-E03
	153	15.8	83.2	15.8	83.2	C 226	15.8	83.2	1242	11	BZ559026	BZ559026 pacs2-164
	154	15.8	83.2	15.8	83.2	C 227	15.8	83.2	1258	9	DN736299	DN736299 CNB86-B03
	155	15.8	83.2	15.8	83.2	C 228	15.8	83.2	1485	14	AV402881	AV402881 Mus muscu
	156	15.8	83.2	15.8	83.2	C 229	15.8	83.2	1766	6	AK008952	AK008952 Mus muscu
	157	15.8	83.2	15.8	83.2	C 230	15.8	83.2	1779	6	AK169602	AK169602 Mus muscu
	158	15.8	83.2	15.8	83.2	C 231	15.8	83.2	1780	6	BC057175	BC057175 Mus muscu
	159	15.8	83.2	15.8	83.2	C 232	15.8	83.2	1848	6	AK011967	AK011967 Mus muscu
	160	15.8	83.2	15.8	83.2	C 233	15.8	83.2	2448	6	AK032901	AK032901 Mus muscu
	161	15.8	83.2	15.8	83.2	C 234	15.8	83.2	2732	6	AK149909	AK149909 Mus muscu
	162	15.8	83.2	15.8	83.2	C 235	15.8	83.2	2732	6	AK149925	AK149925 Mus muscu
	163	15.8	83.2	15.8	83.2	C 236	15.8	83.2	2732	6	AK150180	AK150180 Mus muscu
	164	15.8	83.2	15.8	83.2	C 237	15.8	83.2	2898	6	AK033858	AK033858 Mus muscu
	165	15.8	83.2	15.8	83.2	C 238	15.8	83.2	2929	6	AK019034	AK019034 Mus muscu

239	15.8	83.2	2933	6	AK154308	Mus muscu	AK154308 Mus muscu
240	15.8	83.2	4089	6	AK132171	Mus muscu	AK132171 Mus muscu
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242	15.4	81.1	203	12	CG587905	OST238028	CG587905 OST238028
C 243	15.4	81.1	204	14	DX181091	OR_Aba004	DX181091 OR_Aba004
244	15.4	81.1	254	12	CE046649	tigr-gss-	CE046649 tigr-gss-
C 245	15.4	81.1	286	4	BX610825	BX610825	BX610825 BX610825
C 246	15.4	81.1	296	7	BB526226	BB526226	BB526226 BB526226
C 247	15.4	81.1	337	7	BE624671	mx25a09.Y	BE624671 mx25a09.Y
248	15.4	81.1	386	8	CO741279	Hd mx23.1	CO741279 Hd mx23.1
249	15.4	81.1	396	11	BH250941	SALK_0107	BH250941 SALK_0107
C 250	15.4	81.1	412	13	CW625344	Gsal_17_U	CW625344 Gsal_17_U
C 251	15.4	81.1	424	11	AQ468227	HS_5211_B	AQ468227 HS_5211_B
252	15.4	81.1	456	4	BY364527	BY364527	BY364527 BY364527
253	15.4	81.1	455	4	CB740963	AMGNNUC:M	CB740963 AMGNNUC:M
C 254	15.4	81.1	465	8	CO330281	AK	CO330281 AK
255	15.4	81.1	466	13	CW472625	feb0001f2	CW472625 feb0001f2
C 256	15.4	81.1	488	3	BP810866	BP810866	BP810866 BP810866
C 257	15.4	81.1	492	3	BP752980	BP752980	BP752980 BP752980
258	15.4	81.1	514	3	BU142518	603135523	BU142518 603135523
C 259	15.4	81.1	515	4	BX610657	BX610657	BX610657 BX610657
260	15.4	81.1	516	11	AZ302696	GSSBTru163	AZ302696 GSSBTru163
C 261	15.4	81.1	520	7	AW098292	sd37908.Y	AW098292 sd37908.Y
C 262	15.4	81.1	521	12	CE743051	tigr-gss-	CE743051 tigr-gss-
C 263	15.4	81.1	530	7	BE598128	P11_66_A1	BE598128 P11_66_A1
C 264	15.4	81.1	543	13	CZ426316	1022019_R	CZ426316 1022019_R
C 265	15.4	81.1	548	4	CB826166	rw22a03.Y	CB826166 rw22a03.Y
C 266	15.4	81.1	559	14	DX193129	OR_Aba005	DX193129 OR_Aba005
267	15.4	81.1	579	2	BJ929156	BJ929156	BJ929156 BJ929156
268	15.4	81.1	585	7	BE571264	601330701	BE571264 601330701
269	15.4	81.1	597	11	BH764015	ENBAC321B	BH764015 ENBAC321B
C 270	15.4	81.1	600	13	CZ457136	MCF740F17	CZ457136 MCF740F17
C 271	15.4	81.1	601	12	CG921504	MBEAT94TF	CG921504 MBEAT94TF
272	15.4	81.1	602	5	CK618516	mk13b01.Y	CK618516 mk13b01.Y
273	15.4	81.1	604	11	AZ973824	2N0248L12	AZ973824 2N0248L12
274	15.4	81.1	609	13	CW231906	CW231906	CW231906 CW231906
275	15.4	81.1	614	8	CO429466	UI-M-HW0-	CO429466 UI-M-HW0-
C 276	15.4	81.1	616	8	CK247015	1298851_N	CK247015 1298851_N
C 277	15.4	81.1	619	3	BQ410746	GA_Ed003	BQ410746 GA_Ed003
C 278	15.4	81.1	621	1	AL874369	AL874369	AL874369 AL874369
279	15.4	81.1	625	11	BH066273	ENBAC10P1	BH066273 ENBAC10P1
C 280	15.4	81.1	627	11	AZ378438	IM0133007	AZ378438 IM0133007
C 281	15.4	81.1	631	13	CW399365	fsbb001f0	CW399365 fsbb001f0
282	15.4	81.1	635	12	CE264643	tigr-gss-	CE264643 tigr-gss-
C 283	15.4	81.1	638	7	BB658080	BB658080	BB658080 BB658080
C 284	15.4	81.1	647	8	CE531123	CR531123	CE531123 CR531123
285	15.4	81.1	650	7	BB656927	BB656927	BB656927 BB656927
C 286	15.4	81.1	652	12	CC320357	TAM32-33H	CC320357 TAM32-33H
C 287	15.4	81.1	654	14	DX325904	OR_Aba024	DX325904 OR_Aba024
C 288	15.4	81.1	659	13	DU303654	109844830	DU303654 109844830
C 289	15.4	81.1	669	14	DX054457	KBxB058K2	DX054457 KBxB058K2
290	15.4	81.1	678	11	BH391120	AG-ND-163	BH391120 AG-ND-163
C 291	15.4	81.1	682	1	AL697364	AL697364	AL697364 AL697364
C 292	15.4	81.1	698	4	CB426182	601338_MA	CB426182 601338_MA
C 293	15.4	81.1	707	4	BX609637	BX609637	BX609637 BX609637
C 294	15.4	81.1	711	14	DX237688	OR_Aba012	DX237688 OR_Aba012
C 295	15.4	81.1	726	8	CK312674	JGI_XZT86	CK312674 JGI_XZT86
296	15.4	81.1	735	5	CF882404	tric086xm	CF882404 tric086xm
C 297	15.4	81.1	738	8	CO025053	EST803437	CO025053 EST803437
298	15.4	81.1	739	9	CK447938	JGI_XZG25	CK447938 JGI_XZG25
299	15.4	81.1	745	8	CO507999	Hd mx24_0	CO507999 Hd mx24_0
C 300	15.4	81.1	747	11	BH045554	RFCI-24-3	BH045554 RFCI-24-3

ALIGNMENTS

RESULT 1
 LOCUS BY275654 452 bp mRNA linear EST 11-DEC-2002
 DEFINITION BY275654 RIKEN full-length enriched, visual cortex Mus musculus
 CDNA clone K430314L24 5', mRNA sequence.
 ACCESSION BY275654

VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS

BY275654.1 GI:26465991
 EST.
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
 1 (bases 1 to 452)
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojohori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawai, H., Kawasawa, Y., Kedzierzki, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sadelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Veratara, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wyszewski, B., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Azawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 12466851
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Tissues were provided by Michela Fagiolini and Takao K. Hensch (Laboratory for Neuronal Circuit Development Brain Science Institute RIKEN 2-1 Hirose, Wako-shi, Saitama 351-0198 Japan) whose assistance we gratefully acknowledge. Please visit our web site

TITLE
 JOURNAL
 PUBMED
 COMMENT

(http://genome.gsc.riken.go.jp) for further details.									
FEATURES	source								
	Location/Qualifiers								
1..452									
/organism="Mus musculus"									
/mol_type="mRNA"									
/strain="C57BL/6J"									
/db_xref="taxon:10090"									
/clone="K430314L24"									
/tissue_type="visual cortex"									
/clone_lib="RIKEN full-length enriched, visual cortex"									
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Query Match									
Best Local Similarity 91.6%; Score 17.4; DB 4; Length 452;									
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY 1 GAACGGAAGGCTTTTCGG 19									
Db 255 GAACGGGAGGCTTTTCGG 273									
RESULT 2									
LOCUS BF240426 828 bp mRNA linear EST 14-NOV-2000									
DEFINITION 601905978F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133899 5',									
mRNA sequence.									
ACCESSION BF240426									
VERSION BF240426.1 GI:11154350									
KEYWORDS EST.									
SOURCE Homo sapiens (human)									
ORGANISM Homo sapiens									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;									
Hominidae; Homo.									
1 (bases 1 to 828)									
NIH-MGC http://mgc.nci.nih.gov/.									
National Institutes of Health, Mammalian Gene Collection (MGC)									
Unpublished (1999)									
Contact: Robert Strausberg, Ph.D.									
Email: cgapbs-r@mail.nih.gov									
Tissue Procurement: ATCC									
cDNA Library Preparation: CLONETECH Laboratories, Inc.									
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)									
DNA Sequencing by: Incyte Genomics, Inc.									
Clone distribution: MGC clone distribution information can be									
found through the I.M.A.G.E. Consortium/LNL at:									
http://image.llnl.gov									
Plate: LCM1035 row: k column: 20									
High quality sequence stop: 497.									
Location/Qualifiers									
1..828									
/organism="Homo sapiens"									
/mol_type="mRNA"									
/db_xref="taxon:9606"									
/clone="IMAGE:4133899"									
/tissue_type="from chronic myelogenous leukemia"									
/lab_host="DH10B (T1 phage-resistant)"									
/clone_lib="NTH_MGC 54"									
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);									
Site_1: SfiI (ggcgctcgcc); Site_2: SfiI									
(ggccattagggc); Double-stranded cDNA was prepared from									
cell line RNA. 5' and 3' adaptors were used in cloning as									
follows: 5' adaptor sequence: 5'-CAGGCCATTATGGCC-3' and									
3' adaptor sequence:									
5'-ATTCTAGAGCGGCGGCACATG-dT(30)BN-3' (where B = A,									
C, or G and N = A, C, G, or T). Average insert size									
1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained									
inserts by PCR. This library was enriched for full-length									
clones and was constructed by Clontech Laboratories (Palo									
Alto, CA)."									
ORIGIN									
Query Match									
91.6%; Score 17.4; DB 7; Length 828;									

Best Local Similarity 94.7%; Pred. No. 5.8e+02;									
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY 1 GAACGGAAGGCTTTTCGG 19									
Db 708 GAACGGAAGGCTTTTCGG 690									
RESULT 3									
LOCUS CO684942 305 bp mRNA linear EST 26-JUL-2004									
DEFINITION DG11-193n18 DG11-kidney Canis familiaris cDNA 3', mRNA sequence.									
ACCESSION CO684942									
VERSION CO684942.1 GI:50633608									
KEYWORDS EST.									
SOURCE Canis familiaris (dog)									
ORGANISM Canis familiaris									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;									
Canis.									
1 (bases 1 to 305)									
Schlueter, T., Hermanns, J., Weindel, M., Schuette, D., Kranz, H.,									
Henrich, J. and Loebbert, R.									
Dog arrayTAG cDNA clone collection									
Unpublished (2004)									
Contact: Thomas Schlueter									
LION Bioscience AG									
Walhoferstrasse 98, D-69123 Heidelberg, Germany									
Tel: +49 6221 4038 150									
Fax: +49 6221 4038 290									
Email: Thomas.Schlueter@lionbioscience.com.									
Location/Qualifiers									
1..305									
/organism="Canis familiaris"									
/mol_type="mRNA"									
/strain="Beagle"									
/db_xref="taxon:9615"									
/tissue_type="kidney"									
/dev_stage="adult"									
/lab_host="DH10B"									
/clone_lib="DG11-kidney"									
/note="Organ: kidney; Vector: Dog pBluescript LION"									
ORIGIN									
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Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY 2 AACGGAAGGCTTTTCGG 19									
Db 135 AACGCAAGGCTTTTCGG 152									
RESULT 4									
BB241896/c 312 bp mRNA linear EST 06-JUL-2000									
LOCUS BB241896 RIKEN full-length enriched, 3 days neonate thymus Mus									
DEFINITION musculus cDNA A630089H08 3', mRNA sequence.									
ACCESSION BB241896									
VERSION BB241896.1 GI:8934642									
KEYWORDS EST.									
SOURCE Mus musculus (house mouse)									
ORGANISM Mus musculus									
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;									
Sciurognathi; Muridea; Muridae; Murinae; Mus.									
1 (bases 1 to 312)									
Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T.,									
Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,									
Hirozane, T., Iishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,									
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,									
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C.,									
Kusakabe, M., Matsuyama, T., Maki, R., Sano, Y., Nakamura, M., Oda, H.,									

Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamana, K., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTs (Konno, H., et al.)
 Unpublished (2000)
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216

Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/
 Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagasaka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Thermotabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh, M., Kitsuunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
 Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES

Location/Qualifiers
 1. 312
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="A630089H08"
 /tissue_type="thymus"
 /dev_stage="3 days neonate"
 /lab_host="DH10B"
 /clone_lib="RIKEN full-length enriched, 3 days neonate thymus"

/notes="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGATCCAGAGCTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCGAGTTAAATTAATCCCTCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

ORIGIN

Query Match 86.3%; Score 16.4; DB 7; Length 312;
 Best Local Similarity 94.4%; Pred. No. 1.6e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AACCGAAAGGCTTTTCG 19
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 Db 67 AACCGAAAGGCTTTACG 50

RESULT 5
 BP863510

LOCUS BP863510 412 bp mRNA linear EST 17-FEB-2005
 DEFINITION BP863510 RAFL21 Arabidopsis thaliana cDNA clone RAFL21-66-P16 5', mRNA sequence.

ACCESSION BP863510
 VERSION BP863510.1 GI:59924483
 KEYWORDS EST.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 412)
 AUTHORS Seki, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Akiyama, K., Iida, K., Enju, A., Sakurai, T., Arakawa, T., Carninci, P., Fukuda, S., Iida, J., Kawai, J., Sasaki, D., Shiraki, T., Hayashizaki, Y. and Shinozaki, K.

TITLE Large-Scale Analysis of RIKEN Arabidopsis Full-length cDNAs
 JOURNAL Unpublished (2005)
 COMMENT Contact: Motoaki Seki
 Plant Functional Genomics Research Group
 RIKEN Genomic Sciences Center
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-4359
 Fax: 81-298-36-9060
 Email: mseki@rtc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998, 2002). This clone is in a modified pBluescript vector.
 Please visit our web site (http://pfgweb.gsc.riken.jp) and http://range.gsc.riken.jp) for further details.

FEATURES

Location/Qualifiers
 1. 412
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
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 /clone="RAFL21-66-P16"
 /lab_host="DH10B"
 /clone_lib="RAFL21"
 /notes="Site 1: BamHI; Site 2: SalI; Subtraction Library. The sequence was obtained from samples subjected to various stress and plant hormones-treated"

ORIGIN

Query Match 86.3%; Score 16.4; DB 3; Length 412;
 Best Local Similarity 94.4%; Pred. No. 1.7e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTTTCG 18
 |||||
 Db 197 GAACGGAAGGCTTTTG 214

RESULT 6
 BU398878

LOCUS BU398878 603 bp mRNA linear EST 27-NOV-2002
 DEFINITION 603533950F1 CSBQCHN58 Gallus gallus cDNA clone CHEST492d14 5', mRNA sequence.

ACCESSION BU398878
 VERSION BU398878.1 GI:25767934
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus

REFERENCE 1 (bases 1 to 603)
 AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 TITLE A Comprehensive Collection of Chicken cDNAs
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
 PUBMED 12445392

COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences

University of Manchester Institute of Science and Technology

(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers

FEATURES

source

1. .603
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="CHEST492d14"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQCHN56"
/note="Organ: small intestine; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, following methylation C in the first strand synthesis reaction. EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996) 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Query Match 86.3%; Score 16.4; DB 3; Length 603;
Best Local Similarity 94.4%; Pred. NO. 1.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCTTTTCG 18
DB 273 GAAAGGAAGGCCTTTTCG 290

RESULT 7

LBAF055F03/c LBAF055F03 614 bp DNA linear GSS 20-JUN-2003
LOCUS Leishmania braziliensis GSS, clone LBAF055F03, genomic survey
DEFINITION

sequence.
BX542565
VERSION BX542565.1 GI:32137791
KEYWORDS GSS; genomic survey sequence.
SOURCE Leishmania braziliensis

ORGANISM

Leishmania braziliensis
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Leishmania; Leishmania braziliensis species complex.

REFERENCE

1 Laurentino,E.C., Ruiz,J.C. and Cruz,A.K.

GSS analysis of the Leishmania braziliensis genome

TITLE

Unpublished

JOURNAL

Department of Molecular and Cell Biology, FMRP, Avenida

Bandeirantes 3900, Ribeirao Preto, SP, 14049-900, BRAZIL

Clone requests: akcruz@mrp.usp.br.

Location/Qualifiers

1. .614

/organism="Leishmania braziliensis"

/mol_type="genomic DNA"

/strain="WHOM/BR/75/M2904"

/db_xref="taxon:5660"

/clone="LBAF055F03"

. ORIGIN

Query Match 86.3%; Score 16.4; DB 14; Length 614;
Best Local Similarity 94.4%; Pred. NO. 1.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AACGGAAGGCCTTTTCG 19
DB 31 AACGGAAGGCCTTTAGG 14

RESULT 8

LOCUS BU306528

DEFINITION BU306528 625 bp mRNA linear EST 27-NOV-2002
603739007F1 CSEQCHN56 Gallus gallus cDNA clone CHEST633n2 5', mRNA
sequence.

ACCESSION BU306528

VERSION BU306528.1

KEYWORDS GI:25756262

SOURCE EST.

ORGANISM Gallus gallus (chicken)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 625)

AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,

Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.

A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)

PUBMED 12445392

COMMENT Contact: Simon Hubbard

Department of Biomolecular Sciences

University of Manchester Institute of Science and Technology

(UMIST)

PO Box 88, Manchester, M60 1QD, UK

Tel: 01612008930

Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

FEATURES

source

Location/Qualifiers
1. .625
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton line 151"
/db_xref="taxon:9031"
/clone="CHEST633n2"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQCHN56"
/note="Organ: small intestine; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, following methylation C in the first strand synthesis reaction. EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996) 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Query Match 86.3%; Score 16.4; DB 3; Length 625;
Best Local Similarity 94.4%; Pred. NO. 1.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCTTTTCG 18
DB 290 GAAAGGAAGGCCTTTTCG 307

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RESULT 9
BU283959
LOCUS
DEFINITION BU283959 643 bp mRNA linear EST 27-NOV-2002
603600041F1 CSEQCHN54 Gallus gallus cDNA clone CHEST573a12 5', mRNA
sequence.
ACCESSION BU283959
VERSION BU283959.1 GI:25733402
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 643)
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
FEATURES
source
1..643
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="CHEST573a12"
/sex="Female"
/tissue_type="not cerebrum or cerebellum"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQCHN54"
/notes="Organ: brain; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site_2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunt-ended, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
ORIGIN
Query Match 86.3%; Score 16.4; DB 3; Length 643;
Best Local Similarity 94.4%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTCG 18
||| ||||| ||||| |||||
Db 10 GAAAGGAAGGCGCTTCG 27

RESULT 10
BH794488
LOCUS
DEFINITION BH794488 660 bp DNA linear GSS 02-APR-2002
ME MBA0002P13f Manihot esculenta Manihot esculenta genomic clone
ME MBA0002P13f, genomic survey sequence.
ACCESSION BH794488
VERSION BH794488.1 GI:19892621
KEYWORDS GSS.
SOURCE Manihot esculenta (cassava)

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ORGANISM Manihot esculenta
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eustosids I; Malpighiales; Euphorbiaceae; Crotonoideae;
Manihoteae; Manihot.
REFERENCE 1 (bases 1 to 660)
Tomkins,J., Fregene,M., Main,D., Kim,H., Wing,R. and Tohme,J.
Bacterial artificial chromosome (BAC) library resource for
positional cloning of pest and disease resistance genes in cassava
(Manihot esculenta Crantz)
JOURNAL Plant Mol. Biol. 56 (4), 555-561 (2004)
PUBMED 15630619
COMMENT Contact: Tomkins J
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634, USA
Tel: 864 656 6419
Fax: 864 656 4293
Email: jtmkns@clemson.edu
Total High Quality bases = 281
Seq primer: TAATAGCACTCACTATAGGG
Class: BAC ends
High quality sequence stop: 658.
FEATURES
source
1..660
/organism="Manihot esculenta"
/mol_type="genomic DNA"
/strain="MECW72"
/db_xref="taxon:3983"
/clone="ME MBA0002P13f"
/tissue_type="leaf"
/lab_host="E. coli"
/clone_lib="Manihot esculenta"
/notes="Vector: pCUGIBAC-1; Site 1: HindIII; Site 2: NotI;
For more details on library preparation and sequence
analysis see
http://www.genome.clemson.edu/projects/stc/cassava/ME_MBA
to order clones from this library see
http://www.genome.clemson.edu/orders "
ORIGIN
Query Match 86.3%; Score 16.4; DB 11; Length 660;
Best Local Similarity 94.4%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTCG 18
||| ||||| ||||| |||||
Db 225 GAAAGGAAGGCGCTTCG 242

RESULT 11
BU412995
LOCUS
DEFINITION BU412995 709 bp mRNA linear EST 29-NOV-2002
603154843F1 CSQRBL05 Gallus gallus cDNA clone CHEST167e12 5', mRNA
sequence.
ACCESSION BU412995
VERSION BU412995.1 GI:25905666
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 709)
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)

```

PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@mist.ac.uk.

FEATURES

source
1. .709
Location/Qualifiers
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer"
/db_xref="taxon:9031"
/clone="CHEST174b10"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEORBL05"
/note="Organ: ovary; Vector: pBluescript II KS(+); Site: 1: EcoRI; Site: 2: NotI; Modification of pBluescript II KS(+) [Stratagene] vector to accommodate cDNA produced with the T-trimmed protocol (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved 3' end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BsgI and BamHI sites [5'ggccgcgtcgagcccgatccgaaaaaag] [5'aattcttttcggatccgggctgcagc]"

ORIGIN

Query Match 86.3%; Score 16.4; DB 3; Length 709;
Best Local Similarity 94.4%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCGCTTTCG 18
|||||
DB 354 GAAAGGAAGCGCTTTCG 371

RESULT 12

LOCUS CR077081 835 bp DNA linear GSS 05-JUL-2004
DEFINITION Reverse strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHP284c21, genomic survey sequence.
ACCESSION CR077081
VERSION GSS; genome survey sequence; MICER.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murioidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 835)
AUTHORS Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y., Rogers,J. and Bradley,A.

Direct Submission
TITLE Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
JOURNAL CB10 1SA, UK. http://www.sanger.ac.uk/MICR

FEATURES

source
1. .835
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHP284c21"
/clone_lib="MHPP"

ORIGIN

Query Match 86.3%; Score 16.4; DB 14; Length 835;
Best Local Similarity 94.4%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCGCTTTCG 18
|||||
DB 524 GAAAGGAAGCGCTTTCG 541

RESULT 13

LOCUS BU409605 847 bp mRNA linear EST 29-NOV-2002
DEFINITION 603157733F1 CSEORBL03 Gallus gallus cDNA clone CHEST174b10 5', mRNA sequence.

ACCESSION BU409605
VERSION BU409605.1 GI:25902276
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

REFERENCE

1 (bases 1 to 847)
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
PUBMED 12445392

COMMENT

Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)
PO Box 88, Manchester, M60 1QD, UK

Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@mist.ac.uk.

FEATURES

source
1. .847
Location/Qualifiers
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer and broiler"
/db_xref="taxon:9031"
/clone="CHEST174b10"
/sex="Male and female"
/tissue_type="Chondrocytes isolated from growth plate cartilage"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEORBL03"
/note="Vector: pBluescript II KS(+); Site: 1: EcoRI; Site 2: NotI; Modification of pBluescript II KS(+) [Stratagene] vector to accommodate cDNA produced with the T-trimmed protocol (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved 3' end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BsgI and BamHI sites [5'ggccgcgtcgagcccgatccgaaaaaag] [5'aattcttttcggatccgggctgcagc]"

ORIGIN

Query Match 86.3%; Score 16.4; DB 3; Length 847;
Best Local Similarity 94.4%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCGCTTTCG 18
|||||
DB 278 GAAAGGAAGCGCTTTCG 295

RESULT 14

LOCUS BE881910 872 bp mRNA linear EST 20-OCT-2000
DEFINITION 601504886F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906597 5', mRNA sequence.

ACCESSION BE881910
VERSION BE881910.1 GI:10330686
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 872)
NIH-MGC http://mgs.nci.nih.gov/.
NATIONAL INSTITUTES OF HEALTH, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9715 row: 1 column: 22
High quality sequence start: 49
High quality sequence stop: 593.
Location/Qualifiers
1. .872
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3906597"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_71"
/notes="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI;
Site2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. "

ORIGIN
Query Match 86.3%; Score 16.4; DB 7; Length 872;
Best Local Similarity 94.4%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AACGGAAAGGCCTTCG 19
|||||
Db 762 AACTGAAAGGCCTTCG 779

RESULT 15
DN561788 910 bp mRNA linear EST 14-MAR-2005
LOCUS
DEFINITION
92178421 Sea Urchin primary mesenchyme cell cDNA library
Strongylocentrotus purpuratus cDNA clone PMSPR2-102A16 5', mRNA
sequence.
ACCESSION DN561788
VERSION DN561788.1 GI:61120827
KEYWORDS
SOURCE
ORGANISM
Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
REFERENCE
1 (bases 1 to 910)
Zhu, X., Mahairas, G., Illies, M.R., Cameron, R.A., Davidson, E.H. and
Ertensohn, C.A.
A large scale analysis of mRNAs expressed by primary mesenchyme
cells of the sea urchin embryo
Development 128 (13), 2615-2627 (2001)
11493577
JOURNAL
PUBMED
COMMENT
Contact: Erica Sodergren
Human Genome Sequencing Center
Baylor College of Medicine
One Baylor Plaza, Houston, TX 77030, USA
Tel: 713-798-7676
Fax: 713-798-6977
Email: ericae@bcm.tmc.edu
NCBI Trace Archive: 496682679
Insert Length: 1750 Std Error: 0.25
Plate: 102 row: A column: 16.
Location/Qualifiers

FEATURES
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1. .910
/organism="Strongylocentrotus purpuratus"
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/db_xref="taxon:7668"
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/tissue_type="embryo"
/cell_type="primary mesenchyme cells"
/lab_host="E.coli"
/clone_lib="Sea Urchin primary mesenchyme cell cDNA
library"
/notes="Vector: pSPORT1; Site 1: NotI; Site 2: MluI; oligo
dC priming from poly A+ RNA, directionally cloned"

ORIGIN
Query Match 86.3%; Score 16.4; DB 9; Length 910;
Best Local Similarity 94.4%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGAAAGGCCTTCG 18
|||||
Db 794 GAACGAAAGGCCTTCG 811

RESULT 16
COS83238/c
LOCUS
DEFINITION
ILLUMIGEN MQC 44583 Katze MMLV Macaca mulatta cDNA clone
IBIUM:16736 57 similar to Bases 1 to 944 highly similar to human
ITIH3 (Hs.76716), mRNA sequence.
ACCESSION COS83238
VERSION COS83238.1 GI:50415893
KEYWORDS
SOURCE
ORGANISM
Macaca mulatta (rhesus monkey)
Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecoidea; Macaca.
REFERENCE
1 (bases 1 to 944)
Magness, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agui, M.B.,
Prohl, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. and
Iadonato, S.P.
Analysis of the Macaca mulatta transcriptome and the sequence
divergence between Macaca and human
Genome Biol. 6 (7), R60 (2005)
15998449
Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.06.18. 633 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see
http://www.macaque.org
PCR Primers
FORWARD: CCCTCACTAAAGGGAACAAAA
BACKWARD: CACTATAGGCGAATTGGTA
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Location/Qualifiers
1. .944
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/mol_type="mRNA"
/strain="Indian"
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/clone="IBIUM:16736"
/sex="female"
/dev_stage="adult"
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/clone_lib="Katze_MMLV"

FEATURES
source
1. .944
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/strain="Indian"
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/sex="female"
/dev_stage="adult"
/lab_host="Electromax DH10B"
/clone_lib="Katze_MMLV"

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/notes="Organ: liver; Vector: pDONR 222; Site 1: BsrG I;
Site 2: BsrG I; Created from CloneMiner CDNA_Library
Construction kit (catalog #18249-029)"

ORIGIN
Query Match      86.3%; Score 16.4; DB 8; Length 944;
Best Local Similarity 94.4%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AACGGAAGGCCTTCGG 19
Db 837 AACGGAAGGCCTTCGG 820

RESULT 17
LOCUS BZ548902/c 1330 bp DNA linear GSS 17-DEC-2002
DEFINITION pacsl-60_1548.01 pacsl-60 Pseudomonas aeruginosa genomic clone
ACCESSION BZ548902
VERSION BZ548902.1 GI:27152483
KEYWORDS GSS.
SOURCE Pseudomonas aeruginosa
ORGANISM Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
REFERENCE 1 (bases 1 to 1330)
AUTHORS Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
Burns,J.B., Kaul,R. and Olsen,M.V.
TITLE Whole-Genome-Sequence variation among multiple isolates of
Pseudomonas aeruginosa library
JOURNAL J. Bacteriol. (2002) In press
COMMENT Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 20622216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.
FEATURES
source
1. .1330
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="1-60"
/db_xref="taxon:287"
/clone="pacsl-60_1548"
/clone_lib="pacsl-60"
/notes="clinical isolate 1-60 Whole genomic shotgun
library."

ORIGIN
Query Match      86.3%; Score 16.4; DB 11; Length 1330;
Best Local Similarity 94.4%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AACGGAAGGCCTTCGG 19
Db 1240 AACGGAAGGCCTTCGG 1223

RESULT 18
LOCUS BF851999 268 bp mRNA linear EST 16-JAN-2001
DEFINITION MR3-EN0090-111200-003-f09 EN0090 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF851999
VERSION BF851999.1 GI:12239161
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

```

```

1 (bases 1 to 268)
Dias Neco,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=MR3&t2=MR3-EN0090-
111200-003-f09&t3=2000-12-11&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 21
High quality sequence stop: 174.
FEATURES
source
1. .268
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="EN0090"
/notes="Organ: lung normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Query Match      84.2%; Score 16; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AACGGAAGGCCTTC 17
Db 76 AACGGAAGGCCTTC 91

RESULT 19
LOCUS CC153371 360 bp DNA linear GSS 25-APR-2003
DEFINITION CSU-K34.124M19.SP6 CSU-K34 Aedes aegypti genomic clone
ACCESSION CC153371
VERSION CC153371.1 GI:30106667
KEYWORDS GSS.
SOURCE Aedes aegypti (yellow fever mosquito)
ORGANISM Aedes aegypti
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Culicinae; Culicini; Aedes; Stegomyia.
1 (bases 1 to 360)
Loftus,B., Shetty,J., Knudson,D. and Severson,D.
BAC end sequencing of Aedes aegypti
Unpublished (2003)
Other GSSs: CSU-K34.124M19.T7
Contact: Brendan Loftus
Department of Eukaryotic Genomics
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA

```

Tel: 301-838-3543
 Fax: 301-838-0208
 Email: enta@tigr.org
 Library was provided by Susan Brown and Dennis Knudson at Colorado State University.
 Seq primer: SP6
 Class: BAC ends.

FEATURES

source
 1. .360
 Location/Qualifiers
 /organism="Aedes aegypti"
 /mol_type="genomic DNA"
 /db_xref="taxon:7159"
 /clone="CSU-K34-124M19"
 /clone_lib="CSU-K34"
 /note="Vector: pBACE3.6; Site 1: EcoRI; Source DNA: Aedes aegypti; strain unknown (derived from freshly hatched larvae at the Virus Research Centre, Poona, India. Reference: SINGH, K. R. P., 1967 Cell cultures derived from larvae of Aedes albopictus (Skuse) and Aedes aegypti (L.). Current Science 36: 506-508; ATC-10 cell line ATCC CCL-125"

ORIGIN

Query Match 84.2%; Score 16; DB 12; Length 360;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGGAAAGCGCTTTTCGG 19

Db 246 CGGAAAGCGCTTTTCGG 261

RESULT 20

AW850543
 LOCUS
 DEFINITION IL3-CT0219-160200-060-A03 CT0219 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW850543
 VERSION AW850543.1 GI:7946060
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE

AUTHORS
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Mateukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 PUBMED 10737800

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

PUBMED

COMMENT

Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=at2=IL3-CT0219-160200-060-A03&t3=2000-02-16&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 17
 High quality sequence stop: 129.

FEATURES

source
 1. .590
 Location/Qualifiers
 /organism="Homo sapiens"

/mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="CT0219"

/note="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 84.2%; Score 16; DB 7; Length 590;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGGAAAGCGCTTTTCGG 19

Db 249 CGGAAAGCGCTTTTCGG 264

RESULT 21

BZ688362/c
 LOCUS
 DEFINITION OGDAD75TC ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMA0144N06, genomic survey sequence.

ACCESSION BZ688362

VERSION BZ688362.1

KEYWORDS GI:28275551

SOURCE GSS.

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 661)

AUTHORS White, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

TITLE Consortium for Maize Genomics

JOURNAL Unpublished (2002)

COMMENT Other_GSSs: OGDAD75TM

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TF

Class: methylation filtered.

Location/Qualifiers

1. .661

/organism="Zea mays"

/mol_type="genomic DNA"

/strain="B73"

/db_xref="taxon:4577"

/clone="ZMMBMA0144N06"

/clone_lib="ZM 0.7 1.5_KB"

/note="Vector: pBCK-; Site 1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"

ORIGIN

Query Match 84.2%; Score 16; DB 12; Length 661;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ACGAAAGCGCTTTTCG 18

Db 227 ACGAAAGCGCTTTTCG 212

RESULT 22

DR891379/c

LOCUS	DR891379	JGI_XZT19757.rev NIH_XGC tropTads	663 bp	mRNA	linear	EST 01-AUG-2005
DEFINITION	IMAGE:7596789 3', mRNA sequence.					
ACCESSION	DR891379					
VERSION	DR891379.1	GI:71580631				
KEYWORDS	EST.					
SOURCE	Xenopus tropicalis (western clawed frog)					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus; Silurana.					
REFERENCE	1 (bases 1 to 663)					
AUTHORS	Richardson,P., Lucas,S., Rokhsar,D., Dettter,J.C., Ng,D.C., Brokstein,P. and Lindquist,E.A.					
TITLE	DOE Joint Genome Institute Xenopus tropicalis EST project					
JOURNAL	Unpublished (2004)					
COMMENT	Other_ESTs: JGI_XZT19757.fwd Contact: Lindquist,E.A., Richardson,P. DOE Joint Genome Institute 2800 Mitchell Drive, Walnut Creek, CA 94598, USA Tel: 925 296 5600 Fax: 925 296 5710 Email: cdna@jgi-psf.org Tissue Procurement: Richard M. Harland Laboratory, University of California, Berkeley: http://tropicalis.berkeley.edu/home cDNA Library Preparation: Richard M. Harland Laboratory, University of California, Berkeley DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov Clone Distribution: I.M.A.G.E. Consortium/LLNL: http://image.llnl.gov Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.rev' indicates a reverse sequencing read of the insert. It does not necessarily reflect the orientation of the insert. Poly-A: Based upon the presence of a run of 14 or more T residues at the beginning of the sequence, this clone was polyadenylated. The resulting Poly-T sequence has been removed. Plate: XZT 0205 row: j column: 19 High quality sequence stop: 534 POLYA=Yes.					
FEATURES	Location/Qualifiers 1..663 /organism="Xenopus tropicalis" /mol_type="mRNA" /db_xref="taxon:8364" /clone="IMAGE:7596789" /tissue_type="whole embryo" /dev_stage="Tadpole (st. 36-41)" /lab_host="E. coli XLI-Blue derivative, Stratagene ElectroTen-Blue" /clone_lib="NIH_XGC tropTads" /note="Vector: pCS108; Site_1: SalI; Site_2: NotI; Tadpole library constructed by Russell B. Fletcher in R. Harland's lab using poly A RNA and oligo dt primers (Invitrogen SuperScript Plasmid System for cDNA Synthesis and Cloning). SalI (5' end) -NotI (3' end) cDNA was inserted into vector pCS108 (http://mcb.berkeley.edu/labs/harland/pages/plasmids.html)."					
source	1..663					
Query Match	84.2%;	Score 16;	DB 10;	Length 663;		
Best Local Similarity	100.0%;	Pred. No. 3e+03;				
Matches	16;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	2	AACGGAAGGCCTTTC	17			
Db	459	AACGGAAGGCCTTTC	444			
RESULT 23						
CX793255/c						
LOCUS	CX793255	JGI_CAAJ387.rev NIH_XGC tropBrn2	711 bp	mRNA	linear	EST 31-JAN-2005
DEFINITION	IMAGE:7640427 3', mRNA sequence.					
ACCESSION	DR891379					
VERSION	DR891379.1	GI:71580631				
KEYWORDS	EST.					
SOURCE	Xenopus tropicalis (western clawed frog)					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus; Silurana.					
REFERENCE	1 (bases 1 to 711)					
AUTHORS	Richardson,P., Lucas,S., Rokhsar,D., Dettter,J.C., Ng,D.C., Brokstein,P. and Lindquist,E.A.					
TITLE	DOE Joint Genome Institute Xenopus tropicalis EST project					
JOURNAL	Unpublished (2004)					
COMMENT	Other_ESTs: JGI_CAAJ387.fwd Contact: Lindquist,E.A., Richardson,P. DOE Joint Genome Institute 2800 Mitchell Drive, Walnut Creek, CA 94598, USA Tel: 925 296 5600 Fax: 925 296 5710 Email: cdna@jgi-psf.org Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory, University of California, Berkeley: http://tropicalis.berkeley.edu/home) cDNA Library Preparation: DOE Joint Genome Institute: http://www.jgi.doe.gov DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov Clone Distribution: I.M.A.G.E. Consortium/LLNL: http://image.llnl.gov Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.rev' indicates a reverse sequencing read of the insert. It does not necessarily reflect the orientation of the insert. Plate: CAAJ 0005 row: e column: 1 High quality sequence stop: 645.					
FEATURES	Location/Qualifiers 1..711 /organism="Xenopus tropicalis" /mol_type="mRNA" /db_xref="taxon:8364" /clone="IMAGE:7640427" /tissue_type="Brain" /dev_stage="Adult" /lab_host="ElectroMAX DH10B" /clone_lib="NIH_XGC tropBrn2" /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; This library was made from dt primed cDNA and cloned into Invitrogen pCMVSPORT6 vector. The work was done at DOE Joint Genome Institute. Poly A RNA were primed with 5' GACTAGTTC TAGATCGGAG CGGCGCCCTTTT TTTT TTTT 3'. cDNA were ligated to SalI adapter (5' TCGACCCACGGGCCG and 5'CGACGCGTGGG), digested with NotI, size fractionated in 1.1% agarose gel electrophoresis and ligated into NotI and SalI digested pCMVSPORT6 vector."					
source	1..711					
Query Match	84.2%;	Score 16;	DB 9;	Length 711;		
Best Local Similarity	100.0%;	Pred. No. 3e+03;				
Matches	16;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	2	AACGGAAGGCCTTTC	17			
Db	515	AACGGAAGGCCTTTC	500			
RESULT 24						
CX798411/c						
LOCUS	CX798411	JGI_CAAJ13264.rev NIH_XGC tropBrn2	736 bp	mRNA	linear	EST 28-JUL-2005
DEFINITION	IMAGE:7643358 3', mRNA sequence.					
ACCESSION	DR891379					
VERSION	CX798411.2	GI:71459585				

```

KEYWORDS
SOURCE  EST.
ORGANISM Xenopus tropicalis (western clawed frog)
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
          Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 736)
AUTHORS  Richardson,P., Lucas,S., Rokhsar,D., Dettter,J.C., Ng,D.C.,
          Brokstein,P. and Lindquist,E.A.
TITLE    DOE Joint Genome Institute Xenopus tropicalis EST project
JOURNAL  Unpublished (2004)
COMMENT  On Jan 31, 2005 this sequence version replaced gi:58353040.
          Other_ESTs: JGI_CAAJ13264.fwd
          Contact: Lindquist,E.A., Richardson,P.
          DOE Joint Genome Institute
          2800 Mitchell Drive, Walnut Creek, CA 94598, USA
          Tel: 925 296 5600
          Fax: 925 296 5710
          Email: cdna@jgi-psf.org
          Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory,
          University of California, Berkeley:
          http://tropicalis.berkeley.edu/home)
          cDNA Library Preparation: DOE Joint Genome Institute:
          http://www.jgi.doe.gov
          Naming Conventions: EST name is generated by the concatenation of
          the JGI Clone id and the direction of sequencing. The suffix '.rev'
          indicates a reverse sequencing read of the insert. It does not
          necessarily reflect the orientation of the insert.
          Plate: CAAJ 0137 row: 0 column: 4
          High quality sequence stop: 730
          POLYA=Yes.

FEATURES             Location/Qualifiers
     source           1..736
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="IMAGE:7643358"
                     /tissue_type="Brain"
                     /dev_stage="Adult"
                     /lab_host="ElectroMAX DH10B"
                     /clone_lib="NIH XGC tropBrn2"
                     /notes="vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
                     This library was made from dt primed cDNA and cloned into
                     Invitrogen pCMVSPORT6 vector. The work was done at DOE
                     Joint Genome Institute. Poly A RNA were primed with 5'
                     GACTAGTCTAGATCGGAG CGCGCGCCCTTTT TTTT 3'. cDNA
                     were ligated to SalI adapter (5' TCGACCCACGCGTCG and
                     5'CGACGCGTGGG), digested with NotI, size fractionated in
                     1.1% agarose gel electrophoresis and ligated into NotI and
                     SalI digested pCMVSPORT6 vector."

ORIGIN
Query Match      84.2%; Score 16; DB 9; Length 736;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 AACGGAAGGCTTTC 17
    |||||
Db  509 AACGGAAGGCTTTC 494

RESULT 25
CC684169
LOCUS      CC684169
DEFINITION OGWED19TV ZM 0.7 1.5 KB Zea mays genomic clone ZMMBma0557D14,
          genomic survey sequence.
ACCESSION CC684169
VERSION   CC684169.1 GI:32088945
KEYWORDS  GSS.
SOURCE    Zea mays

Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 763)
Whiteclaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGWED19TH
Contact: Cathy Whitelaw
TIGR      9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
Class: methylation filtered.
          Location/Qualifiers
     source           1..763
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBma0557D14"
                     /notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
                     methylation filtered genomic DNA library"

ORIGIN
Query Match      84.2%; Score 16; DB 12; Length 763;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  3 ACGGAAGGCTTTC 18
    |||||
Db  328 ACGGAAGGCTTTC 343

RESULT 26
CX797048/c
LOCUS      CX797048
DEFINITION JGI_CAAJ12493.rev NIH XGC tropBrn2 Xenopus tropicalis cDNA clone
          IMAGE:7642446 3', mRNA sequence.
ACCESSION  CX797048
VERSION    CX797048.2 GI:71459157
KEYWORDS   EST.
SOURCE     Xenopus tropicalis (western clawed frog)
ORGANISM   Xenopus tropicalis
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
          Xenopodinae; Xenopus; Silurana.
REFERENCE  1 (bases 1 to 803)
AUTHORS    Richardson,P., Lucas,S., Rokhsar,D., Dettter,J.C., Ng,D.C.,
          Brokstein,P. and Lindquist,E.A.
TITLE      DOE Joint Genome Institute Xenopus tropicalis EST project
JOURNAL    Unpublished (2004)
COMMENT    On Jan 31, 2005 this sequence version replaced gi:58351677.
          Other_ESTs: JGI_CAAJ12493.fwd
          Contact: Lindquist,E.A., Richardson,P.
          DOE Joint Genome Institute
          2800 Mitchell Drive, Walnut Creek, CA 94598, USA
          Tel: 925 296 5600
          Fax: 925 296 5710
          Email: cdna@jgi-psf.org
          Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory,
          University of California, Berkeley:
          http://tropicalis.berkeley.edu/home)
          cDNA Library Preparation: DOE Joint Genome Institute:
          http://www.jgi.doe.gov
          DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
          Clone Distribution: I.M.A.G.E. Consortium/LLNL:
          http://image.llnl.gov
          Naming Conventions: EST name is generated by the concatenation of
          the JGI Clone id and the direction of sequencing. The suffix '.rev'
          indicates a reverse sequencing read of the insert. It does not
          necessarily reflect the orientation of the insert.
          Plate: CAAJ 0137 row: 0 column: 4
          High quality sequence stop: 730
          POLYA=Yes.

FEATURES             Location/Qualifiers
     source           1..736
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="IMAGE:7643358"
                     /tissue_type="Brain"
                     /dev_stage="Adult"
                     /lab_host="ElectroMAX DH10B"
                     /clone_lib="NIH XGC tropBrn2"
                     /notes="vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
                     This library was made from dt primed cDNA and cloned into
                     Invitrogen pCMVSPORT6 vector. The work was done at DOE
                     Joint Genome Institute. Poly A RNA were primed with 5'
                     GACTAGTCTAGATCGGAG CGCGCGCCCTTTT TTTT 3'. cDNA
                     were ligated to SalI adapter (5' TCGACCCACGCGTCG and
                     5'CGACGCGTGGG), digested with NotI, size fractionated in
                     1.1% agarose gel electrophoresis and ligated into NotI and
                     SalI digested pCMVSPORT6 vector."

ORIGIN
Query Match      84.2%; Score 16; DB 9; Length 736;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 AACGGAAGGCTTTC 17
    |||||
Db  509 AACGGAAGGCTTTC 494

RESULT 25
CC684169
LOCUS      CC684169
DEFINITION OGWED19TV ZM 0.7 1.5 KB Zea mays genomic clone ZMMBma0557D14,
          genomic survey sequence.
ACCESSION  CC684169
VERSION    CC684169.1 GI:32088945
KEYWORDS   GSS.
SOURCE    Zea mays

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http://image.llnl.gov
Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.rev' indicates a reverse sequencing read of the insert. It does not necessarily reflect the orientation of the insert.
Plate: CAAJ 0129 row: i column: 4
High quality sequence stop: 760
POLYA=Yes.

FEATURES
source Location/Qualifiers
1..803
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:7642446"
/tissue_type="Brain"
/dev_stage="Adult"
/lab_host="ElectromAX DH10B"
/clone_lib="NIH XGC tropBn2"
/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
This library was made from dt primed cDNA and cloned into Invitrogen pCMVSPORT6 vector. The work was done at DOE Joint Genome Institute. Poly A RNA were primed with 5' GACTAGTTCTAGATCGGAG CGCGCGCTTTT TTTT 3'. CDNA were ligated to SalI adapter (5' TCGACCCAGCGTCCG and 5'CGGACGCTGGG), digested with NotI, size fractionated in 1.1% agarose gel electrophoresis and ligated into NotI and SalI digested pCMVSPORT6 vector."

ORIGIN
Query Match 84.2%; Score 16; DB 9; Length 803;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AACGGAAGGCTTTC 17
Db 391 AACGGAAGGCTTTC 376
|||||

RESULT 27
CX815303
LOCUS
DEFINITION
JGI CAAK1288.fwd NIH XGC tropBn3 Xenopus tropicalis cDNA clone
IMAGE:7652603 5', mRNA sequence.
ACCESSION
CX815303.1 GI:58369930
VERSION
CX815303
KEYWORDS
EST.
Xenopus tropicalis (western clawed frog)
ORGANISM
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 829)
Richardson,P., Lucas,S., Rokhsar,D., Dettter,J.C., Ng,D.C.,
Brokstein,P. and Lindquist,E.A.
DOE Joint Genome Institute Xenopus tropicalis EST project
Unpublished (2004)
Other ESTs: JGI CAAK1288.rev
Contact: Lindquist,E.A., Richardson,P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory,
University of California, Berkeley:
http://tropicalis.berkeley.edu/home)
cDNA Library Preparation: DOE Joint Genome Institute:
http://www.jgi.doe.gov

NAME
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Clone Distribution: I.M.A.G.E. Consortium/LLNL:
http://image.llnl.gov
Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.fwd' indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.

indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.
Plate: CAAK 0013 row: p column: 9
High quality sequence stop: 817.

FEATURES
source Location/Qualifiers
1..829
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:7652603"
/tissue_type="Brain"
/dev_stage="Adult"
/lab_host="ElectromAX DH10B"
/clone_lib="NIH XGC tropBn3"
/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
This library was made from dt primed cDNA and cloned into Invitrogen pCMVSPORT6 vector. The work was done at DOE Joint Genome Institute. Poly A RNA were primed with 5' GACTAGTTCTAGATCGGAG CGCGCGCTTTT TTTT 3'. CDNA were ligated to SalI adapter (5' TCGACCCAGCGTCCG and 5'CGGACGCTGGG), digested with NotI, size fractionated in 1.1% agarose gel electrophoresis and ligated into NotI and SalI digested pCMVSPORT6 vector."

ORIGIN
Query Match 84.2%; Score 16; DB 9; Length 829;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AACGGAAGGCTTTC 17
Db 636 AACGGAAGGCTTTC 651
|||||

RESULT 28
CX815302/c
LOCUS
DEFINITION
JGI CAAK1288.rev NIH XGC tropBn3 Xenopus tropicalis cDNA clone
IMAGE:7652603 3', mRNA sequence.
ACCESSION
CX815302
VERSION
CX815302.2 GI:71464988
KEYWORDS
EST.
Xenopus tropicalis (western clawed frog)
ORGANISM
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 853)
Richardson,P., Lucas,S., Rokhsar,D., Dettter,J.C., Ng,D.C.,
Brokstein,P. and Lindquist,E.A.
DOE Joint Genome Institute Xenopus tropicalis EST project
Unpublished (2004)
On Jan 31, 2005 this sequence version replaced gi:58369929.
Other ESTs: JGI CAAK1288.fwd
Contact: Lindquist,E.A., Richardson,P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory,
University of California, Berkeley:
http://tropicalis.berkeley.edu/home)
cDNA Library Preparation: DOE Joint Genome Institute:
http://www.jgi.doe.gov

NAME
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Clone Distribution: I.M.A.G.E. Consortium/LLNL:
http://image.llnl.gov
Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.rev' indicates a reverse sequencing read of the insert. It does not necessarily reflect the orientation of the insert.
Plate: CAAK 0013 row: p column: 9

LOCUS	949 bp	DNA	linear	GSS 19-JUN-2003
CC678267				
OGUJ28TH ZM	0.7	1.5 KB	Zea mays genomic clone ZM5BMA0440F04,	
DEFINITION				

```

genomic survey sequence.
ACCESSION CC678267
VERSION CC678267.1 GI:32083043
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 949)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGULJ26TV
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: methylation filtered.
Location/Qualifiers
1..949
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone_lib="ZMBMa0440F04"
/notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match 84.2%; Score 16; DB 12; Length 949;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ACGGAAGGCGTTTCG 18
|||||
Db 63 ACGGAAGGCGTTTCG 48

RESULT 32
CC712366
LOCUS CC712366
DEFINITION CC712366
ACCESSION CC712366
VERSION CC712366
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1009)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGULG58TH
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: methylation filtered.
Location/Qualifiers
1..1009
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone_lib="ZMBMa0467I19"
/notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match 84.2%; Score 16; DB 12; Length 1009;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ACGGAAGGCGTTTCG 18
|||||
Db 555 ACGGAAGGCGTTTCG 570

RESULT 33
DN695496
LOCUS DN695496
DEFINITION DN695496
ACCESSION DN695496
VERSION DN695496.1 GI:62053862
KEYWORDS EST.
SOURCE Gasterosteus aculeatus (three spined stickleback)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
Gasterosteidae; Gasterosteus.
1 (bases 1 to 1136)
Kingsley,D.M., Peichel,C., Balabhadra,S., Grimwood,J., Dickson,M.,
Schmutz,J. and Myers,R.M.
Expressed sequence tags from Gasterosteus aculeatus
Unpublished (2003)
Contact: Grimwood, Jane
Stanford Human Genome Center
Stanford University School of Medicine
975 S California Ave, Palo Alto, CA 94304, USA
Tel: 650 320 5917
Fax: 650 320 5801
Email: jane@shgc.stanford.edu
Plate: 01
High quality sequence stop: 812.
Location/Qualifiers
1..1136
/organism="Gasterosteus aculeatus"
/mol_type="mRNA"
/strain="Bitruifjordur marine sticklebacks, Iceland"
/db_xref="taxon:69293"
/clone_lib="CLJ01-D08"
/sex="mixed male and female"
/tissue_type="whole larva"
/db_xref="taxon:69293"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="SHGC-CLJ"
/notes="Vector: Express 1; Total and poly A+ RNA was
isolated from the indicated stickleback tissue, and a cDNA
library was constructed in the Express 1 plasmid vector by
Open Biosystems. First strand cDNA synthesis was primed
with an 54 bp linker primer containing an oligodT sequence
preceded by a synthetic NotI site (first strand primer:
5'-GACTAGTTCTAGATCGAGCGGCCG(T)25-3'). Following
second strand synthesis, cDNAs were made blunt at the end
corresponding to the original 5 prime end of mRNA, and
cloned directionally into the NotI and EcoRV sites of
Express 1. Note that the EcoRV site is typically destroyed
```

in the blunt end cloning, leaving a junction of the form 'xxxATC' (where is ATC is the second half of the EcorV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at:
http://www.openbiosystems.com/cdna_library_construction_fa_q.php#8 The primary library was transformed and amplified in DH10B (T1 phage resistant) bacteria. Clones available from Open Biosystems:
<http://www.openbiosystems.com/stickleback>

ORIGIN

Query Match 84.2%; Score 16; DB 9; Length 1136;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AACGGAAGGCGCTTTC 17
 |||||
 Db 947 AACGGAAGGCGCTTTC 962

RESULT 34

DT995972 1390 bp mRNA linear EST 22-SEP-2005
 LOCUS CNB181-G02.yld-s SHGC-CNB Gasterosteus aculeatus cDNA clone
 DEFINITION
 DT995972
 VERSION
 DT995972.1 GI:76119782
 KEYWORDS
 EST.
 SOURCE
 Gasterosteus aculeatus (three spined stickleback)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes; Gasterosteidae; Gasterosteus.

REFERENCE

1 (bases 1 to 1390)
 Kingsley, D.M., Peichel, C., Balabhadra, S., Grimwood, J., Dickson, M., Schmutz, J., and Myers, R.M.

AUTHORS

Expressed sequence tags from *Gasterosteus aculeatus*

TITLE

Unpublished (2003)

JOURNAL

Contact: Grimwood, Jane

COMMENT

Stanford Human Genome Center

Stanford University School of Medicine

975 S California Ave, Palo Alto, CA 94304, USA

Tel: 650 320 5917

Fax: 650 320 5801

Email: jane@hgsc.stanford.edu

Plate: 181

High quality sequence start: 26

High quality sequence stop: 835.

Location/Qualifiers

1. .1390

/organism="Gasterosteus aculeatus"

/mol_type="mRNA"

/strain="Conner Creek sticklebacks, WA USA"

/db_xref="taxon:69293"

/clone="CNB181-G02"

/sex="mixed male and female"

/tissue_type="brain"

/dev_stage="adult"

/lab_hosts="DH10B (T1 phage resistant)"

/clone_lib="SHGC-CNB"

/note="Vector: Express 1; Total and poly A+ RNA was isolated from the indicated stickleback tissue, and a cDNA library was constructed in the Express 1 plasmid vector by Open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceded by a synthetic NotI site (first strand primer: 5'-GACAGTCTAGATCGGAGCGGCC(T)25-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5 prime end of mRNA, and cloned directionally into the NotI and EcorV sites of Express 1. Note that the EcorV site is typically destroyed in the blunt end cloning, leaving a junction of the form

'xxxATC' (where is ATC is the second half of the EcorV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at:
http://www.openbiosystems.com/cdna_library_construction_fa_q.php#8 The primary library was transformed and amplified in DH10B (T1 phage resistant) bacteria. Clones available from Open Biosystems:
<http://www.openbiosystems.com/stickleback>

ORIGIN

Query Match 84.2%; Score 16; DB 10; Length 1390;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AACGGAAGGCGCTTTC 17
 |||||
 Db 1273 AACGGAAGGCGCTTTC 1288

RESULT 35

BM633199 169 bp mRNA linear EST 26-FEB-2002
 LOCUS 17000687506761 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
 DEFINITION
 BM633199
 VERSION
 BM633199.1 GI:18932710
 KEYWORDS
 EST.
 SOURCE
 Anopheles gambiae (African malaria mosquito)

ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae; Anophelinae; Anopheles.

REFERENCE

1 (bases 1 to 169)

AUTHORS

Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.

TITLE

Celera Anopheles gambiae EST project

JOURNAL

Unpublished (2002)

COMMENT

Contact: Holt R.A.

Celera Genomics

45 W. Gude Dr., Rockville, MD 20850, USA

Tel: 2404533151

Fax: 2404534580

Email: HoltRA@celera.com

Plate: NU01004AY7 row: H column: 16

Seq primer: M13 Reverse.

Location/Qualifiers

1. .169

/organism="Anopheles gambiae"

/mol_type="mRNA"

/strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"

/db_xref="taxon:7165"

/clone="19600449642370"

/dev_stage="Adult"

/lab_host="DH10B"

/clone_lib="A.Gam.ad.cDNA1"

/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."

ORIGIN

Query Match 83.2%; Score 15.8; DB 3; Length 169;
 Best Local Similarity 89.8%; Pred. No. 3.1e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCGCTTTCGG 19
 |||||
 Db 52 GAACGGAAAGCGCTTTCGG 70

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RESULT 36
DT929107
LOCUS
DEFINITION PCRS10047 Hematopoietic stem cells Mus musculus CDNA, mRNA
sequence.
ACCESSION DT929107
VERSION DT929107.1 GI:75959729
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 225)
AUTHORS Pritsker,M., Doniger,T.T., Kramer,L.C., Westcot,S.E. and
Lemischka,I.R.
TITLE Diversification of Stem Cell Molecular Repertoire by Alternative
Splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. (2005) In press
COMMENT Lab of Thor Lemischka, Department of Molecular Biology
Princeton University
Princeton, NJ 08544, USA
Tel: 609 258 5657
Fax: 609 258 1704
Email: pritsker@molbio.princeton.edu.
FEATURES
source
1..225
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue="Hematopoietic stem cells"
/cell_type="Hematopoietic stem cells"
/clone_lib="Hematopoietic stem cells"
/notes="cDNA library was made from FACS-purified
hematopoietic stem cells"
ORIGIN
Query Match 83.2%; Score 15.8; DB 10; Length 225;
Best Local Similarity 89.5%; Pred. No. 3.2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GAACGGAAGGCCTTCGG 19
Db 122 GAACGGAAGGCCTTCGG 140
RESULT 37
CV341801/c
LOCUS
DEFINITION MR0-HT0559-160500-019-b11 HT0559 Homo sapiens CDNA, mRNA sequence.
ACCESSION CV341801
VERSION CV341801.1 GI:52665015
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 255)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. http://www.ludwig.org.br.
LOCATION/Qualifiers
1..255
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0559"
/notes="Organ: head neck; Vector: puc18; Site:1: SmaI;
Site:2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
ORIGIN
Query Match 83.2%; Score 15.8; DB 8; Length 255;
Best Local Similarity 89.5%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GAACGGAAGGCCTTCGG 19
Db 250 GAATGGAAGGCTTCGG 232
RESULT 38
CV341780/c
LOCUS
DEFINITION MR0-HT0559-060600-030-b12 HT0559 Homo sapiens cDNA, mRNA sequence.
ACCESSION CV341780
VERSION CV341780.1 GI:52664994
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 256)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. http://www.ludwig.org.br.
LOCATION/Qualifiers
1..256
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0559"
/notes="Organ: head neck; Vector: puc18; Site:1: SmaI;

```


Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 83.2%; Score 15.8; DB 8; Length 256;
 Best Local Similarity 89.5%; Pred. No. 3.3e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTTCGG 19
 |||||
 Db 250 GAATGGAAGGCTTTCGG 232

RESULT 39

BB276884/c
 LOCUS
 DEFINITION BB276884 RIKEN full-length enriched, 10 days neonate cortex Mus
 musculus cDNA clone A830099J18 3' similar to AF040965 Homo sapiens
 unknown protein IT12 mRNA, mRNA sequence.

ACCESSION

VERSION BB276884.1 GI:8973905

KEYWORDS

SOURCE EST.

Mus musculus (house mouse)

ORGANISM

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Muridae; Mus.

REFERENCE

AUTHORS

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T.,
 Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
 Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
 Irawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
 Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C.,
 Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H.,
 Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K.,
 Shibata, Y., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T.,
 Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A.,
 Takahashi, F., Tomimaga, N., Toya, T., Tsunoda, Y., Watanishi, A.,
 Watanabe, S., Yamamura, T., Yamakawa, I., Yano, R., Yasunishi, A.,
 Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and
 Hayashizaki, Y.

RIKEN Mouse ESTs (Konno, H., et al.)

TITLE

JOURNAL

COMMENT

Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216

Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/
 Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoaka, S.,
 Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Thermostabilization and thermoactivation of thermolabile enzymes by
 trehalose and its application for the synthesis of full length
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh, M., Ktsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,
 Okazaki, Y. and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)

Please visit our web site (http://genome.rtc.riken.go.jp) for
 further details.

FEATURES

source

Location/Qualifiers

1..263

/organism="Mus musculus"

/mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="A830099J18"
 /tissue_type="cortex"
 /dev_stage="10 days neonate"
 /lab_host="DH10B"
 /clone_lib="RIKEN full-length enriched, 10 days neonate
 cortex"

/notes="Site 1: Sali; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTNN 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. cDNA went through one round of normalization
 to Rot = 20.0 and subtraction to Rot = 459.0. Second
 strand cDNA was prepared with the primer adapter of
 sequence [5' GAGAGAGAGATTCGAGTTAAATTAATCCCCCCCCCCC
 3']. cDNA was cleaved with XhoI and BamHI. Vector: a
 modified pBluescript KS(+) after bulk excision from Lambda
 FLC I."

ORIGIN

Query Match 83.2%; Score 15.8; DB 7; Length 263;
 Best Local Similarity 89.5%; Pred. No. 3.3e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTTCGG 19
 |||||
 Db 112 GAATGGAAGGCTTTCGG 94

RESULT 40

CF045077
 LOCUS
 DEFINITION CF045077 Zea mays cDNA clone QJC8a11, mRNA sequence.
 ACCESSION
 VERSION CF045077.1 GI:32940258

KEYWORDS

SOURCE EST.

Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Genoplatte
 Genoplatte
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplatte' (http://www.genoplatte.com
 and http://genoplatte-info.infobiogen.fr).

FEATURES

source

1..267

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="F2"

/db_xref="taxon:4577"

/clone="QJC8a11"

/tissue_type="cell lignification part of the 6th leaf"

/clone_lib="QJC"

ORIGIN

Query Match 83.2%; Score 15.8; DB 5; Length 267;
 Best Local Similarity 89.5%; Pred. No. 3.3e+03;

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

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FEATURES
  source
    1..279
      /location/Qualifiers
        /organism="Mus musculus"
        /mol_type="mRNA"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="D930045D23"
        /sex="mixed"
        /tissue_type="head"
        /dev_stage="15 days embryo"
        /lab_host="DH10B"
        /clone_lib="RIKEN full-length enriched, 15 days embryo
head"
        /notes="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'
GAGAGAGAGATTCTCAGTTAATTAATATCCCCCCCCC 3']. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I"
ORIGIN
  Query Match      83.2%; Score 15.8; DB 7; Length 279;
  Best Local Similarity 89.5%; Pred. No. 3.3e+03;
  Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

  QY      1 GAACGGAAGGCGCTTTTCGG 19
          |||||
  Db      231 GAACGGAATGCTTTCAG 213

RESULT 43
LOCUS      CF044432
DEFINITION CFJ29g07.yg QCJ Zea mays cDNA clone QCJ29g07, mRNA sequence.
ACCESSION CF044432
VERSION    CF044432.1 GI:32939613
KEYWORDS   EST.
SOURCE     Zea mays
ORGANISM   Zea mays
REFERENCE   1 (bases 1 to 288)
AUTHORS    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
JOURNAL    clade; Panicoideae; Andropogoneae; Zea.
COMMENT    Genoplante.
            Genoplante, a major partnership french program in plant genomics
            Unpublished (2003)
            Contact: Genoplante
            Genoplante
            93, rue Henri Rochefort 91025 EVRY CEDEX France
            Tel: 33 1 69 47 54 00
            Fax: 33 1 69 47 54 10
            This sequence has been generated in the framework of the french
            plant genomics programme 'Genoplante' (http://www.genoplante.com
            and http://genoplante-info.infobiogen.fr).
FEATURES
  source
    1..288
      /location/Qualifiers
        /organism="Zea mays"
        /mol_type="mRNA"
        /cultivar="F2"
        /db_xref="taxon:4577"
        /clone="QCJ29g07"

/issue_type="cell lignification part of the 6th leaf"
/clone_lib="QCJ"

ORIGIN
  Query Match      83.2%; Score 15.8; DB 5; Length 288;
  Best Local Similarity 89.5%; Pred. No. 3.3e+03;
  Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

  QY      1 GAACGGAAGGCGCTTTTCGG 19
          |||||
  Db      209 GAACCGAAGGCGCTTCGG 227

RESULT 44
LOCUS      CB710003
DEFINITION AMGNNUC.NRDG1-00123-A7-A nrdg1 (10855) Rattus norvegicus cDNA clone
nrdg1-00123-a7 5', mRNA sequence.
ACCESSION CB710003
VERSION    CB710003.1 GI:29767151
KEYWORDS   EST.
SOURCE     Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridea; Muridae; Murinae; Rattus.
            1 (bases 1 to 292)
            Angen EST Program.
            Angen Rat EST Program
            Unpublished (2003)
            Contact: Dan Fitzpatrick
            Angen, Inc
            One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
            Tel: 805 447-4881
            Plate: 00123 row: a column: 7.
FEATURES
  source
    1..292
      /location/Qualifiers
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        /mol_type="mRNA"
        /db_xref="taxon:10116"
        /clone="nrdg1-00123-a7"
        /tissue_type="Dorsal Root Ganglia"
        /clone_lib="nrdg1 (10855)"
        /notes="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; rat
dorsal root ganglia"

ORIGIN
  Query Match      83.2%; Score 15.8; DB 4; Length 292;
  Best Local Similarity 89.5%; Pred. No. 3.4e+03;
  Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

  QY      1 GAACGGAAGGCGCTTTTCGG 19
          |||||
  Db      137 GAACGGAAGGCGCTTCGG 155

RESULT 45
LOCUS      CC939630/c
DEFINITION ZMMBBb0239D20.r ZMMBBb Zea mays genomic clone ZMMBBb0239D20 3',
genomic survey sequence.
ACCESSION CC939630
VERSION    CC939630.1 GI:33625477
KEYWORDS   GSS.
SOURCE     Zea mays
ORGANISM   Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
            1 (bases 1 to 299)
            Yu, Y., Kim, H.R., Hatfield, J., Soderlund, C., Bharti, A.K., Messing, J.
            and Wing, R.
            Sequencing of the maize genome

FEATURES
  source
    1..288
      /location/Qualifiers
        /organism="Zea mays"
        /mol_type="mRNA"
        /cultivar="F2"
        /db_xref="taxon:4577"
        /clone="QCJ29g07"
```

JOURNAL COMMENT
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: T7
BACKWARD: M13r
Plate: 0239 row: D column: 20
Seq primer: M13r
Class: BAC ends.

FEATURES
source
Location/Qualifiers
1..299
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/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZM5BB0239D20"
/lab_host="DH10B"
/notes="Vector: pBelobAC11; Site 1: HindIII; Site 2: HindIII; Zea mays L. ssp. mays"

ORIGIN
Query Match 83.2%; Score 15.8; DB 12; Length 299;
Best Local Similarity 89.5%; Pred. No. 3.4e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GAACGGAAGGCGCTTCGG 19
|||||
Db 45 GAACGGAAGGCGCTTCGG 27

RESULT 46
BZ866870
LOCUS
DEFINITION
BZ866870 302 bp DNA linear GSS 18-MAR-2003
CH240_248M13.TJ CHORI-240 Bos taurus genomic clone CH240_248M13,
genomic survey sequence.
ACCESSION
BZ866870 1 GI:29094275
VERSION
GSS.
KEYWORDS
Bos taurus (cattle)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 302)
Zhao,S., Shetty,J., Shatsman,S., Teegaye,G., Geer,K.,
Shvartsbeyn,A., Gebregiorgis,E., Chen,D., Riggs,F., de Jong,P.,
Crawford,A.M. and McEwan,J.C.
Bovine BAC End Sequences from Library CHORI-240
Unpublished (2003)
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the bovine BAC library CHORI-240
(<http://www.chori.org/bacpac/bovine240.htm>). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(<http://www.chori.org/bacpac/ordering/information.htm>). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by AgResearch Ltd., New Zealand and The
Institute of Genomic Research (TIGR), USA.
Plate: 248 row: M column: 13
Seq primer: SP6

Class: BAC ends.
Location/Qualifiers
1..302
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/cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
Hereford bull Ll Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN
Query Match 83.2%; Score 15.8; DB 12; Length 302;
Best Local Similarity 89.5%; Pred. No. 3.4e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GAACGGAAGGCGCTTCGG 19
|||||
Db 219 GAACGGAAGGCGCTCACGG 237

RESULT 47
BF451770
LOCUS
DEFINITION
BF451770 308 bp mRNA linear EST 29-DEC-2000
uz79a11.y1 NCI_CGAP Lu29 Mus musculus cDNA clone IMAGE:3675260 5',
similar to TR:Q9UDN0 Q9UDN0 SIMILAR TO COCH-5B2. ;, mRNA sequence.
ACCESSION
BF451770 1 GI:11517939
VERSION
EST.
KEYWORDS
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 308)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
MGI:14336028
Seq primer: -40RP from Gibco
High quality sequence stop: 295.

FEATURES
source
Location/Qualifiers
1..308
/organism="Mus musculus"
/mol_type="mRNA"
/strain="Czech II"
/db_xref="taxon:10090"
/clone="IMAGE:3675260"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 83.2%; Score 15.9; DB 7; Length 308;
 Best Local Similarity 89.5%; Pred. No. 3.4e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCGCTTCCGG 19
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 Db 239 GAACGGAAAGCGCTTCCGG 257
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AV304782 316 bp mRNA linear EST 10-NOV-1999
 AV304782 RIKEN full-length enriched, 8 days embryo Mus musculus
 cDNA clone 5730523G20 3' similar to AB000467 Homo sapiens mRNA,
 mRNA sequence.

ACCESSION AV304782.1 GI:6337296
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 316)

REFERENCE
 KONNO, H., AIZAWA, K., AKAHIRA, S., AKIYAMA, J., CARNINCI, P., ENDO, T.,
 FUKUDA, S., FUKUNISHI, Y., HARA, A., HAYATSU, N., HIROZANE, T., HORI, F.,
 ISHII, Y., ISHIKAWA, T., ITOH, M., IZAWA, M., KADOTA, K., KAGAWA, I.,
 KAI, C., KAWAI, J., KIKUCHI, N., KOJIMA, Y., KOYA, S., KUSAKABE, M.,
 MATSUYAMA, T., MIKI, R., MIZUNO, Y., NAKAMURA, M., ODA, H., OKAZAKI, Y.,
 OWA, C., OZAWA, Y., SAIJO, H., SANO, M., SATO, K., SHIBATA, K.,
 SHIBATA, Y., SHIGEMOTO, Y., SHIRAKI, T., SOGABE, Y., SUGAHARA, Y.,
 SUZUKI, H., SUZUKI, H., TAKAHASHI, F., TATENO, M., TOMINAGA, N.,
 TEUNODA, Y., WACHIKI, A., WATANABE, S., YAMAMURA, T., YASUNISHI, A.,
 YOKOTA, T., YOSHIOKI, A., YOSHINO, M., MURAMATSU, M. and HAYASHIZAKI, Y.,
 RIKEN Mouse ESTs (Konno, H., et al. 1999)
 Unpublished (1999)

TITLE RIKEN Mouse ESTs (Konno, H., et al. 1999)
 JOURNAL Contact: Yoshihide Hayashizaki
 COMMENT Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
 Sasaki, N., Izawa, M., Watahiki, M., Ozawa, K., Tanaka, T., Yoneda, Y.,
 Matsuura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and
 Hayashizaki, Y.
 Transcriptional sequencing: A method for DNA sequencing using RNA
 polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
 Itoh, M., Ktsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,
 Okazaki, Y. and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for
 further details.

FEATURES
 source Location/Qualifiers
 1. 316
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="5730523G20"
 /sex="mixed"
 /dev_stage="8 days embryo"
 /lab_host="DH10B"
 /clone_lib="RIKEN full-length enriched, 8 days embryo"
 /note="Site 1: Sali; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pW42 (G14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 83.2%; Score 15.8; DB 11; Length 325;
Best Local Similarity 89.5%; Pred. No. 3.4e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTCGG 19
|||||
Db 262 GAACGGAAGGCGCTTCGG 280

RESULT 50

BY343361/c

LOCUS BY343361 RIKEN full-length enriched, whole joints Mus musculus cDNA clone L230045E11 5', mRNA sequence. EST 12-DEC-2002

ACCESSION BY343361
VERSION BY343361.1 GI:26572849
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 331)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Osato, R., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Brad, D., Brusci, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawai, H., Kawasawa, Y., Kedzierzki, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Perlea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kigawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

TITLE

Nature 420, 563-573 (2002)

JOURNAL

PUBLISHED

COMMENT

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Vassilis Aidinis (Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES

source

Location/Qualifiers
1..331
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="L230045E11"
/tissue_type="whole joints"
/clone_fib="RIKEN full-length enriched, whole joints"

ORIGIN

Query Match 83.2%; Score 15.8; DB 4; Length 331;
Best Local Similarity 89.5%; Pred. No. 3.4e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTCGG 19

|||||

Db 55 GAATGGAGAGGCGCTTCGG 37

RESULT 51

BY335795/c

LOCUS

DEFINITION

BY335795 RIKEN full-length enriched, synovial fibroblasts Mus

musculus cDNA clone L130045U21 5', mRNA sequence.

BY335795

VERSION BY335795.1 GI:26530055

EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 335)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaide, I., Osato, R., Saito, R., Suzuki, H., Yamanaka, I.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,

Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,

Batalov, S., Beisel, K. W., Blake, J. A., Brad, D., Brusci, V.,

Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N.,
Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suto,K.H., Tagawa,A., Takahashi,F., Takaku-Akaira,S.,
Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
2001)

TITLE

JOURNAL

COMMENT

Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9226
Fax: 81-45-503-9216
Email: genome-res@gscc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Itoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
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sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
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Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.

e mouse tissues.

FEATURES

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   Genomic Sciences Center and Genome Science Laboratory in
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   contributed to prepare mouse tissues. 1st strand cDNA was
   primed with a primer [5'
   GAGAGAGAGCGCGCGCACTCGAGTTTTTTTTTTTTTTVN 3'], cDNA was
   prepared by using trehalose thermo-activated reverse
   transcriptase and subsequently enriched for full-length by
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   primer adapter of sequence [5'
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   cDNA was cleaved with XhoI and SstI."
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LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

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Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
Shimobach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
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Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
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Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
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Analysis of the mouse transcriptome based on functional annotation
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Nature 420, 563-573 (2002)

TITLE

JOURNAL

PUBMED

COMMENT

12456851
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to

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<p>Encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)</p> <p>cDNA library was prepared and sequenced in Mouse Genome Encyclopedic Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues</p> <p>Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose</p>				
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1 (bases 1 to 369)				
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,				
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12466851				
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Sciences Center (GSC), Yokohama Institute				
The Institute of Physical and Chemical Research (RIKEN)				
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan				
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The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
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Trust/MRC building Addenbrookes Hospital Cambridge) whose
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further details.

FEATURES

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ORIGIN
Query Match      83.2%; Score 15.8; DB 4; Length 369;
Best Local Similarity 89.5%; Pred.No. 3.5e+03;
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ACCESSION	
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SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	

EST 10-DEC-2002
linear mRNA
370 bp
RIKEN full-length enriched, activated spleen Mus musculus
cDNA clone F830230123 5', mRNA sequence.

BY222901	GI:26404004
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Mus musculus	
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Mammalia;	Eutheria; Euarchontoglires; Glires; Rodentia;
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	FEATURES	SOURCE
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8.	Easy to Fold & Store	Malaysia
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Query Match 83.2%; Score 15.8; DB 4; Length 370;
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Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DEFINITION

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VERSION

KEYWORDS

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Mus musculus

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REFERENCE

AUTHORS

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierzki, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J. Z., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wyszynski, B., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE

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JOURNAL

PUBLISHED

Nature 420, 563-573 (2002)

CONTACT: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

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Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC Building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

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FEATURES

Location/Qualifiers

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Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCTTTTCGG 19
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RESULT 60

AA652906

LOCUS

DEFINITION

AA652906.1 GI:25845558

EST.

SOURCE

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ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 379)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuquai, M.D., Michael Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: David B. Krizman, Ph.D.

cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 705 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 1.

FEATURES

Location/Qualifiers

1..379

/organism="Homo sapiens"

/mol_type="mRNA"

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/notes="vector: pAMP10; Site 1: NotI; Site 2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from
5,000-10,000 microdissected preneoplastic cells
histologically-determined to be prostatic intraepithelial
neoplasia 2 (PIN2) cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."

ORIGIN
Query Match      83.2%; Score 15.8; DB 1; Length 379;
Best Local Similarity 89.5%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCCTTCGG 19
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RESULT 61
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DEFINITION ur58d11.y1 NCI CGAP Mam3 Mus musculus cDNA clone IMAGE:3154485 5'
similar to TR:Q26422 Q26422 FACTOR C. [1] ;, mRNA sequence.
ACCESSION  AW762692
VERSION     AW762692.1 GI:7694623
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SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
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            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 379)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml

MGI:1057241
Seq primer: -40RP from Gibco
High quality sequence stop: 378.
Location/Qualifiers
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Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
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ORIGIN

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Query Match      83.2%; Score 15.8; DB 7; Length 379;
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RESULT 62

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BY280232/c
LOCUS      384 bp mRNA linear EST 11-DEC-2002
DEFINITION BY280232 RIKEN full-length enriched, visual cortex Mus musculus
cDNA clone K430345N21 5', mRNA sequence.
ACCESSION  BY280232
VERSION     BY280232.1 GI:26470569
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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REFERENCE

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1 (bases 1 to 384)
Okazaki, F., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamana, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V.,
Ciothia, C., Corbani, L. E., Cousins, S., Dalia, E., Dragani, T. A.,
Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
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Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
Kawai, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,
Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,
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Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kigawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
```

TITLE

```

JOURNAL     Nature 420, 563-573 (2002)
PUBMED      12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-resgsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
            Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
            Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
            Ono, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
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FEATURES

source

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/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
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/clone_lib="NCI_CGAP Mam3"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
```

*Tissues were provided by Michela Fagiolini and Takao K. Hensch (Laboratory for Neuronal Circuit Development Brain Science Institute RIKEN 2-1 Hiroswa, Wako-shi, Saitama 351-0198 Japan) whose assistance we gratefully acknowledge. Please visit our web site (<http://genome.qsc.riken.co.jp>) for further details.

Genomic Sciences Center and Genome Science Laboratory in RIKEN.
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Email: genome_res@gs.c.riken.jp, URL: <http://genome.gs.c.riken.jp/>

Db 115 GAACGGAACGCCCTTCGG 131

RESULT 65
BY268029/c
LOCUS BY268029 RIKEN full-length enriched, visual cortex Mus musculus
DEFINITION cDNA clone K430020M20 5', mRNA sequence.
ACCESSION BY268029
VERSION BY268029.1 GI:26458236
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 388)
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nkado, I., Otsu, N., Sato, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierzki, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Tasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBLISHED 12466851
COMMENT Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-resseqc.riken.jp, URL: http://genome.gsc.riken.jp/
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Tissues were provided by Michela Fagiolini and Takao K. Hensch (Laboratory for Neuronal Circuit Development Brain Science Institute RIKEN 2-1 Hirosewa, Wako-shi, Saitama 351-0198 Japan) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES
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QY 1 GAACGGAAGGCGCTTCGG 19
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 Db 58 GAATGGAGAGCGCTTCGG 40

RESULT 66
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LOCUS DT906610 Hematopoietic stem cells Mus musculus cDNA, mRNA
DEFINITION S25-20013 Hematopoietic stem cells Mus musculus cDNA, mRNA
ACCESSION DT906610
VERSION DT906610.1 GI:75887096
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
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REFERENCE 1 (bases 1 to 388)
AUTHORS Pritsker, M., Doniger, T. T., Kramer, L. C., Westcot, S. E. and Lemischka, I. R.
TITLE Diversification of Stem Cell Molecular Repertoire by Alternative Splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. (2005) In press
COMMENT Contact: Pritsker M
 Lab of Thor Lemischka, Department of Molecular Biology
 Princeton University
 Princeton, NJ 08544, USA
 Tel: 609 258 5657
 Fax: 609 258 1704
 Email: pritsker@molbio.princeton.edu.

FEATURES
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 Best Local Similarity 89.5%; Pred. No. 3.5e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 Db 58 GAATGGAGAGCGCTTCGG 40

Db	115 GAACGAAACGCCTTCGG 133	
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DEFINITION	CDNA clone F930036019 5', mRNA sequence.	
ACCESSION	BY234732	
VERSION	BY234732.1	GI:26415842
KEYWORDS	EST.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS	1 (bases 1 to 392)	
	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanpin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Brad, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, J.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Saitana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wyshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Haehizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.	
TITLE	Analysis of the mouse transcriptome based on functional annotation	
JOURNAL	Of 60,770 full-length cDNAs	
PUBMED	Nature 420, 563-573 (2002)	
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suenhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/ Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)	
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	Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
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DEFINITION	AMGNNUC:SRPB2-00154-F5-A srpb2 (10220) Rattus norvegicus CDNA clone srpb2-00154-f5 5', mRNA sequence.	
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VERSION	CB811973.1	GI:29935343
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SOURCE	Rattus norvegicus (Norway rat)	
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REFERENCE	1 (bases 1 to 404)	
AUTHORS	Amgen EST Program	
TITLE	Amgen Rat EST Program	
JOURNAL	Unpublished (2003)	
COMMENT	Contact: Dan Fitzpatrick Amgen, Inc One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA Tel: 805 447-4881 Plate: 00154 row: f column: 5.	
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	/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; rat prostate normalized double selected poly(A+) mRNA size fraction > 1 kb"	
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	Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	1 GAACGAAAGGCGCTTCGG 19	
DB	106 GAACGAAAGGCGCTTCGG 124	

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Kirk W. Beisel (Boys Town National Research Hospital 555 North 30th Street Omaha, NE 68131 USA) whose assistance we gratefully acknowledge. Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

Location/Qualifiers
1. .392
/organism="Mus musculus"
/mol_type="mRNA"
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/clone_lib="RIKEN full-length enriched, adult inner ear"

Query Match 83.2%; Score 15.8; DB 4; Length 392;
Best Local Similarity 89.5%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGAAAGGCGCTTCGG 19
DB 52 GAATGGAGGCGCTTCGG 34

RESULT 68

CB811973

LOCUS

DEFINITION

AMGNNUC:SRPB2-00154-F5-A srpb2 (10220) Rattus norvegicus CDNA clone

srpb2-00154-f5 5', mRNA sequence.

ACCESSION

CB811973

VERSION

CB811973.1 GI:29935343

KEYWORDS

EST.

SOURCE

Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE

1 (bases 1 to 404)

AUTHORS

Amgen EST Program

TITLE

Amgen Rat EST Program

JOURNAL

Unpublished (2003)

COMMENT

Contact: Dan Fitzpatrick

Amgen, Inc

One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA

Tel: 805 447-4881

Plate: 00154 row: f column: 5.

Location/Qualifiers

1. .404

/organism="Rattus norvegicus"

/mol_type="mRNA"

/db_xref="taxon:10116"

/clone="srpb2-00154-f5"

/tissue_type="prostate tissue"

/clone_lib="srpb2 (10220)"

/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; rat

prostate normalized double selected poly(A+) mRNA size

fraction > 1 kb"

ORIGIN

Query Match 83.2%; Score 15.8; DB 4; Length 404;

Best Local Similarity 89.5%; Pred. No. 3.5e+03;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGAAAGGCGCTTCGG 19

DB 106 GAACGAAAGGCGCTTCGG 124

```

RESULT 69
BY268165/c
LOCUS
DEFINITION
  BY268165 RIKEN full-length enriched, visual cortex Mus musculus
  cDNA clone K430022A21 5', mRNA sequence.
ACCESSION
  BY268165
VERSION
  BY268165.1 GI:26458372
KEYWORDS
  EST.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
  1 (bases 1 to 411)
REFERENCE
  Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
  Nikaido, I., Oeato, N., Saito, R., Suzuki, H., Yamanaka, I.,
  Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
  Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
  Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
  Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
  Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
  Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
  Gariboldi, M., Glissi, C., Godzik, A., Gough, J., Grimmond, S.,
  Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
  Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
  Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
  Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
  Numata, K., Okido, T., Pavan, W.J., Pertea, G., Resole, G.,
  Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
  Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
  Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
  Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
  Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y.,
  Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
  Yang, J., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
  Hayashizaki, Y., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
  Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
  Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
  Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
  Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
  Rogers, J., Birney, E. and Hayashizaki, Y.
  Analysis of the mouse transcriptome based on functional annotation
  of 60,770 full-length cDNAs
  Nature 420, 563-573 (2002)
  12466851
  Contact: Yoshihide Hayashizaki
  Laboratory for Genome Exploration Research Group, RIKEN Genomic
  Sciences Center (GSC), Yokohama Institute
  The Institute of Physical and Chemical Research (RIKEN)
  1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
  Tel: 81-45-503-9222
  Fax: 81-45-503-9216
  Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
  Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
  Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
  Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
  Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
  Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
  Hayashizaki, Y. Direct Submission
  Computational Analysis of Full-length Mouse cDNAs Compared with
  Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
  Normalization and subtraction of cap-trapper-selected cDNAs to
  prepare full-length cDNA libraries for rapid discovery of new
  genes. Genome Res. 10 (10), 1617-1630 (2000)
  RIKEN integrated sequence analysis (RISA) system--384-format
  sequencing pipeline with 384 multicapillary sequencer. Genome Res.
  10 (11), 1757-1771 (2000)
  Computer-based methods for the mouse full-length cDNA
  encyclopedia: real-time sequence clustering for construction of a
  nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
  cDNA library was prepared and sequenced in Mouse Genome
  Encyclopedia Project of Genome Exploration Research Group in Riken

```

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Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Michela Pagiolini and Takao K. Hensch (
Laboratory for Neuronal Circuit Development Brain Science Institute
RIKEN 2-1 Hirose, Wako-shi, Saitama 351-0198 Japan ) whose
assistance we gratefully acknowledge. Please visit our web site
(http://genome.gsc.riken.go.jp) for further details.
FEATURES
  Location/Qualifiers
    source
      1..411
      /organism="Mus musculus"
      /mol_type="mRNA"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="K430022A21"
      /tissue_type="visual cortex"
      /clone_lib="RIKEN full-length enriched, visual cortex"
ORIGIN
  Query Match      83.2%; Score 15.8; DB 4; Length 411;
  Best Local Similarity 89.5%; Pred. No. 3.5e+03;
  Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
  QY 1 GAACGGAAGGCGCTTTTCGG 19
  DB 58 GAATGGAGAGCGCTTTTCGG 40
  RESULT 70
  BM654471
  LOCUS
  DEFINITION
    BM654471 417 bp mRNA linear EST 26-FEB-2002
    17000687383524 A.Gam.ad.cdna1 Anopheles gambiae cDNA clone
    19600449670164 5', mRNA sequence.
  ACCESSION
    BM654471
  VERSION
    BM654471.1 GI:18953982
  KEYWORDS
  SOURCE
    Anopheles gambiae (African malaria mosquito)
  ORGANISM
    Anopheles gambiae
    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
    Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
    Culicidae; Anophelinae; Anopheles.
  REFERENCE
    1 (bases 1 to 417)
    Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L.,
    Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
    Celera Anopheles gambiae EST project
    Unpublished (2002)
    Contact: Holt R.A.
    Celera Genomics
    45 W. Gude Dr., Rockville, MD 20850, USA
    Tel: 2404533151
    Fax: 2404534580
    Email: Holtra@celera.com
    Plate: NU010049WN row: N column: 18
    Seq primer: M13 Reverse.
    Location/Qualifiers
      1..417
      /organism="Anopheles gambiae"
      /mol_type="mRNA"
      /strain="RSP-ST (Reduced ausc. to Permethrin - std.
      chromosome)"
      /db_xref="taxon:7165"
      /clone="19600449670164"
      /dev_stage="Adult"
      /lab_host="DH10b"
      /clone_lib="A.Gam.ad.cdna1"
      /note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
      adult mosquitoes (mixed sex) frozen on liquid nitrogen.
      cDNA inserts >500 bp cloned directionally into pSport 1.
      Not 1 site is 3'. Clones available through the Malaria
      Research and Reference Reagent Resource Center
      (www.malaria.mr4.org)."
  ORIGIN

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CB758843
LOCUS      CB758843      434 bp      mRNA      linear      EST 16-MAY-2003
DEFINITION AMGNNUC:NRW3-00049-A9-A white adipose tiss (10469) Rattus
            norvegicus cDNA clone nrwa3-00049-a9 5', mRNA sequence.
ACCESSION  CB758843
VERSION     CB758843.1  GI:29847234
KEYWORDS   EST.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM    Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidae; Muridae; Murinae; Rattus.
            1 (bases 1 to 434)
REFERENCE   Angen EST Program.
AUTHORS     Angen Rat EST Program
TITLE       Unpublished (2003)
JOURNAL     Contact: Dan Fitzpatrick
COMMENT     Angen, Inc
            One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
            Tel: 805 447-4881
            Plate: 00049 row: a column: 9.
FEATURES   Location/Qualifiers
            1..434
            /organism="Rattus norvegicus"
            /mol_type="mRNA"
            /db_xref="taxon:10116"
            /clone="nrwa3-00049-a9"
            /tissue_type="adipose tiss"
            /clone_lib="white adipose tiss (10469)"
            /note="vector: pSPORT1; Site_1: SalI; Site_2: NotI; white
            adipose tiss adult female Wistar rats, >250 grams"
ORIGIN
Query Match      83.2%; Score 15.8; DB 4; Length 434;
Best Local Similarity 89.5%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGCCTTCGG 19
    |||||
Db 117 GAACGGAAAGCCTTCGG 135

RESULT 74
CO651130
LOCUS      CO651130      441 bp      mRNA      linear      EST 01-MAY-2005
DEFINITION ccp23_D04 08 Chondrus crispus protoplasts Zap Express Library
            Chondrus crispus cDNA clone ccp23 D04 08 5' similar to orf [Ricin
            communis] with an e-value of 5,00E-23, mRNA sequence.
ACCESSION  CO651130
VERSION     CO651130.1  GI:62994086
KEYWORDS   EST.
SOURCE      Chondrus crispus (carrageen)
ORGANISM    Chondrus crispus
            Eukaryota; Rhodophyta; Florideophyceae; Gigartinales;
            Gigartiniaceae; Chondrus.
            1 (bases 1 to 441)
REFERENCE   Collen, J., Roeder, V., Rousvoal, S., Collin, O., Kloareg, B. and
AUTHORS     Boyen, C.
TITLE       An expressed sequence tag analysis of thallus and regenerating
JOURNAL     protoplasts of Chondrus crispus (Gigartinales, Rhodophyceae)
COMMENT     Unpublished (2004)
            Contact: Collen J.
            CNRS UMR 7139 Vegetaux marins et biomolécules
            Station Biologique de Roscoff
            Place Georges Teissier, 29680 ROSCOFF, FRANCE
            Tel: 33 2 98 29 23 23
            Fax: 33 2 98 29 23 24
            Email: collen-roscoff.fr
            http://www.sb-roscoff.fr/chondrus.html
            PCR Primers
            FORWARD: Universal T3
            BACKWARD: Universal T7
            Seq primer: AATTAAACCCCTCACTAAAGG (T3)

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FEATURES   High quality sequence stop: 441.
            Location/Qualifiers
            1..441
            /organism="Chondrus crispus"
            /mol_type="mRNA"
            /db_xref="taxon:2769"
            /clone="ccp23_D04_08"
            /cell_type="protoplasts"
            /clone_lib="Chondrus crispus protoplasts Zap Express
            Library"
            /note="Vector: pbK-CMV; Site_1: Eco RI; Site_2: XbaI"
ORIGIN
Query Match      83.2%; Score 15.8; DB 8; Length 441;
Best Local Similarity 89.5%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGCCTTCGG 19
    |||||
Db 372 GAACGGAAAGCCTTCGG 390

RESULT 75
AI225711/c
LOCUS      AI225711      449 bp      mRNA      linear      EST 29-OCT-1998
DEFINITION uf10f05.y1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone
            IMAGE:1510977 5', mRNA sequence.
ACCESSION  AI225711
VERSION     AI225711.1  GI:3808764
KEYWORDS   EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidae; Muridae; Murinae; Mus.
            1 (bases 1 to 449)
REFERENCE   Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
AUTHORS     Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
            Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
            Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
            Waterston, R.
            The WashU-HMNI Mouse EST Project
            Unpublished (1996)
            Contact: Marra M/Mouse EST Project
            WashU-HMNI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:937829
            Seq primer: -40RP from Gibco
            High quality sequence stop: 441.
            Location/Qualifiers
            1..449
            /organism="Mus musculus"
            /mol_type="mRNA"
            /db_xref="taxon:10090"
            /clone="IMAGE:1510977"
            /sex="female (lactating)"
            /tissue_type="mammary gland"
            /lab_host="DH10B"
            /clone_lib="Soares mammary_gland_NMLMG"
            /note="Vector: pT73D-FacI; 1st strand cDNA was prepared
            from mammary gland tissue from a lactating female, and was
            then primed with a Not I - oligo(dT) primer.
            Double-stranded cDNA was ligated to Eco RI adaptors
            (Pharmacia), digested with Not I and cloned into the Not
            I and Eco RI sites of the modified pT7T3 vector. Library
            is normalized. Library was constructed by Bento Soares
            and M. Fatima Bonaldo."
FEATURES   source

```

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lucy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Septoo, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mousest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:923651
Seq primer: custom primer used
High quality sequence stop: 475.

FEATURES
source
1..487
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1450335"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME18S-FL3; Site 1: DraIII
(CACTGTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTCTTTTCTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTGGCTTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCGTCTTAAAGCTGG and 3' end
primer CGACCTGCAGCTCGAGCACA."

ORIGIN
Query Match 83.2%; Score 15.8; DB 1; Length 487;
Best Local Similarity 89.5%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTTCGG 19
|||||
Db 25 GAATGGAGGCGCTTTCGG 7

ORIGIN
Query Match 83.2%; Score 15.8; DB 1; Length 487;
Best Local Similarity 89.5%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTTCGG 19
|||||
Db 25 GAATGGAGGCGCTTTCGG 7

RESULT 79
BM649929
LOCUS
DEFINITION
17000687370141 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
19600449640353 5', mRNA sequence.
BM649929
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Anopheles gambiae (African malaria mosquito)
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Culicidae; Anophelinae; Anopheles.
1 (bases 1 to 489)
Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L.,
Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
Celera Genomics
Unpublished (2002)
Contact: Holt R.A.
45 w. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580

Email: Holtra@celera.com
Plate: NU01004A9Q row: D column: 15
Seq primer: M13 Reverse.

FEATURES
source
1..489
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std.
chromosome)"
/db_xref="taxon:7165"
/clone="19600449640353"
/dev_stage="Adult"
/lab_host="DH10B"
/clone_lib="A.Gam.ad.cDNA1"
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
adult mosquitoes (mixed sex) frozen on liquid nitrogen.
cDNA inserts >500 bp cloned directionally into pSport 1.
Not 1 site is 3'. Clones available through the Malaria
Research and Reference Reagent Resource Center
(www.malaria.mr4.org)."

ORIGIN
Query Match 83.2%; Score 15.8; DB 3; Length 489;
Best Local Similarity 89.5%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTTCGG 19
|||||
Db 36 GAACGGAAGTACTTTCGG 54

RESULT 80
BM623849
LOCUS
DEFINITION
17000687489874 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
19600449655267 5', mRNA sequence.
BM623849
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Anopheles gambiae (African malaria mosquito)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Culicidae; Anophelinae; Anopheles.
1 (bases 1 to 492)
Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L.,
Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
Celera Genomics
Unpublished (2002)
Contact: Holt R.A.
45 w. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: Holtra@celera.com
Plate: NU01004A9Q row: B column: 01
Seq primer: M13 Reverse.

FEATURES
source
1..492
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std.
chromosome)"
/db_xref="taxon:7165"
/clone="19600449655267"
/dev_stage="Adult"
/lab_host="DH10B"
/clone_lib="A.Gam.ad.cDNA1"
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
adult mosquitoes (mixed sex) frozen on liquid nitrogen.
cDNA inserts >500 bp cloned directionally into pSport 1.
Not 1 site is 3'. Clones available through the Malaria
Research and Reference Reagent Resource Center

(www.malaria.mr4.org)."

ORIGIN

Query Match 83.2%; Score 15.8; DB 3; Length 492;
 Best Local Similarity 89.5%; Pred. No. 3.6e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTTTCGG 19

Db 285 GAACGGAAGTACTTTTCGG 303

RESULT 81

AW090720/c

LOCUS xc95e03.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2592028 3',
 DEFINITION mRNA sequence.

ACCESSION AW090720

VERSION AW090720.1 GI:6048064

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE 1 (bases 1 to 495)

NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS National Cancer Institute / National Institute of Neurological

TITLE Disorders and Stroke, Brain Tumor Genome Anatomy Project

(CGAP/STGAP), Tumor Gene Index

Unpublished (1998)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rc@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco

High quality sequence stop: 426.

FEATURES

source

1..495
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2592028"
 /tissue_type="tumor, 5 pooled (see description)"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Brn35"
 /note="Organ: Brain; Vector: pCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dn.
 Average insert size 1.33 Kb. Tumor types include:
 meningioma, oligodendroglioma, astrocytoma (grade II),
 medulloblastoma, astrocytoma (grade IV). Life Technologies
 catalog #: 11544-012"

ORIGIN

Query Match 83.2%; Score 15.8; DB 7; Length 495;
 Best Local Similarity 89.5%; Pred. No. 3.6e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTTTCGG 19

Db 249 GAACGGAAGGCTTTTCGG 231

RESULT 82

BF362878/c

LOCUS BF362878 517 bp mRNA linear EST 24-NOV-2000
 DEFINITION MR0-NN0087-260600-017-f09 NN0087 Homo sapiens cDNA, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homnidae; Homo.

1 (bases 1 to 517)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.A.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

10737800

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR0&t2=MR0-NN0087-260600-017-f09&t3=2000-06-26&t4=1>)

Seq primer: puc 18 forward

High quality sequence start: 5

High quality sequence stop: 33.

Location/Qualifiers

1..517

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="NN0087"

/note="Organ: nervous normal; Vector: puc18; Site 1: SmaI;

Site 2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the puc 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

0;

Qy 1 GAACGGAAGGCTTTTCGG 19

Db 394 GAACGGAAGGCTTTTCGG 376

RESULT 83

CO651195

LOCUS

DEFINITION

ccp24_E05_09 Chondrus crispus protoplasts Zap Express Library

Chondrus crispus cDNA clone ccp24_E05_09 5' similar to orf [Ricinus

communis] with an e-value of 5.00E-23, mRNA sequence.

CO651195

CO651195.1 GI:62994151

EST.

Chondrus crispus (carrageen)

Chondrus crispus

Eukaryota; Rhodophyta; Florideophyceae; Gigartinales;

Gigartinales; Chondrus.

REFERENCE 1 (bases 1 to 517)

AUTHORS Collen,J., Roeder,V., Rousvoal,S., Collin,O., Kloareg,B. and Boyen,C.

TITLE An expressed sequence tag analysis of thallus and regenerating protoplasts of *Chondrus crispus* (Gigartinales, Rhodophyceae)

JOURNAL Unpublished (2004)

COMMENT Contact: Collen J.
 CNRS UMR 7139 Vegetaux marins et biomolécules
 Station Biologique de Roscoff
 Place Georges Teissier, 29680 ROSCOFF, FRANCE
 Tel: 33 2 98 29 23 23
 Fax: 33 2 98 29 23 24
 Email: collen-roscoff.fr
<http://www.sbr-roscoff.fr/chondrus.html>

PCR Primers
 FORWARD: Universal T3
 BACKWARD: Universal T7
 Seq primer: AATTAAACCTCACTAAAGGG (T3)
 High quality sequence stop: 517.

FEATURES
 source
 1. .517
 /organism="Chondrus crispus"
 /mol_type="mRNA"
 /db_xref="taxon:2769"
 /clone="ccp24_E05_09"
 /cell_type="protoplasts"
 /clone_lib="Chondrus crispus protoplasts Zap Express Library"
 /note="vector: pbK-CMV; Site_1: Eco R1; Site_2: Xho1"

ORIGIN
 Query Match 83.2%; Score 15.8; DB 8; Length 517;
 Best Local Similarity 89.5%; Pred. No. 3.7e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGCCTTTCGG 19
 |||||
Db 365 GAACGGAAAGCCTTTCGG 383

RESULT 84
A1226747/c
LOCUS A1226747 519 bp mRNA linear EST 29-OCT-1998
DEFINITION U15B10.y1 Sugano mouse kidney mKia Mus musculus cDNA clone
IMAGE:1908091 5', mRNA sequence.

ACCESSION A1226747
VERSION A1226747.1 GI:3809800
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS 1 (bases 1 to 519)
 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:976287
 Seq primer: custom primer used
 High quality sequence stop: 516.
 Location/Qualifiers

source
 1. .519
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone="IMAGE:1908091"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="Sugano mouse kidney mKia"
 /note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII (CACTGTG); Site_2: DraIII (CACTGTG); 1st strand cDNA was primed with an oligo(dT) primer
 [ATGTGGCCTTTTITTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTGGCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGACACA."

ORIGIN
 Query Match 83.2%; Score 15.8; DB 1; Length 519;
 Best Local Similarity 89.5%; Pred. No. 3.7e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGCCTTTCGG 19
 |||||
Db 162 GAATGGAGAGCGCTTTCGG 144

RESULT 85
AA510135/c
LOCUS AA510135 522 bp mRNA linear EST 08-JUL-1997
DEFINITION VH57E02.r1 Soares mammary gland NbMMG Mus musculus cDNA clone
IMAGE:891098 5', mRNA sequence.

ACCESSION AA510135
VERSION AA510135.1 GI:2247989
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS 1 (bases 1 to 522)
 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:519058
 Seq primer: -28ml3 rev2 ET from Amersham
 High quality sequence stop: 494.
 Location/Qualifiers

FEATURES
 source
 1. .522
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"

AUTHORS Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L.,
 Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
TITLE Celera Anopheles gambiae EST project
JOURNAL Unpublished (2002)
COMMENT Contact: Holt R.A.
 Celera Genomics
 45 W. Gude Dr., Rockville, MD 20850, USA
 Tel: 2404533151
 Fax: 2404534580
 Email: HoltRA@celera.com
 Plate: NU01003CY0 row: B column: 20
 Seq primer: M13 Reverse.

FEATURES
 source
 Location/Qualifiers
 1..526

/organism="Anopheles gambiae"
 /mol_type="mRNA"
 /strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"
 /db_xref="taxon:7165"
 /clone="19600449640310"
 /dev_stage="Adult"
 /lab_host="DH10b"
 /clone_lib="A.Gam.ad.cdna1"
 /note="Vector: pSport1; Site_1: SalI; Site_2: NotI; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."

ORIGIN

Query Match 83.2%; Score 15.8; DB 3; Length 526;
 Best Local Similarity 89.5%; Pred. No. 3.7e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGCCTTTTCGG 19
 |||||
 Db 101 GAACGGAAAGTACTTTTCGG 119

RESULT 89
DB281202
LOCUS DB281202 UTERU3 Homo sapiens cDNA clone UTERU3008097 5', mRNA
DEFINITION sequence.
ACCESSION DB281202
VERSION DB281202.1 GI:83211312
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 537)
 Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Iehi,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,I., Nagai,K., Kikuchi,H., Nakai,K., Isogai,I. and Sugano,S.
TITLE Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes
JOURNAL Genome Res. 16 (1), 55-65 (2006)
PUBLISHED 16344560
COMMENT Contact: Takao Isogai
 FLJ Project (HRI Team)
 Helix Research Institute
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: flj-cdna@nifty.com
 NEDO human cDNA project (New Energy and Industrial Technology

FEATURES
 source
 Location/Qualifiers
 1..537

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UTERU3008097"
 /tissue_type="uterus"
 /clone_lib="UTERU3"
 /note="Vector: pME18SFL3".

ORIGIN

Query Match 83.2%; Score 15.8; DB 9; Length 537;
 Best Local Similarity 89.5%; Pred. No. 3.7e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGCCTTTTCGG 19
 |||||
 Db 519 GAATCGAAGGCTTTTCGG 537

RESULT 90

DB642702
LOCUS BX642702.1 GI:34477035
DEFINITION DKFZp781D1916 r1 781 (synonym: hlcc4) Homo sapiens cDNA clone
 DKFZp781D1916 5', mRNA sequence.
ACCESSION BX642702
VERSION BX642702.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 540)
 Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.
TITLE EST (Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS
 MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by BMFZ (Biomedical Research Center at the Heinrich-Heine-University, Duesseldorf/Germany) within the cDNA sequencing consortium of the German Genome Project. No si sequence available.
 This clone (DKFZp781D1916) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
 source
 Location/Qualifiers
 1..540

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZp781D1916"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="781 (synonym: hlcc4)"
 /note="Vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiIB; cDNA-collection"

ORIGIN

Query Match 83.2%; Score 15.8; DB 4; Length 540;
 Best Local Similarity 89.5%; Pred. No. 3.7e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGCCTTTTCGG 19

Db

|||||
506 GAATGGAAAGGCTTTTCGG 524

RESULT 91
AL699601
LOCUS
DEFINITION
AL699601.1 GI:19620141 linear EST 04-SEP-2003
DKFP686J07114_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFP686J07114_5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Koehler,K., Beyer,A., Mewes,W., Weil,B. and Wiemann,S.
EST (Koehler,K., Beyer,A., Mewes,H.W., Weil,B. and Wiemann,S.)
Unpublished (1999)
Contact: MIPS

MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charité,
Berlin/Germany) within the cDNA sequencing consortium of the German
Genome Project.
No sl sequence available.
This clone (DKFP686J07114) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1..551
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFP686J07114"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pTripEx2; Site_1: SfIIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN

Query Match 83.2%; Score 15.8; DB 1; Length 551;
Best Local Similarity 89.5%; Pred. No. 3.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCTTTCGG 19
|||||
497 GAATGGAAAGGCTTTTCGG 515

Db

RESULT 92
AI528048/c
LOCUS
DEFINITION
AI528048.1 GI:4442183 linear EST 18-MAR-1999
uj39d01.y1 Sugano mouse kidney mkia Mus musculus cDNA clone
IMAGE:1922305 5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
Waterston,R., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.

Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info:image.llnl.gov) for further information.
MGI:978597
Seq primer: custom primer used
High quality sequence stop: 463.
Location/Qualifiers
1..553
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1922305"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Sugano mouse kidney mkia"
/note="Organ: kidney; Vector: pME18S-FL3; Site 1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGCCCTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCACTGCG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCGTCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGACACA."

ORIGIN

Query Match 83.2%; Score 15.8; DB 1; Length 553;
Best Local Similarity 89.5%; Pred. No. 3.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCTTTCGG 19
|||||
108 GAATGGAGAGGCCTTTCGG 90

Db

RESULT 93
AI316240/c
LOCUS
DEFINITION
AI316240.1 GI:4031507 linear EST 17-DEC-1998
uj26f04.y1 Sugano mouse kidney mkia Mus musculus cDNA clone
IMAGE:1921087 5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.

The WashU-HMMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMMI Mouse EST Project

TITLE
JOURNAL
COMMENT

Query Match	83.2%;	Score 15.8;	DB 10;	Length 557;
Best Local Similarity	89.5%;	Pred. No. 3.7e+03;		
Matches 17: Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Lenischka, I.R.
Diversification of Stem Cell Molecular Repertoire by Alternative Splicing

TITLE
JOURNAL
COMMENT
Proc. Natl. Acad. Sci. U.S.A. (2005) In press
Contact: Pritsker M
Lab of Ihor Lemischka, Department of Molecular Biology
Princeton University
Princeton, NJ 08544, USA
Tel: 609 258 5657
Fax: 609 258 1704
Email: pritsker@molbio.princeton.edu.

FEATURES
source

```
1..567
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="Hematopoietic stem cells"
/cell_type="Hematopoietic stem cells"
/clone_lib="Hematopoietic stem cells"
/note="cDNA library was made from FACS-purified
hematopoietic stem cells"
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ORIGIN

Query Match 83.2%; Score 15.8; DB 10; Length 567;
Best Local Similarity 89.5%; Pred. No. 3.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCCTTCGG 19
|||||
Db 115 GAACGGAAGCCCTTCGG 133

RESULT 99

BM631920 568 bp mRNA linear EST 26-FEB-2002
LOCUS 17000687503458 A.Gam ad.cDNA1 Anopheles gambiae cDNA clone
DEFINITION 13600449625277 5', mRNA sequence.

ACCESSION BM631920
VERSION BM631920.1 GI:18931431
KEYWORDS EST.

SOURCE Anopheles gambiae (African malaria mosquito)

ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Anophelinae; Anopheles.

REFERENCE 1 (bases 1 to 568)

AUTHORS Holt R.A., Lin J.-J., Murphy S.D., Evans C.A., Kraft C.L.,

Charlab R., Collins F.H., Venter J.C. and Hoffman S.L.

Celera Genomics

Unpublished (2002)

TITLE Anopheles gambiae EST project

JOURNAL Contact: Holt R.A.

COMMENT Celera Genomics

45 W. Gude Dr., Rockville, MD 20850, USA

Tel: 2404533151

Fax: 2404534580

Email: HoltRA@celera.com

Plate: NU01004NEV row: P column: 11

Seq primer: M13 Reverse.

FEATURES
source

```
1..568
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std.
chromosome)"
/db_xref="taxon:7165"
/clone="19600449625277"
/dev_stage="Adult"
/lab_host="DH10b"
/clone_lib="A.Gam.ad.cDNA1"
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
adult mosquitoes (mixed sex) frozen on liquid nitrogen.
cDNA inserts >500 bp cloned directionally into pSport 1.
Not 1 site is 3'. Clones available through the Malaria
```

ORIGIN

Query Match 83.2%; Score 15.8; DB 3; Length 568;
Best Local Similarity 89.5%; Pred. No. 3.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCCTTCGG 19
|||||
Db 455 GAACGGAAGCTACTTCGG 473

RESULT 100

DA720663

LOCUS DA720663

DEFINITION DA720663 NT2RI3 Homo sapiens cDNA clone NT2RI3000855 5', mRNA

sequence.

ACCESSION DA720663

VERSION DA720663.1 GI:82366406

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE 1 (bases 1 to 575)

AUTHORS Kimura K., Wakamatsu A., Suzuki Y., Ota T., Nishikawa T.,

Yamashita R., Yamamoto J., Sekine M., Tsuritani K., Wakaguri H.,

Ishii S., Sugiyama T., Saito K., Isono Y., Irie R., Kushida N.,

Yoneyama T., Otsuka R., Kanda K., Yokoi T., Kondo H., Wagatsuma M.,

Murakawa K., Ishida S., Ishibashi T., Takahashi-Fujii A.,

Tanase T., Nagai K., Kikuchi H., Nakai K., Isogai T. and Sugano S.

Diversification of Transcriptional Modulation: Large-scale

Identification and Characterization of Putative Alternative

Promoters of Human Genes

Genome Res. 16 (1), 55-65 (2006)

JOURNAL 16344560

PUBMED Contact: Takao Isogai

COMMENT FLJ Project (HRI Team)

Helix Research Institute

2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: flj-cdna@nifty.com

NEDO human cDNA project (New Energy and Industrial Technology

Developmental Organization, Japan); cDNA library construction;

Helix Research Institute (HRI); 5'-end one pass sequencing; HRI,

Research Association for Biotechnology (RAB) and Biotechnology

Center, National Institute of Technology and Evaluation; 3'-end one

pass sequencing; RAB.

FEATURES Location/Qualifiers

1..575

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="NT2RI3000855"

/cell_type="teratocarcinoma"

/cell_line="NT2"

/clone_lib="NT2RI3"

/note="Vector: pME18SFLJ3; majorly NT2 neuron; mRNA from

NT2 neuronal precursor cells treated 2-weeks mitotic

inhibitor after 5-weeks retinoic acid (RA) induction"

ORIGIN

Query Match 83.2%; Score 15.8; DB 9; Length 575;
Best Local Similarity 89.5%; Pred. No. 3.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCCTTCGG 19
|||||
Db 517 GAATGGAAGGCTTCGG 535

Research and Reference
(www.malaria.mr4.org)."

Search completed: May 19, 2006, 07:06:51
Job time : 1282.71 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 03:46:33 ; Search time 762.175 Seconds
(without alignments)
306.314 Million cell updates/sec

Title: US-10-665-708-24

Perfect score: 19

Sequence: 1 gaacggaaagccttcg 19

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Published Applications NA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	18	94.7	24	10	US-10-665-708-22
7	18	94.7	25	3	US-09-738-274-21
8	18	94.7	25	10	US-10-665-708-21
9	17.4	91.6	25	8	US-10-220-212A-31
10	17.4	91.6	25	8	US-10-220-212A-33
11	17.4	91.6	454	7	US-10-438-774-15
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635	9	US-10-425-115-59269	Sequence 59269, A
638	6	US-10-027-632-292604	Sequence 292604,
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1443	13	US-11-035-295-1	Sequence 1, Appli
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1461	10	US-10-697-802A-7	Sequence 7, Appli
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1480	16	US-11-228-416-7	Sequence 8, Appli
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1482	16	US-11-228-416-4	Sequence 4, Appli
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2896	10	US-10-488-528-3	Sequence 3, Appli
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6883	7	US-10-242-515-3363	Sequence 3363, Ap
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297	10	US-10-779-543-22422	Sequence 22422, A
301	9	US-10-425-115-24598	Sequence 24598, A
592	7	US-10-029-386-13162	Sequence 13162, A
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1429	8	US-10-841-643-689	Sequence 689, App
1453	8	US-10-296-115-424	Sequence 424, App
2173	8	US-10-221-625-108	Sequence 108, App
2196	15	US-11-000-688-253	Sequence 253, App
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5913	8	US-10-437-963-66272	Sequence 66272, A
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369	8	US-10-437-963-65383	Sequence 62893, A
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C 104	14.8	77.9	89328	3	US-09-873-367C-332	Sequence 332, App	C 177	14.4	75.8	836	6	US-10-027-632-125589	Sequence 125589,
C 105	14.8	77.9	89328	10	US-10-843-641A-332	Sequence 332, App	C 178	14.4	75.8	1158	13	US-11-097-143-33038	Sequence 33038, A
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C 108	14.8	77.9	715517	6	US-10-027-632-53712	Sequence 53712, A	C 181	14.4	75.8	1384	9	US-10-425-113-30454	Sequence 30454, A
C 109	14.8	77.9	715517	7	US-10-027-632-53712	Sequence 53712, A	C 182	14.4	75.8	1384	9	US-10-425-113-30454	Sequence 30454, A
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C 113	14.4	75.8	25	13	US-11-036-317-479488	Sequence 479488,	C 186	14.4	75.8	1384	9	US-10-425-113-30454	Sequence 30454, A
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C 115	14.4	75.8	28	3	US-09-738-972-15	Sequence 15, Appl	C 188	14.4	75.8	1384	9	US-10-425-113-30454	Sequence 30454, A
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C 118	14.4	75.8	32	3	US-09-738-972-7	Sequence 7, Appl	C 191	14.4	75.8	1384	9	US-10-425-113-30454	Sequence 30454, A
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C 120	14.4	75.8	32	9	US-10-862-026-7	Sequence 7, Appl	C 193	14.4	75.8	1384	9	US-10-425-113-30454	Sequence 30454, A
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C 131	14.4	75.8	352	3	US-09-764-869-154	Sequence 154, App	C 204	14.4	75.8	1384	9	US-10-425-113-30454	Sequence 30454, A
C 132	14.4	75.8	352	6	US-10-091-504-154	Sequence 154, App	C 205	14.4	75.8	1384	9	US-10-425-113-30454	Sequence 30454, A
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C 134	14.4	75.8	380	4	US-09-925-065A-526657	Sequence 526657,	C 207	14.4	75.8	1384	9	US-10-425-113-30454	Sequence 30454, A
C 135	14.4	75.8	380	5	US-09-925-065A-526657	Sequence 526657,	C 208	14.4	75.8	1384	9	US-10-425-113-30454	Sequence 30454, A
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C 142	14.4	75.8	560	10	US-10-478-633A-23	Sequence 23, Appl	C 215	14.4	75.8	1384	9	US-10-425-113-30454	Sequence 30454, A
C 143	14.4	75.8	561	4	US-09-925-065A-171262	Sequence 171262,	C 216	14.4	75.8	1384	9	US-10-425-113-30454	Sequence 30454, A
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C 160	14.4	75.8	600	10	US-10-972-079-6009	Sequence 6009, Ap	C 233	14.4	75.8	1384	9	US-10-425-113-30454	Sequence 30454, A
C 161	14.4	75.8	607	4	US-09-925-065A-398677	Sequence 398677,	C 234	14.4	75.8	1384	9	US-10-425-113-30454	Sequence 30454, A
C 162	14.4	75.8	607	4	US-09-925-065A-398678	Sequence 398678,	C 235	14.4	75.8	1384	9	US-10-425-113-30454	Sequence 30454, A
C 163	14.4	75.8	607	5	US-09-925-065A-398677	Sequence 398677,	C 236	14.4	75.8	1384	9	US-10-425-113-30454	Sequence 30454, A

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237 14.2 74.7 201 15 US-11-124-368A-15160
238 14.2 74.7 243 9 US-10-425-115-31222
239 14.2 74.7 251 3 US-09-783-590-860
240 14.2 74.7 289 9 US-10-425-115-133799
241 14.2 74.7 301 3 US-09-759-143-247
242 14.2 74.7 301 3 US-09-780-669-247
243 14.2 74.7 301 3 US-09-822-827-247
244 14.2 74.7 301 3 US-09-232-880-247
245 14.2 74.7 301 3 US-09-895-793-247
246 14.2 74.7 301 3 US-09-895-814-247
247 14.2 74.7 301 6 US-10-012-896-247
248 14.2 74.7 301 6 US-10-010-940-247
249 14.2 74.7 301 6 US-10-144-678A-247
250 14.2 74.7 301 7 US-10-294-025-247
251 14.2 74.7 301 16 US-11-234-786-247
252 14.2 74.7 341 9 US-10-696-639-2052
253 14.2 74.7 387 9 US-10-425-115-169553
254 14.2 74.7 410 4 US-09-925-065A-468366
255 14.2 74.7 410 5 US-09-925-065A-468366
256 14.2 74.7 411 3 US-09-960-352-4970
257 14.2 74.7 418 12 US-10-301-480-523819
258 14.2 74.7 418 12 US-10-301-480-1137228
259 14.2 74.7 424 8 US-10-276-774-350
260 14.2 74.7 449 9 US-10-425-115-19918
261 14.2 74.7 455 4 US-09-925-065A-827898
262 14.2 74.7 455 5 US-09-925-065A-827898
263 14.2 74.7 456 10 US-10-467-657-2667
264 14.2 74.7 459 4 US-09-925-065A-166580
265 14.2 74.7 459 4 US-09-925-065A-166581
266 14.2 74.7 459 5 US-09-925-065A-166580
267 14.2 74.7 459 5 US-09-925-065A-166581
268 14.2 74.7 477 12 US-10-301-480-258793
269 14.2 74.7 477 12 US-10-301-480-258794
270 14.2 74.7 477 12 US-10-301-480-872202
271 14.2 74.7 477 12 US-10-301-480-872203
272 14.2 74.7 499 3 US-09-918-995-261
273 14.2 74.7 502 8 US-10-240-425-1143
274 14.2 74.7 503 8 US-10-260-238-286
275 14.2 74.7 511 9 US-10-653-047-963
276 14.2 74.7 530 8 US-10-767-701-30317
277 14.2 74.7 540 4 US-09-925-065A-314724
278 14.2 74.7 540 5 US-09-925-065A-314724
279 14.2 74.7 550 6 US-10-027-632-40715
280 14.2 74.7 550 6 US-10-027-632-40716
281 14.2 74.7 550 7 US-10-027-632-40715
282 14.2 74.7 550 7 US-10-027-632-40716
283 14.2 74.7 551 4 US-09-925-065A-160078
284 14.2 74.7 551 5 US-09-925-065A-160078
285 14.2 74.7 551 12 US-10-301-480-375576
286 14.2 74.7 551 12 US-10-301-480-988985
287 14.2 74.7 555 4 US-09-925-065A-298956
288 14.2 74.7 555 5 US-09-925-065A-298956
289 14.2 74.7 558 8 US-10-424-599-138429
290 14.2 74.7 560 3 US-09-796-692-4435
291 14.2 74.7 560 6 US-10-040-862-4435
292 14.2 74.7 560 7 US-10-057-475B-4435
293 14.2 74.7 560 7 US-10-154-884B-4435
294 14.2 74.7 560 9 US-10-764-324-4435
295 14.2 74.7 563 12 US-10-301-480-252901
296 14.2 74.7 563 12 US-10-301-480-389774
297 14.2 74.7 563 12 US-10-301-480-866310
298 14.2 74.7 563 12 US-10-301-480-1003183
299 14.2 74.7 570 4 US-09-925-065A-746395
300 14.2 74.7 570 5 US-09-925-065A-746395
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ALIGNMENTS

RESULT 1

US-09-738-274-24

; Sequence 24, Application US/09738274

; Publication No. US20030165824A1

```
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GPI07-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-24
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Query Match 100.0%; Score 19; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GAACGGAAGGCTTTTCGG 19
Db 1 GAACGGAAGGCTTTTCGG 19
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RESULT 2

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US-10-665-708-24
; Sequence 24, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GPI07-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-10-665-708-24
```

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Query Match 100.0%; Score 19; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GAACGGAAGGCTTTTCGG 19
Db 1 GAACGGAAGGCTTTTCGG 19
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RESULT 3

US-09-738-274-23
; Sequence 23, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-23

Query Match 100.0%; Score 19; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTCGG 19
|||||
DB 4 GAACGGAAGGCTTCGG 22

RESULT 4
US-10-665-708-23
; Sequence 23, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR FILING DATE: US/09/738,274
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-10-665-708-23

Query Match 100.0%; Score 19; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTCGG 19
|||||
DB 4 GAACGGAAGGCTTCGG 22

RESULT 5
US-09-738-274-22
; Sequence 22, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-22

Query Match 94.7%; Score 18; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTCG 18
|||||
DB 7 GAACGGAAGGCTTCG 24

RESULT 6
US-10-665-708-22
; Sequence 22, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-10-665-708-22

Query Match 94.7%; Score 18; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTTTCG 18
 Db 7 GAACGGAAGGCTTTTCG 24

RESULT 7

US-09-738-274-21
 ; Sequence 21, Application US/09738274
 ; Publication No. US20030165824A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BRENTANO, Steven T.
 ; APPLICANT: JUCKER, Markus T.
 ; APPLICANT: DELGADO, Francisco D.
 ; APPLICANT: CLEUZIAI, Philippe
 ; APPLICANT: RODRIGUE, Marc
 ; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
 ; MYCOBACTERIUM SPECIES
 ; FILE REFERENCE: GP107-02.UT
 ; CURRENT APPLICATION NUMBER: US/09/738,274
 ; CURRENT FILING DATE: 2000-12-15
 ; PRIOR FILING DATE: 1999-12-17
 ; PRIOR FILING DATE: 1999-12-17
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 21
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: primer
 ; OTHER INFORMATION: oligonucleotide
 US-09-738-274-21

Query Match 94.7%; Score 18; DB 3; Length 25;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTTTCG 18
 Db 8 GAACGGAAGGCTTTTCG 25

RESULT 8

US-10-665-708-21
 ; Sequence 21, Application US/10665708
 ; Publication No. US20050100915A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BRENTANO, Steven T.
 ; APPLICANT: JUCKER, Markus T.
 ; APPLICANT: DELGADO, Francisco D.
 ; APPLICANT: CLEUZIAI, Philippe
 ; APPLICANT: RODRIGUE, Marc
 ; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
 ; MYCOBACTERIUM SPECIES
 ; FILE REFERENCE: GP107-02.UT
 ; CURRENT APPLICATION NUMBER: US/10/665,708
 ; CURRENT FILING DATE: 2003-09-18
 ; PRIOR FILING DATE: US/09/738,274
 ; PRIOR FILING DATE: 2000-12-15
 ; PRIOR FILING DATE: 2000-12-15
 ; PRIOR FILING DATE: 1999-12-17
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 21
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: primer
 ; OTHER INFORMATION: oligonucleotide
 US-10-665-708-21

Query Match 94.7%; Score 18; DB 10; Length 25;

Best Local Similarity 100.0%; Pred. No. 33;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GAACGGAAGGCTTTTCG 18
 Db 8 GAACGGAAGGCTTTTCG 25

RESULT 9

US-10-220-212A-31
 ; Sequence 31, Application US/10220212A
 ; Publication No. US20040110129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Government of the United States of America as represented by the
 ; SECRETARY, Department of Health & Human Services, the National Institutes
 ; of Health
 ; APPLICANT: Beckman Coulter, Inc.
 ; TITLE OF INVENTION: Multiplex Hybridization System for the Identification of Pathogen
 ; MYCOBACTERIUM
 ; FILE REFERENCE: 4239-58135
 ; CURRENT APPLICATION NUMBER: US/10/220,212A
 ; CURRENT FILING DATE: 2002-08-27
 ; PRIOR APPLICATION NUMBER: 60/186,840
 ; PRIOR FILING DATE: 2000-03-03
 ; NUMBER OF SEQ ID NOS: 35
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 31
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Mycobacterium-specific oligonucleotide
 US-10-220-212A-31

Query Match 91.6%; Score 17.4; DB 8; Length 25;
 Best Local Similarity 94.7%; Pred. No. 69;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTTTCG 19
 Db 1 GAACGGAAGGCTTTTCG 19

RESULT 10

US-10-220-212A-33
 ; Sequence 33, Application US/10220212A
 ; Publication No. US20040110129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Government of the United States of America as represented by the
 ; SECRETARY, Department of Health & Human Services, the National Institutes
 ; of Health
 ; APPLICANT: Beckman Coulter, Inc.
 ; TITLE OF INVENTION: Multiplex Hybridization System for the Identification of Pathogen
 ; MYCOBACTERIUM
 ; FILE REFERENCE: 4239-58135
 ; CURRENT APPLICATION NUMBER: US/10/220,212A
 ; CURRENT FILING DATE: 2002-08-27
 ; PRIOR APPLICATION NUMBER: 60/186,840
 ; PRIOR FILING DATE: 2000-03-03
 ; NUMBER OF SEQ ID NOS: 35
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 33
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Mycobacterium-specific oligonucleotide
 US-10-220-212A-33

Query Match 91.6%; Score 17.4; DB 8; Length 25;
 Best Local Similarity 94.7%; Pred. No. 69;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCTTCGG 19
Db 1 GAACGGAAGGCCTTCGG 19

RESULT 11
US-10-438-774-15
; Sequence 15, Application US/10438774
; Publication No. US20040010504A1
; GENERAL INFORMATION:
; APPLICANT: Hinrichs, Steven
; APPLICANT: Mohammed, Amr
; APPLICANT: Ali, Hesham
; APPLICANT: Kuyper, Dan
; TITLE OF INVENTION: Custom Sequence Databases and Methods of
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: UNMC.63174-US
; CURRENT APPLICATION NUMBER: US/10/438,774
; CURRENT FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: 60/381,015
; PRIOR FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-438-774-15

Query Match 91.6%; Score 17.4; DB 7; Length 454;
Best Local Similarity 94.7%; Pred. No. 72;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCTTCGG 19
Db 4 GAACGGAAGGCCTTCGG 22

RESULT 12
US-10-697-802A-6
; Sequence 6, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 6
; LENGTH: 1449
; TYPE: DNA
; ORGANISM: Mycobacterium fortuitum
US-10-697-802A-6

Query Match 91.6%; Score 17.4; DB 10; Length 1449;
Best Local Similarity 94.7%; Pred. No. 74;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCTTCGG 19
Db 27 GAACGGAAGGCCTTCGG 45

RESULT 13
US-10-697-802A-13
; Sequence 13, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG

; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 13
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Mycobacterium mucogenicum
US-10-697-802A-13

Query Match 91.6%; Score 17.4; DB 10; Length 1455;
Best Local Similarity 94.7%; Pred. No. 74;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCTTCGG 19
Db 37 GAACGGAAGGCCTTCGG 55

RESULT 14
US-10-697-802A-5
; Sequence 5, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 5
; LENGTH: 1482
; TYPE: DNA
; ORGANISM: Mycobacterium farcinogenes
US-10-697-802A-5

Query Match 91.6%; Score 17.4; DB 10; Length 1482;
Best Local Similarity 94.7%; Pred. No. 74;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCTTCGG 19
Db 35 GAACGGAAGGCCTTCGG 53

RESULT 15
US-10-779-543-8365
; Sequence 8365, Application US/10779543
; Publication No. US20050227917A1
; GENERAL INFORMATION:
; APPLICANT: Williams et al
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
; FILE REFERENCE: 2300-21302
; CURRENT APPLICATION NUMBER: US/10/779,543
; CURRENT FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 10/076,555
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 09/217,471
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/068,755
; PRIOR FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: 60/080,664
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/105,234
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 09/297,648
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: PCT/US99/01619
; PRIOR FILING DATE: 1999-01-28

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; PRIOR APPLICATION NUMBER: 60/072,910
; PRIOR FILING DATE: 1998-01-28
; PRIOR APPLICATION NUMBER: 60/075,954
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/080,114
; PRIOR FILING DATE: 1998-03-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 23767
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8365
; LENGTH: 935
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 13, 17, 18, 20, 21, 25, 35, 37, 43, 46, 48, 52, 57, 81, 89,
; LOCATION: 108, 116, 127, 138, 139, 142, 144, 168, 169, 172, 178, 179,
; LOCATION: 184, 185, 204, 222, 231, 234, 242, 248, 258, 263, 279, 287,
; LOCATION: 291, 304, 310, 317, 319, 328, 335, 337, 350, 357, 362
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 363, 365, 375, 387, 390, 391, 401, 433, 434, 436, 455, 460,
; LOCATION: 468, 476, 479, 489, 495, 500, 502, 506, 515, 529, 530, 534,
; LOCATION: 543, 553, 563, 564, 565, 566, 592, 627, 628, 631, 642, 645,
; LOCATION: 650, 653, 662, 668, 670, 680, 681, 682, 684, 685, 691
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 696, 703, 707, 741, 745, 752, 756, 763, 767, 770, 771, 779,
; LOCATION: 795, 823, 824, 829, 830, 846, 850, 854, 855, 873, 874, 878,
; LOCATION: 887, 890, 894, 907, 910, 920, 922, 929, 935
; OTHER INFORMATION: n = A,T,C or G
US-10-779-543-8365

Query Match      84.2%; Score 16; DB 10; Length 935;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GAACGGAAAGCGCTTTTCGG 19
Db      452 GAANGGANGCGCTTTTNGG 470

RESULT 16
US-10-062-727-254
; Sequence 254, Application US/10062727
; Publication No. US20030018185A1
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka
; APPLICANT: Bloksberg, Leonard
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Plant Microsatellite Markers and Methods
; FILE REFERENCE: 11000.1006CIP
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 09/105,307
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 1057
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254
; LENGTH: 170
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: {1}...(170)
; OTHER INFORMATION: n = A,T,C or G
US-10-062-727-254

Query Match      83.2%; Score 15.8; DB 6; Length 170;
Best Local Similarity 89.5%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GAACGGAAAGCGCTTTTCGG 19
Db      69 GAACGGAAAGCGCTTTTAGG 87

RESULT 17
US-10-062-727-376
; Sequence 376, Application US/10062727
; Publication No. US20030018185A1
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka
; APPLICANT: Bloksberg, Leonard
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Plant Microsatellite Markers and Methods
; FILE REFERENCE: 11000.1006CIP
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US/10/062,727
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 09/105,307
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 1057
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 376
; LENGTH: 305
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-062-727-376

Query Match      83.2%; Score 15.8; DB 6; Length 305;
Best Local Similarity 89.5%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GAACGGAAAGCGCTTTTCGG 19
Db      70 GAACGGAAAGCGCTTTTAGG 88

RESULT 18
US-10-062-674-613/c
; Sequence 613, Application US/10062674
; Publication No. US20040005559A1
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.
; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
; FILE REFERENCE: PA-0026-1 CIP
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: US 09/625,102
; PRIOR FILING DATE: 2000-07-24
; NUMBER OF SEQ ID NOS: 2217
; SOFTWARE: PERL Program
; SEQ ID NO 613
; LENGTH: 367
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040005559A1 92292157
US-10-062-674-613

Query Match      83.2%; Score 15.8; DB 7; Length 367;
Best Local Similarity 89.5%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GAACGGAAAGCGCTTTTCGG 19
Db      37 GAATGGAGAGCGCTTTTCGG 19

RESULT 19
US-09-925-065A-544396
```

```
; Sequence 544396, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 544396
; LENGTH: 513
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-544396
```

```
Query Match      83.2%; Score 15.8; DB 4; Length 513;
Best Local Similarity 89.5%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GAACGGAAAGGCGCTTTCGG 19
      ||| ||||| ||||| |||||
Db      226 GAAGGAAAGGCCATTCGG 244
```

```
RESULT 20
US-09-925-065A-544397
; Sequence 544397, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 544397
; LENGTH: 513
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-544397
```

```
Query Match      83.2%; Score 15.8; DB 4; Length 513;
Best Local Similarity 89.5%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GAACGGAAAGGCGCTTTCGG 19
      ||| ||||| ||||| |||||
Db      226 GAAGGAAAGGCCATTCGG 244
```

```
RESULT 21
US-09-925-065A-544396
; Sequence 544396, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 544396
; LENGTH: 513
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-544396
```

```
Query Match      83.2%; Score 15.8; DB 5; Length 513;
Best Local Similarity 89.5%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GAACGGAAAGGCGCTTTCGG 19
      ||| ||||| ||||| |||||
Db      226 GAAGGAAAGGCCATTCGG 244
```

```
RESULT 22
US-09-925-065A-544397
; Sequence 544397, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 544397
; LENGTH: 513
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-544397
```

```
Query Match      83.2%; Score 15.8; DB 5; Length 513;
Best Local Similarity 89.5%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GAACGGAAAGGCGCTTTCGG 19
```

```
Db      226 GAAGGGAAGGCCATTTCGG 244
||||| ||||| ||||| ||||| |||||
Query Match      83.2%; Score 15.8; DB 8; Length 620;
Best Local Similarity 89.5%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 23
US-10-450-763-3105
; Sequence 3105, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR FILING DATE: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 3105
; LENGTH: 576
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (419)..(3)
; OTHER INFORMATION: 32% homologous to Santalum album proline rich
; OTHER INFORMATION: protein, accession number AF020261, Smith-Waterman Score=109.
US-10-450-763-3105

Query Match      83.2%; Score 15.8; DB 10; Length 576;
Best Local Similarity 89.5%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GAACGGAAAGCCTTTTCGG 19
||||| ||||| ||||| ||||| |||||
Db      512 GAATGGAAGGCTTTTCGG 530

RESULT 24
US-10-437-963-34505
; Sequence 34505, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 34505
; LENGTH: 620
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(620)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_38514C.1
US-10-437-963-34505

Db      226 GAAGGGAAGGCCATTTCGG 244
||||| ||||| ||||| ||||| |||||
Query Match      83.2%; Score 15.8; DB 8; Length 620;
Best Local Similarity 89.5%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 25
US-10-425-115-59269
; Sequence 59269, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 59269
; LENGTH: 635
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_15404C.1
US-10-425-115-59269

Query Match      83.2%; Score 15.8; DB 9; Length 635;
Best Local Similarity 89.5%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GAACGGAAAGCCTTTTCGG 19
||||| ||||| ||||| ||||| |||||
Db      454 GAGCGGAAGGCTTTCGG 472

RESULT 26
US-10-027-632-292604
; Sequence 292604, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 292604
; LENGTH: 638
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-292604
```

Query Match 83.2%; Score 15.8; DB 6; Length 638;
Best Local Similarity 89.5%; Pred. No. 5e+02; 2; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTCGG 19
||| ||||| |||||
Db 228 GAAGGGAAGGCCATTCGG 246

RESULT 27
US-10-027-632-292605
; Sequence 292605, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 292605
; LENGTH: 638
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-292605

Query Match 83.2%; Score 15.8; DB 6; Length 638;
Best Local Similarity 89.5%; Pred. No. 5e+02; 2; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTCGG 19
||| ||||| |||||
Db 228 GAAGGGAAGGCCATTCGG 246

RESULT 28
US-10-027-632-292604
; Sequence 292604, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 292604
; LENGTH: 638
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-292604

Query Match 83.2%; Score 15.8; DB 7; Length 638;
Best Local Similarity 89.5%; Pred. No. 5e+02; 2; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTCGG 19
||| ||||| |||||
Db 228 GAAGGGAAGGCCATTCGG 246

RESULT 29
US-10-027-632-292605
; Sequence 292605, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 292605
; LENGTH: 638
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-292605

Query Match 83.2%; Score 15.8; DB 7; Length 638;
Best Local Similarity 89.5%; Pred. No. 5e+02; 2; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTCGG 19
||| ||||| |||||
Db 228 GAAGGGAAGGCCATTCGG 246

RESULT 30
US-10-522-454-1
; Sequence 1, Application US/10522454
; Publication No. US20050244938A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Russell T.
; APPLICANT: Hamann, Mark T.
; APPLICANT: Peraud, Olivier
; APPLICANT: Kasanah, Noer
; TITLE OF INVENTION: MANZAMINE-PRODUCING ACTINOMYCETES

```

: GENERAL INFORMATION:
: APPLICANT: E. I. duPont de Nemours, Inc.
: TITLE OF INVENTION: GENES ENCODING BAEYER-VILLIGER MONOOXYGENASES
: FILE REFERENCE: C11789 PCT
: CURRENT APPLICATION NUMBER: US/10/486,307
: CURRENT FILING DATE: 2004-02-05
: PRIOR APPLICATION NUMBER: 60/315,546
: PRIOR FILING DATE: 2001-08-29
: NUMBER OF SEQ ID NOS: 113
:

```

; APPLICANT: LAZZARINI, Ameriga
 ; APPLICANT: GASTALDO, Luciano
 ; APPLICANT: CANDIANI, Gianpaolo
 ; APPLICANT: CICILIATO, Ismaela
 ; APPLICANT: LOSI, Daniele


```
; APPLICANT: MARINELLI, Flavia
; APPLICANT: SELVA, Enrico
; APPLICANT: PARENTI, Franco
; TITLE OF INVENTION: ANTIBIOTIC 107891, ITS FACTORS A1 AND A2, PHARMACEUTICALLY
; TITLE OF INVENTION: ACCEPTABLE SALTS AND COMPOSITIONS, AND USE THEREOF
; FILE REFERENCE: 892,280-500
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: US 11/045,628
; PRIOR FILING DATE: 2005-01-12
; PRIOR APPLICATION NUMBER: US 10/521,336
; PRIOR FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: PCT/EP2004/007658
; PRIOR FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: EP 03016306.7
; PRIOR FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Microbispora sp. ATCC PTA-5024
US-11-045-628-1

Query Match      83.2%; Score 15.8; DB 13; Length 1443;
Best Local Similarity 89.5%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGAAAGGCGCTTCGG 19
Db 37 GAGCGAAAGGCGCTTCGG 55

RESULT 35
US-10-697-802A-7
; Sequence 7, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 7
; LENGTH: 1461
; TYPE: DNA
; ORGANISM: Mycobacterium goodnae
US-10-697-802A-7

Query Match      83.2%; Score 15.8; DB 10; Length 1461;
Best Local Similarity 89.5%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGAAAGGCGCTTCGG 19
Db 27 GAACGTAAGGCGCTTCGG 45

RESULT 36
US-11-228-416-5
; Sequence 5, Application US/11228416
; Publication No. US2006000852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15
```

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; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1480
; TYPE: DNA
; ORGANISM: Salinospira sp. CNH898 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1423)..(1423)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
US-11-228-416-5

Query Match      83.2%; Score 15.8; DB 16; Length 1480;
Best Local Similarity 89.5%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGAAAGGCGCTTCGG 19
Db 57 GAGCGAAAGGCGCTTCGG 75

RESULT 37
US-11-228-416-6
; Sequence 6, Application US/11228416
; Publication No. US2006000852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1480
; TYPE: DNA
; ORGANISM: Salinospira sp. CNH440 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
```

Db 57 GAGCGGAAAGGCCCTTCGG 75

RESULT 39

US-11-228-416-9

; Sequence 9, Application US/11228416

; Publication No. US20060008852A1

; GENERAL INFORMATION:

; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO

; APPLICANT: FENICAL, William

; APPLICANT: JENSEN, Paul R.

; APPLICANT: MINCER, Tracy J.

; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCTION

; FILE REFERENCE: UCS01630-1

; CURRENT APPLICATION NUMBER: US/11/228,416

; CURRENT FILING DATE: 2005-09-15

; PRIOR APPLICATION NUMBER: US/09/991,518B

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: US 60/249,356

; PRIOR FILING DATE: 2000-11-16

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 9

; LENGTH: 1480

; TYPE: DNA

; ORGANISM: *Salinospira* sp. CNH964 16S ribosomal RNA gene, partial sequence

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (198)..(198)

; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (351)..(351)

; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (442)..(442)

; OTHER INFORMATION: n is signature nucleotide t position 467 of 16S rDNA

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (443)..(443)

; OTHER INFORMATION: n is signature nucleotide t position 468 of 16S rDNA

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1423)..(1423)

; OTHER INFORMATION: n is signature nucleotide g position 1456 of 16S rDNA

US-11-228-416-9

Query Match 83.2%; Score 15.8; DB 16; Length 1480;

Best Local Similarity 89.5%; Pred.No. 5.1e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCCCTTCGG 19

||| ||||| ||||| |||||

Db 57 GAGCGGAAAGGCCCTTCGG 75

RESULT 40

US-11-228-416-3

; Sequence 3, Application US/11228416

; Publication No. US20060008852A1

; GENERAL INFORMATION:

; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO

; APPLICANT: FENICAL, William

; APPLICANT: JENSEN, Paul R.

; APPLICANT: MINCER, Tracy J.

; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCTION

; FILE REFERENCE: UCS01630-1

; CURRENT APPLICATION NUMBER: US/11/228,416

; CURRENT FILING DATE: 2005-09-15

; PRIOR APPLICATION NUMBER: US/09/991,518B

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: US 60/249,356

```

; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1481
; TYPE: DNA
; ORGANISM: Salinospora sp. CNH643 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (352)..(352)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (444)..(444)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1424)..(1424)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
US-11-228-416-3
```

```

Query Match      83.2%; Score 15.8; DB 16; Length 1481;
Best Local Similarity 89.5%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

Qy 1 GAACGGAAGGCGCTTCGG 19
Db 57 GAGCGGAAGGCGCTTCGG 75
```

```

RESULT 41
US-11-228-416-4
; Sequence 4, Application US/11228416
; Publication No. US20060008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1482
; TYPE: DNA
; ORGANISM: Salinospora sp. CNH646 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
```

```

; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1425)..(1425)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
US-11-228-416-4
```

```

Query Match      83.2%; Score 15.8; DB 16; Length 1482;
Best Local Similarity 89.5%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

Qy 1 GAACGGAAGGCGCTTCGG 19
Db 57 GAGCGGAAGGCGCTTCGG 75
```

```

RESULT 42
US-11-228-416-7
; Sequence 7, Application US/11228416
; Publication No. US20060008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1483
; TYPE: DNA
; ORGANISM: Salinospora sp. CNH536 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (444)..(444)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1426)..(1426)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
US-11-228-416-7
```

```

Query Match      83.2%; Score 15.8; DB 16; Length 1483;
Best Local Similarity 89.5%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

Qy 1 GAACGGAAGGCGCTTCGG 19
Db 57 GAGCGGAAGGCGCTTCGG 75
```

```
RESULT 43
US-10-488-528-3
; Sequence 3, Application US/10488528
; Publication No. US20050119459A1
; GENERAL INFORMATION:
; APPLICANT: Kaplan, Feige
; APPLICANT: Swezey, Neil B.
; TITLE OF INVENTION: Late Gestation Lung Genes, Fragments and Uses Thereof
; FILE REFERENCE: 457-110pct
; CURRENT APPLICATION NUMBER: US/10/488,528
; CURRENT FILING DATE: 2004-03-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2896
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (32)...(1525)
US-10-488-528-3
Query Match      83.2%; Score 15.8; DB 10; Length 2896;
Best Local Similarity 89.5%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1  GAACGGAAGCCCTTCGG 19
Db      1486 GAACGGAAGCCCTTCGG 1504

RESULT 44
US-10-488-528-1
; Sequence 1, Application US/10488528
; Publication No. US20050119459A1
; GENERAL INFORMATION:
; APPLICANT: Kaplan, Feige
; APPLICANT: Swezey, Neil B.
; TITLE OF INVENTION: Late Gestation Lung Genes, Fragments and Uses Thereof
; FILE REFERENCE: 457-110pct
; CURRENT APPLICATION NUMBER: US/10/488,528
; CURRENT FILING DATE: 2004-03-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3054
; TYPE: DNA
; ORGANISM: rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (86)...(1576)
US-10-488-528-1
Query Match      83.2%; Score 15.8; DB 10; Length 3054;
Best Local Similarity 89.5%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1  GAACGGAAGCCCTTCGG 19
Db      1540 GAACGGAAGCCCTTCGG 1558

RESULT 45
US-09-764-877-3363
; Sequence 3363, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper

; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3363
; LENGTH: 6883
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-242-515-3363
Query Match      83.2%; Score 15.8; DB 7; Length 6883;
Best Local Similarity 89.5%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1  GAACGGAAGCCCTTCGG 19
Db      478  GAATGGAAGGTCTTCGG 496

RESULT 46
US-10-242-515-3363
; Sequence 3363, Application US/10242515
; Publication No. US20040009488A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005C1
; CURRENT APPLICATION NUMBER: US/10/242,515
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/764,877
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3363
; LENGTH: 6883
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-242-515-3363
Query Match      83.2%; Score 15.8; DB 7; Length 6883;
Best Local Similarity 89.5%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1  GAACGGAAGCCCTTCGG 19
Db      478  GAATGGAAGGTCTTCGG 496

RESULT 47
US-10-856-499-60
; Sequence 60, Application US/10856499
; Publication No. US20040259145A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
```

```
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021C2
; CURRENT APPLICATION NUMBER: US/10/856,499
; CURRENT FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 2370
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-856-499-60

Query Match      81.1%; Score 15.4; DB 9; Length 455;
Best Local Similarity 94.1%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTC 17
Db 27 GACCGGAAGGCGCTTTC 43

RESULT 48
US-10-856-499-1958
; Sequence 1958, Application US/10856499
; Publication No. US20040259145A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021C2
; CURRENT APPLICATION NUMBER: US/10/856,499
; CURRENT FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 2370
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1958
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-856-499-1958

Query Match      81.1%; Score 15.4; DB 9; Length 455;
Best Local Similarity 94.1%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTC 17
Db 27 GACCGGAAGGCGCTTTC 43

RESULT 49
US-10-767-701-30317/c
; Sequence 30317, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 30317
; LENGTH: 530
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:

; OTHER INFORMATION: Clone ID: 9853201
US-10-767-701-30317

Query Match      81.1%; Score 15.4; DB 8; Length 530;
Best Local Similarity 94.1%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ACGGAAGGCGCTTTCG 19
Db 305 ACTGAAGGCGCTTTCG 289

RESULT 50
US-10-301-480-442948
; Sequence 442948, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 442948
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-442948

Query Match      81.1%; Score 15.4; DB 12; Length 625;
Best Local Similarity 94.1%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTC 17
Db 277 GAACGGAAGGCGCTTTC 293

RESULT 51
US-10-301-480-1056357
; Sequence 1056357, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1056357
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1056357

Query Match      81.1%; Score 15.4; DB 12; Length 625;
Best Local Similarity 94.1%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTC 17
```

Db 277 GAACGGAAGGCTCTTC 293

RESULT 52

US-09-925-065A-373045
; Sequence 373045, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 373045
; LENGTH: 634
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-373045

Query Match 81.1%; Score 15.4; DB 4; Length 634;
Best Local Similarity 94.1%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTCTTC 17

Db 286 GAACGGAAGGCTCTTC 302

RESULT 53

US-09-925-065A-373045
; Sequence 373045, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 373045
; LENGTH: 634
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-373045

Query Match 81.1%; Score 15.4; DB 5; Length 634;
Best Local Similarity 94.1%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTCTTC 17

Db 286 GAACGGAAGGCTCTTC 302

RESULT 54

US-10-750-185-42960
; Sequence 42960, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42960
; LENGTH: 1187
; TYPE: DNA
; ORGANISM: Bovine 19866881327789
US-10-750-185-42960

Query Match 81.1%; Score 15.4; DB 10; Length 1187;
Best Local Similarity 94.1%; Pred. No. 8.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTCTTC 17

Db 224 GAACGGAAGGCTCTTC 240

RESULT 55

US-10-750-623-42960
; Sequence 42960, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42960
; LENGTH: 1187
; TYPE: DNA
; ORGANISM: Bovine 19866881327789
US-10-750-623-42960

Query Match 81.1%; Score 15.4; DB 10; Length 1187;
Best Local Similarity 94.1%; Pred. No. 8.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTCTTC 17

Db 177 GAACGGAAGGCTCTTC 177

Db 224 GAACGAAAGGCCTTTC 240

RESULT 56

US-10-750-185-34543

; Sequence 34543, Application US/10750185

; Publication No. US20050260603A1

; GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.

; APPLICANT: DENISE, Sue K.

; APPLICANT: KERR, Richard

; APPLICANT: ROSENFELD, David

; APPLICANT: HOLM, Tom

; APPLICANT: BATES, Stephen

; APPLICANT: FANTIN, Dennis

; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

; FILE REFERENCE: MM1100-2

; CURRENT APPLICATION NUMBER: US/10/750,185

; PRIOR FILING DATE: 2003-12-31

; PRIOR APPLICATION NUMBER: US 60/437,482

; PRIOR FILING DATE: 2002-12-31

; NUMBER OF SEQ ID NOS: 64922

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 34543

; LENGTH: 2665

; TYPE: DNA

; ORGANISM: Bovine 19866880465649

US-10-750-185-34543

Query Match 81.1%; Score 15.4; DB 10; Length 2665;

Best Local Similarity 94.1%; Pred. No. 8.3e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGAAAGGCCTTTC 17

Db 916 GAACAGAAAGGCCTTTC 932

RESULT 57

US-10-750-623-34543

; Sequence 34543, Application US/10750623

; Publication No. US20050287531A1

; GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.

; APPLICANT: DENISE, Sue K.

; APPLICANT: KERR, Richard

; APPLICANT: ROSENFELD, David

; APPLICANT: HOLM, Tom

; APPLICANT: BATES, Stephen

; APPLICANT: FANTIN, Dennis

; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS

; FILE REFERENCE: MM1100-1

; CURRENT APPLICATION NUMBER: US/10/750,623

; CURRENT FILING DATE: 2003-12-31

; PRIOR APPLICATION NUMBER: US 60/437,482

; PRIOR FILING DATE: 2002-12-31

; NUMBER OF SEQ ID NOS: 64922

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 34543

; LENGTH: 2665

; TYPE: DNA

; ORGANISM: Bovine 19866880465649

US-10-750-623-34543

Query Match 81.1%; Score 15.4; DB 10; Length 2665;

Best Local Similarity 94.1%; Pred. No. 8.3e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGAAAGGCCTTTC 17

Db 916 GAACAGAAAGGCCTTTC 932

RESULT 58

US-11-097-143-3737

; Sequence 3737, Application US/11097143

; Publication No. US20050208558A1

; GENERAL INFORMATION:

; APPLICANT: Venter, J. Craig

; APPLICANT: et al.

; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

; FILE REFERENCE: CL000728

; CURRENT APPLICATION NUMBER: US/11/097,143

; CURRENT FILING DATE: 2005-04-04

; PRIOR APPLICATION NUMBER: 60/157,832

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: 60/160,191

; PRIOR FILING DATE: 1999-10-19

; PRIOR APPLICATION NUMBER: 60/161,932

; PRIOR FILING DATE: 1999-10-28

; PRIOR APPLICATION NUMBER: 60/164,769

; PRIOR FILING DATE: 1999-11-12

; PRIOR APPLICATION NUMBER: 60/173,383

; PRIOR FILING DATE: 1999-12-28

; PRIOR APPLICATION NUMBER: 60/175,693

; PRIOR FILING DATE: 2000-01-12

; PRIOR APPLICATION NUMBER: 60/184,831

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: 60/191,637

; PRIOR FILING DATE: 2000-03-23

; NUMBER OF SEQ ID NOS: 43008

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3737

; LENGTH: 5433

; TYPE: DNA

; ORGANISM: DROSOPHILA

US-11-097-143-3737

Query Match 81.1%; Score 15.4; DB 13; Length 5433;

Best Local Similarity 94.1%; Pred. No. 8.5e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AACGAAAGGCCTTTCG 18

Db 1687 AACGTAAGGCCTTTCG 1703

RESULT 59

US-11-097-143-3736/c

; Sequence 3736, Application US/11097143

; Publication No. US20050208558A1

; GENERAL INFORMATION:

; APPLICANT: Venter, J. Craig

; APPLICANT: et al.

; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

; FILE REFERENCE: CL000728

; CURRENT APPLICATION NUMBER: US/11/097,143

; CURRENT FILING DATE: 2005-04-04

; PRIOR APPLICATION NUMBER: 60/157,832

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: 60/160,191

; PRIOR FILING DATE: 1999-10-19

; PRIOR APPLICATION NUMBER: 60/161,932

; PRIOR FILING DATE: 1999-10-28

; PRIOR APPLICATION NUMBER: 60/164,769

; PRIOR FILING DATE: 1999-11-12

; PRIOR APPLICATION NUMBER: 60/173,383

; PRIOR FILING DATE: 1999-12-28

; PRIOR APPLICATION NUMBER: 60/175,693

; PRIOR FILING DATE: 2000-01-12

; PRIOR APPLICATION NUMBER: 60/184,831

; PRIOR FILING DATE: 2000-02-24


```
; Sequence 24598, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 24598
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_122440C.1
US-10-425-115-24598

Query Match      78.9%; Score 15; DB 9; Length 301;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AACGGAAGGCCCTTT 16
Db      94 AACGGAAGGCCCTTT 80

RESULT 63
US-10-029-386-13162
; Sequence 13162, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 13162
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR19.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.97
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
; OTHER INFORMATION: NT HIT: g114758021, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q14585, EVALUE 1.00e-48
; OTHER INFORMATION: EST_HUMAN HIT: BE742835.1, EVALUE 0.00e+00
US-10-029-386-13162

Query Match      78.9%; Score 15; DB 7; Length 592;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GGAAGGCCCTTTCCG 19
Db      532 GGAAGGCCCTTTCCG 546

RESULT 64
US-10-641-643-689
; Sequence 689, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; Susan G. Stuart
; Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 689:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1429 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: TLYMNOT02
; CLONE: 450088
; SEQUENCE DESCRIPTION: SEQ ID NO: 689 :
US-10-641-643-689

Query Match      78.9%; Score 15; DB 8; Length 1429;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GGAAGGCCCTTTCCG 19
Db      264 GGAAGGCCCTTTCCG 278

RESULT 65
US-10-296-115-424/c
; Sequence 424, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1e1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 424
; LENGTH: 1453
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-296-115-424
```

```
;
;
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequences:primer
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(2196)
; OTHER INFORMATION: zinc finger protein 463(ZNF463) gene.
US-11-000-688-253

Query Match      78.9%; Score 15; DB 15; Length 2196;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5  GGAAGGCGCTTTCGG 19
Db      1173  GGAAGGCGCTTTCGG 1159

RESULT 66
US-10-221-625-108
; Sequence 108, Application US/10221625
; Publication No. US20040033942A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: BANDMAN, Olga
; APPLICANT: TANG, Y. Tom
; APPLICANT: MATHUR, Preete
; APPLICANT: SHAH, Purvi
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: REDDY, Roopa
; TITLE OF INVENTION: TRANSCRIPTION FACTORS
; FILE REFERENCE: PF-0761 PCT
; CURRENT APPLICATION NUMBER: US/10/221.625
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: PERL Program
; SEQ ID NO 108
; LENGTH: 2173
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040033942A1 095210CB1
US-10-221-625-108

Query Match      78.9%; Score 15; DB 8; Length 2173;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5  GGAAGGCGCTTTCGG 19
Db      989  GGAAGGCGCTTTCGG 1003

RESULT 67
US-11-000-688-253
; Sequence 253, Application US/11000688
; Publication No. US20050287544A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois
; APPLICANT: HOULGATTE, Remi
; APPLICANT: BIRNBAUM, Daniel
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; FILE REFERENCE: 1423-R-03
; CURRENT APPLICATION NUMBER: US/11/000.688
; CURRENT FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US 60/525,987
; PRIOR FILING DATE: 2003-12-01
; NUMBER OF SEQ ID NOS: 1596
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 253
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Artificial Sequence
;
;
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequences:primer
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(2196)
; OTHER INFORMATION: zinc finger protein 463(ZNF463) gene.
US-11-000-688-253

Query Match      78.9%; Score 15; DB 15; Length 2196;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5  GGAAGGCGCTTTCGG 19
Db      1320  GGAAGGCGCTTTCGG 1334

RESULT 68
US-11-097-143-7973
; Sequence 7973, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097.143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7973
; LENGTH: 3003
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-7973

Query Match      78.9%; Score 15; DB 13; Length 3003;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GAACGGAAAGGCCTT 15
Db      2424  GAACGGAAAGGCCTT 2438

RESULT 69
US-09-764-864-123
; Sequence 123, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ23
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
```



```
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 91974
; LENGTH: 275
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_90498C.1
US-10-437-963-91974

Query Match          77.9%; Score 14.8; DB 8; Length 275;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2 AACGGAAGGCCTTTCCG 19
Db  222 AACGGAAGGCCTGTCCG 239

RESULT 74
US-10-424-599-79317
; Sequence 79317, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 79317
; LENGTH: 362
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_42639C.1
US-10-424-599-79317

Query Match          77.9%; Score 14.8; DB 8; Length 362;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2 AACGGAAGGCCTTTCCG 19
Db  59 AAAGGAAGGCCTTTGG 76

RESULT 75
US-10-717-897-63/c
; Sequence 63, Application US/10717897
; Publication No. US20040163146A1
; GENERAL INFORMATION:
; APPLICANT: PHILLIPS, JONATHAN
; APPLICANT: PUTHIGAE, SATHISH
; APPLICANT: YAO, JIALONG
; APPLICANT: FLINN, BARRY
; APPLICANT: FORSTER, RICHARD S.
; APPLICANT: EGGLETON, CLARE
; TITLE OF INVENTION: VASCULAR-PREFERRED PROMOTERS
; FILE REFERENCE: 044463-0264
; CURRENT APPLICATION NUMBER: US/10/717,897
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: 60/428,287
; PRIOR FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 86
```

```
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 63
; LENGTH: 365
; TYPE: DNA
; ORGANISM: Pinus radiata
US-10-717-897-63

Query Match          77.9%; Score 14.8; DB 8; Length 365;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2 AACGGAAGGCCTTTCCG 19
Db  158 AACGGAAGGCCTTTCCG 141

RESULT 76
US-10-437-963-65283/c
; Sequence 65283, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 65283
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_66346C.1
US-10-437-963-65283

Query Match          77.9%; Score 14.8; DB 8; Length 369;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2 AACGGAAGGCCTTTCCG 19
Db  210 AACGGAAGGCCTGTCCG 193

RESULT 77
US-10-424-599-36941/c
; Sequence 36941, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 36941
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_13335C.1
```

```

US-10-424-599-36941

Query Match      77.9%; Score 14.8; DB 8; Length 414;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 AACCGAAGGCCTTTCG 19
    |||||
Db  127 AACCGAAGGCCTGCTG 110

RESULT 78
US-09-925-065A-187308/c
; Sequence 187308, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187308
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-187308

Query Match      77.9%; Score 14.8; DB 4; Length 529;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1 GAACGGAAGGCCTTTCG 18
    |||||
Db  126 GAGTGAAGGCCTTTCG 109

RESULT 79
US-09-925-065A-187308/c
; Sequence 187308, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187308
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-187308

Query Match      77.9%; Score 14.8; DB 8; Length 529;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1 GAACGGAAGGCCTTTCG 18
    |||||
Db  126 GAGTGAAGGCCTTTCG 109

RESULT 80
US-10-301-480-277352/c
; Sequence 277352, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 277352
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-277352

Query Match      77.9%; Score 14.8; DB 12; Length 529;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1 GAACGGAAGGCCTTTCG 18
    |||||
Db  126 GAGTGAAGGCCTTTCG 109

RESULT 81
US-10-301-480-890761/c
; Sequence 890761, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 890761
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-890761

Query Match      77.9%; Score 14.8; DB 12; Length 529;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1 GAACGGAAGGCCTTTCG 18
    |||||
Db  126 GAGTGAAGGCCTTTCG 109

RESULT 82
US-10-301-480-890761/c
; Sequence 890761, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 890761
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-890761

Query Match      77.9%; Score 14.8; DB 12; Length 529;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1 GAACGGAAGGCCTTTCG 18
    |||||
Db  126 GAGTGAAGGCCTTTCG 109

RESULT 83
US-10-301-480-890761/c
; Sequence 890761, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 890761
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-890761

Query Match      77.9%; Score 14.8; DB 12; Length 529;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1 GAACGGAAGGCCTTTCG 18
    |||||
Db  126 GAGTGAAGGCCTTTCG 109

RESULT 84
US-10-301-480-890761/c
; Sequence 890761, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 890761
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-890761

Query Match      77.9%; Score 14.8; DB 12; Length 529;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1 GAACGGAAGGCCTTTCG 18
    |||||
Db  126 GAGTGAAGGCCTTTCG 109

RESULT 85
US-10-301-480-890761/c
; Sequence 890761, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 890761
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-890761

Query Match      77.9%; Score 14.8; DB 12; Length 529;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1 GAACGGAAGGCCTTTCG 18
    |||||
Db  126 GAGTGAAGGCCTTTCG 109

RESULT 86
US-10-301-480-890761/c
; Sequence 890761, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms

```

Qy 1 GAACGGAAGGCCCTTTCG 18
Db 126 GAGTGGAAAGGCCCTTTCG 109

```

RESULT 82
US-09-925-065A-632445
; Sequence 632445, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 632445
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-632445

```

```

RESULT 83
US-09-925-065A-632445
; Sequence 632445, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 632445
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-632445

```

```

Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 AACGGAAGGCGCTTTGGG 19
      ||| ||||| ||||| |||
Db      354 AACAGAAAGCGCTTTGGG 371

RESULT 84
US-09-864-761-16483/c
; Sequence 16483, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aescmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 16483
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC013568.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
US-09-864-761-16483

```

QY 1 GAACGAAAGGCCTTTCG 18
|||
Db 266 GATGGGAAAGGCCTTTCG 249

```

RESULT 85
US-09-925-065A-848570/c
; Sequence 848570, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 848570
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-848570

```

Query Match	77.9%	Score 14.8;	DB 4;	Length 597;
Best Local Similarity	88.9%	Pred. No. 1.7e+03;		
Matches 16;	Conservative	0;	Mismatches 2;	Indels 0;
				Gaps 0;

QY 2 AACGAAAGGCCTTTTCGG 19
Db 240 AAAGGAAAGGACTTTTCGG 223

```

RESULT 86
US-09-925-065A-848570/c
; Sequence 848570, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of
; TITLE OF INVENTION: Nucleotide Polymorphisms
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 848570
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-848570

```

Query Match 77.9%; Score 14.8; DB 5; Length 597;

Best Local Similarity	88.9%;	Pred. No. 1.7e+03;
Matches	16; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
Qy	2 AACGGAAGGCTTTTCGG	19
Db	240 AAAGGAAGGACTTTTCGG	223

```

RESULT 87
US-09-925-065A-692790
; Sequence 692790, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 692790
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 64
; OTHER INFORMATION: n = A,T,C or G
US-09-925-065A-692790

```

Query Match	77.9%;	Score 14.8;	DB 4;	Length 633;
Best Local Similarity	88.9%;	Pred. No. 1.7e+03;		
Matches 16;	Conservative	0;	Mismatches 2;	Indels 0;
	Gaps	0;		

Qy 1 GAACGGAAGCCTTTCG 18
Db 178 GAATGGAAGGTCTTTCG 195

```

RESULT 88
US-09-925-065A-692790
; Sequence 692790, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0

```

Query Match	77.9%;	Score 14.8;	DB 4;	Length 633;
Best Local Similarity	88.9%;	Pred. No. 1.7e+03;		
Matches 16;	Conservative	0;	Mismatches 2;	Indels 0;
	Gaps	0;		

Qy 1 GAACGGAAGCCTTTCG 18
Db 178 GAATGGAAGGTCTTTCG 195

```
; SEQ ID NO 692790
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 64
; OTHER INFORMATION: n = A,T,C or G
US-09-925-065A-692790

Query Match      77.9%; Score 14.8; DB 5; Length 633;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GAACGGAAGCCCTTCG 18
      ||||| ||||| |||||
Db      178 GAATGGAAGGCTTTTCG 195

RESULT 89
US-09-925-065A-481777
; Sequence 481777, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 481777
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-481777

Query Match      77.9%; Score 14.8; DB 4; Length 654;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 AACGGAAGCCCTTCG 19
      ||||| ||||| |||||
Db      409 AACGGAACGGCCTTTTCAG 426

RESULT 90
US-09-925-065A-481777
; Sequence 481777, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 481777
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-481777

Query Match      77.9%; Score 14.8; DB 4; Length 654;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 AACGGAAGCCCTTCG 19
      ||||| ||||| |||||
Db      409 AACGGAACGGCCTTTTCAG 426

RESULT 91
US-09-925-065A-220788
; Sequence 220788, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 220788
; LENGTH: 658
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-220788

Query Match      77.9%; Score 14.8; DB 4; Length 658;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 AACGGAAGCCCTTCG 19
      ||||| ||||| |||||
Db      621 AACGGAAGGCATTTTGG 638

RESULT 92
US-09-925-065A-220788
; Sequence 220788, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 220788
; LENGTH: 658
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-220788

Query Match      77.9%; Score 14.8; DB 4; Length 658;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 AACGGAAGCCCTTCG 19
      ||||| ||||| |||||
Db      621 AACGGAAGGCATTTTGG 638

RESULT 92
US-09-925-065A-220788
; Sequence 220788, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 220788
; LENGTH: 658
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-220788

Query Match      77.9%; Score 14.8; DB 4; Length 654;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 AACGGAAGCCCTTCG 19
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Db      409 AACGGAACGGCCTTTTCAG 426
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; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 220788
; LENGTH: 658
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-220788

Query Match      77.9%; Score 14.8; DB 5; Length 658;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 AACGGAAAGGCCTTTTCG 19
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Db      621 AACGGAAAGGCATTTCG 638

RESULT 93
US-10-282-122A-15227
; Sequence 15227, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Onisen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15227
; LENGTH: 981
; TYPE: DNA
; ORGANISM: Bordetella pertussis

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US-10-282-122A-15227

Query Match      77.9%; Score 14.8; DB 8; Length 981;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GAACGGAAAGGCCTTTTCG 18
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Db      169 GAACGGAAAGGCATCG 186

RESULT 94
US-11-136-527-2075/c
; Sequence 2075, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2075
; LENGTH: 4591
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-11-136-527-2075

Query Match      77.9%; Score 14.8; DB 16; Length 4591;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GAACGGAAAGGCCTTTTCG 18
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Db      1046 GACTGGAAAGGCCTTCG 1029

RESULT 95
US-10-270-333-106
; Sequence 106, Application US/10270333
; Publication No. US20030092124A1
; GENERAL INFORMATION:
; APPLICANT: Cravchik, Anibal
; TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF AS INSECTICIDAL TARGETS
; FILE REFERENCE: CL000733CON
; CURRENT APPLICATION NUMBER: US/10/270,333
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/168,677
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/175,691
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/191,638
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106
; LENGTH: 7564
; TYPE: DNA
; ORGANISM: Drosophila
; US-10-270-333-106

Query Match      77.9%; Score 14.8; DB 6; Length 7564;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 4458 AACGAAATGCTTCG 4475

RESULT 96

US-11-097-143-19213
; Sequence 19213, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19213
; LENGTH: 7564
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-19213

Query Match 77.9%; Score 14.8; DB 13; Length 7564;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AACGAAAGGCTTCG 19

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Db 4458 AACGAAATGCTTCG 4475

RESULT 97

US-09-764-877-2799
; Sequence 2799, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2799
; LENGTH: 19183
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-2799

Query Match 77.9%; Score 14.8; DB 3; Length 19183;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGAAAGGCTTCG 18

Db 3573 GTACGGAAGGCCTTTG 3590

RESULT 98

US-10-242-515-2799
; Sequence 2799, Application US/10242515
; Publication No. US20040009488A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005C1
; CURRENT APPLICATION NUMBER: US/10/242,515
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/764,877
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2799
; LENGTH: 19183
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-242-515-2799

Query Match 77.9%; Score 14.8; DB 7; Length 19183;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCTTCG 18

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Db 3573 GTACGGAAGGCCTTTG 3590

RESULT 99

US-09-764-869-2314/c
; Sequence 2314, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2314
; LENGTH: 32249
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-869-2314

Query Match 77.9%; Score 14.8; DB 3; Length 32249;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;

Matches	16;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
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Qy 2 AACGGAAGGCCTTTCGG 19

Db 13291 AAAGGAAGGCCATTCCG 13274

RESULT 100

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US-10-091-504-2314/c
; Sequence 2314, Application US/10091504
; Publication No. US20030059908A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007C3
; CURRENT APPLICATION NUMBER: US/10/091,504
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2442
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2314
; LENGTH: 32249
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-091-504-2314

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Query Match 77.9%; Score 14.8; DB 6; Length 32249;

Best Local Similarity 88.9%; Pred. No. 1.8e+03;

Matches	16;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
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QY 2 AACGGAAGGCCTTTCGG 19

Db 13291 AAAGGAAAGGCCATTCCG 13274

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Job time : 774.175 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 03:57:04 ; Search time 11.7892 Seconds
(without alignments)
113.711 Million cell updates/sec

Title: US-10-665-708-24

Perfect score: 19

Sequence: 1 gaacggaagccttcg 19

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 224314 seqs, 35277956 residues

Total number of hits satisfying chosen parameters: 448628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications NA New.*

- 1: /EMC_Celleria_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 2: /EMC_Celleria_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /EMC_Celleria_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /EMC_Celleria_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq.*
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- 7: /EMC_Celleria_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 8: /EMC_Celleria_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	14.4	75.8	2454	7 US-11-217-529-6038	Sequence 6038, Ap
2	14.2	74.7	1950	7 US-11-217-529-77876	Sequence 77876, A
3	13.4	70.5	762	7 US-11-217-529-5130	Sequence 5130, Ap
4	13.4	70.5	814	6 US-10-525-126-124	Sequence 124, App
5	13.4	70.5	11611	6 US-10-541-993-4	Sequence 4, Appli
6	13.2	69.5	471	7 US-11-217-529-77805	Sequence 77805, A
7	13.2	69.5	492	7 US-11-217-529-173378	Sequence 173378, A
8	13.2	69.5	498	7 US-11-217-529-76021	Sequence 76021, A
9	13.2	69.5	1269	7 US-11-217-529-75	Sequence 75, Appl
10	13.2	69.5	3102	7 US-11-217-529-82302	Sequence 82302, A
11	13	68.4	25	7 US-11-217-529-91576	Sequence 91576, A
12	13	68.4	25	7 US-11-217-529-152160	Sequence 152160, A
13	13	68.4	404	6 US-10-488-619-347	Sequence 347, App
14	13	68.4	702	7 US-11-217-529-81537	Sequence 81537, A
15	13	68.4	2853	7 US-11-217-529-76130	Sequence 76130, A
16	12.8	67.4	25	7 US-11-217-529-115745	Sequence 115745, A
17	12.8	67.4	25	7 US-11-217-529-152423	Sequence 152423, A
18	12.8	67.4	617	6 US-10-488-619-1860	Sequence 1860, Ap
19	12.8	67.4	711	6 US-10-488-619-1859	Sequence 1859, Ap
20	12.8	67.4	806	6 US-10-488-619-2939	Sequence 2939, Ap
21	12.8	67.4	1098	7 US-11-217-529-2939	Sequence 5765, Ap
22	12.8	67.4	1242	7 US-11-217-529-75628	Sequence 75628, A
23	12.8	67.4	1260	7 US-11-217-529-5375	Sequence 5375, Ap
24	12.8	67.4	1653	6 US-10-468-193-25	Sequence 25, Appl
25	12.8	67.4	1695	7 US-11-217-529-4098	Sequence 4098, Ap

7	1785	67.4	US-11-217-529-81561	Sequence 81561, A
7	2178	67.4	US-11-217-529-76599	Sequence 76599, A
7	2223	67.4	US-11-217-529-78291	Sequence 78291, A
7	2387	67.4	US-11-226-605-50	Sequence 50, Appl
7	2454	67.4	US-11-217-529-6038	Sequence 6038, Ap
7	2850	67.4	US-11-217-529-79139	Sequence 79139, A
7	2976	67.4	US-11-217-529-80319	Sequence 80319, A
7	3267	67.4	US-11-217-529-79139	Sequence 79139, A
6	7873	67.4	US-10-485-397-7	Sequence 8066, A
6	7943	67.4	US-10-485-397-8	Sequence 8066, A
7	8090	67.4	US-11-226-605-86	Sequence 86, Appl
7	95	66.3	US-11-264-784-222	Sequence 222, App
7	95	66.3	US-11-264-784-223	Sequence 223, App
7	264	66.3	US-11-264-784-246	Sequence 246, App
7	483	66.3	US-11-217-529-174297	Sequence 174297, A
6	587	66.3	US-10-488-619-2986	Sequence 2986, Ap
6	687	66.3	US-10-488-619-2985	Sequence 2985, Ap
7	829	66.3	US-11-252-080-11	Sequence 11, Appl
1	1095	66.3	US-09-949-925-23	Sequence 23, Appl
7	1242	66.3	US-11-217-529-78935	Sequence 78935, A
7	1269	66.3	US-11-264-784-255	Sequence 255, App
7	1270	66.3	US-11-264-784-209	Sequence 209, App
7	1272	66.3	US-11-264-784-48	Sequence 48, Appl
7	1272	66.3	US-11-264-784-263	Sequence 263, App
7	1758	66.3	US-11-217-529-1422	Sequence 1422, Ap
7	1788	66.3	US-11-217-529-182	Sequence 182, App
7	1824	66.3	US-11-217-529-79690	Sequence 79690, A
7	1852	66.3	US-11-264-784-250	Sequence 250, App
7	1898	66.3	US-11-264-784-251	Sequence 251, App
7	1920	66.3	US-11-217-529-1481	Sequence 1481, Ap
6	2208	66.3	US-10-505-928-487	Sequence 487, App
7	2286	66.3	US-11-217-529-728	Sequence 728, App
7	2397	66.3	US-11-217-529-254	Sequence 254, App
6	2883	66.3	US-10-196-749-157	Sequence 157, App
6	3015	66.3	US-11-217-529-76510	Sequence 76510, A
6	3396	66.3	US-10-505-928-346	Sequence 346, App
6	3869	66.3	US-10-511-937-2853	Sequence 2853, Ap
6	4204	66.3	US-10-505-928-188	Sequence 188, App
6	5223	66.3	US-11-217-529-3246	Sequence 3246, Ap
7	7008	66.3	US-11-263-326-98	Sequence 98, Appl
7	7087	66.3	US-11-263-326-104	Sequence 104, App
7	10448	66.3	US-11-024-544-129	Sequence 129, App
7	10448	66.3	US-11-190-750-112	Sequence 112, App
7	10448	66.3	US-11-264-784-123	Sequence 123, App
6	12918	66.3	US-10-501-834-4	Sequence 4, Appli
7	13295	66.3	US-11-264-784-125	Sequence 125, App
7	15543	66.3	US-11-264-784-124	Sequence 124, App
7	16325	66.3	US-11-264-784-127	Sequence 127, App
7	42999	66.3	US-11-284-877-17	Sequence 17, Appl
7	25	65.3	US-11-217-529-103956	Sequence 103956, A
7	108	65.3	US-11-217-529-81840	Sequence 81840, A
6	462	65.3	US-10-488-619-319	Sequence 319, App
6	526	65.3	US-10-488-619-2561	Sequence 2561, App
6	529	65.3	US-10-488-619-1653	Sequence 1653, Ap
6	786	65.3	US-10-488-619-1654	Sequence 1654, Ap
6	927	65.3	US-10-473-173-107	Sequence 107, App
7	1003	65.3	US-11-226-605-7	Sequence 7, Appli
7	1003	65.3	US-11-226-605-11	Sequence 11, Appl
7	1158	65.3	US-11-217-529-79938	Sequence 79938, A
7	1275	65.3	US-11-217-529-76861	Sequence 76861, A
7	1377	65.3	US-11-217-529-4877	Sequence 4877, Ap
7	1695	65.3	US-11-217-529-79055	Sequence 79055, A
7	1731	65.3	US-11-217-529-78343	Sequence 78343, A
7	2646	65.3	US-11-217-529-77238	Sequence 77238, A
7	2871	65.3	US-11-217-529-76779	Sequence 76779, A
7	3669	65.3	US-11-181-115-36	Sequence 36, Appl
7	25	64.2	US-11-217-529-36553	Sequence 36553, A
7	25	64.2	US-11-217-529-48962	Sequence 48962, A
7	25	64.2	US-11-217-529-61824	Sequence 61824, A
7	25	64.2	US-11-217-529-110320	Sequence 110320, A
7	25	64.2	US-11-217-529-132068	Sequence 132068, A
7	390	64.2	US-11-301-554-1419	Sequence 1419, Ap
7	402	64.2	US-11-217-529-173452	Sequence 173452, A

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101	12.2	64.2	573	7	US-11-217-529-81230	Sequence 81230, A	174	11.8	62.1	213	7	US-11-139-257-12	Sequence 12, Appl
102	12.2	64.2	636	7	US-11-217-529-79746	Sequence 79746, A	175	11.8	62.1	279	7	US-11-217-529-1024	Sequence 1024, Ap
C 103	12.2	64.2	858	7	US-11-217-529-1257	Sequence 1257, App	176	11.8	62.1	362	6	US-10-488-619-1084	Sequence 1084, Ap
C 104	12.2	64.2	858	7	US-11-217-529-77141	Sequence 77141, A	177	11.8	62.1	378	7	US-11-301-554-889	Sequence 889, App
C 105	12.2	64.2	883	6	US-10-488-619-2064	Sequence 2064, Ap	178	11.8	62.1	443	7	US-11-301-554-162	Sequence 162, App
C 106	12.2	64.2	906	7	US-11-217-529-2768	Sequence 2768, Ap	179	11.8	62.1	447	6	US-10-473-173-139	Sequence 139, App
C 107	12.2	64.2	918	7	US-11-217-529-5478	Sequence 5478, Ap	180	11.8	62.1	501	7	US-11-217-529-17344	Sequence 17344, A
C 108	12.2	64.2	933	7	US-11-217-529-4222	Sequence 4222, Ap	181	11.8	62.1	505	6	US-10-488-619-96	Sequence 96, Appl
C 109	12.2	64.2	1029	7	US-11-217-529-81270	Sequence 81270, A	182	11.8	62.1	523	6	US-10-488-619-2036	Sequence 2026, Ap
C 110	12.2	64.2	1082	6	US-10-511-937-2916	Sequence 2916, Ap	183	11.8	62.1	581	6	US-10-488-619-2947	Sequence 2947, Ap
C 111	12.2	64.2	1089	7	US-11-217-529-4005	Sequence 4005, Ap	184	11.8	62.1	619	6	US-10-488-619-2110	Sequence 2110, Ap
C 112	12.2	64.2	1143	7	US-11-217-529-3940	Sequence 3940, Ap	185	11.8	62.1	627	6	US-11-217-529-79008	Sequence 79008, A
C 113	12.2	64.2	1155	7	US-11-217-529-999	Sequence 999, App	186	11.8	62.1	630	6	US-10-488-619-1455	Sequence 1455, Ap
C 114	12.2	64.2	1197	7	US-11-217-529-5027	Sequence 5027, App	187	11.8	62.1	658	6	US-10-488-619-2511	Sequence 2511, Ap
C 115	12.2	64.2	1326	7	US-11-217-529-80747	Sequence 80747, A	188	11.8	62.1	669	7	US-11-257-062-37	Sequence 37, Appl
C 116	12.2	64.2	1344	7	US-11-217-529-4610	Sequence 4610, A	189	11.8	62.1	733	6	US-10-488-619-2084	Sequence 2084, Ap
C 117	12.2	64.2	1410	6	US-10-511-937-447	Sequence 447, App	190	11.8	62.1	744	7	US-11-217-529-4512	Sequence 4512, Ap
C 118	12.2	64.2	1422	7	US-11-136-524-69	Sequence 69, Appl	191	11.8	62.1	791	6	US-10-488-619-2086	Sequence 2086, Ap
C 119	12.2	64.2	1473	6	US-10-528-032-6	Sequence 6, Appli	192	11.8	62.1	792	6	US-10-488-619-2510	Sequence 2510, Ap
C 120	12.2	64.2	1565	6	US-10-505-928-93	Sequence 93, Appl	193	11.8	62.1	819	7	US-11-217-529-1255	Sequence 1255, Ap
C 121	12.2	64.2	1594	6	US-10-196-749-183	Sequence 183, App	194	11.8	62.1	861	7	US-11-217-529-2572	Sequence 2572, Ap
C 122	12.2	64.2	1687	6	US-10-528-032-7	Sequence 7, Appli	195	11.8	62.1	921	6	US-10-488-619-948	Sequence 948, App
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C 124	12.2	64.2	1816	6	US-10-528-032-3	Sequence 3, Appli	197	11.8	62.1	948	7	US-11-249-111-60	Sequence 60, Appl
C 125	12.2	64.2	1847	6	US-10-528-032-1	Sequence 1, Appli	198	11.8	62.1	975	7	US-11-217-529-82684	Sequence 82684, A
C 126	12.2	64.2	1869	7	US-11-217-529-78128	Sequence 78128, A	199	11.8	62.1	987	7	US-11-217-529-79848	Sequence 79848, A
C 127	12.2	64.2	1893	7	US-11-217-529-77547	Sequence 77547, A	200	11.8	62.1	996	7	US-11-217-529-490	Sequence 490, App
C 128	12.2	64.2	1950	6	US-10-528-032-4	Sequence 4, Appli	201	11.8	62.1	1003	7	US-11-226-605-56	Sequence 56, Appl
C 129	12.2	64.2	1959	7	US-11-217-529-75971	Sequence 75971, A	202	11.8	62.1	1006	6	US-10-525-126-108	Sequence 108, App
C 130	12.2	64.2	1968	7	US-11-312-958-13	Sequence 13, Appl	203	11.8	62.1	1032	7	US-11-217-529-80676	Sequence 80676, A
C 131	12.2	64.2	1980	7	US-11-217-529-76411	Sequence 76411, A	204	11.8	62.1	1074	7	US-11-217-529-76912	Sequence 76912, A
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C 133	12.2	64.2	2010	7	US-11-217-529-3479	Sequence 3479, Ap	206	11.8	62.1	1134	7	US-11-217-529-81013	Sequence 81013, A
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C 135	12.2	64.2	2079	7	US-11-217-529-76446	Sequence 76446, A	208	11.8	62.1	1197	7	US-11-217-529-1881	Sequence 1881, Ap
C 136	12.2	64.2	2115	7	US-11-217-529-76502	Sequence 76502, A	209	11.8	62.1	1212	7	US-11-217-529-4487	Sequence 4487, Ap
C 137	12.2	64.2	2179	7	US-11-217-529-3141	Sequence 3141, Ap	210	11.8	62.1	1272	7	US-11-217-529-78453	Sequence 78453, A
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C 148	12.2	64.2	4329	7	US-11-217-529-1487	Sequence 1487, Ap	221	11.8	62.1	1790	7	US-11-242-505A-1	Sequence 1, Appli
C 149	12.2	64.2	4773	6	US-10-511-455-1	Sequence 1, Appli	222	11.8	62.1	1809	7	US-11-217-529-174100	Sequence 174100, A
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C 151	12.2	64.2	70665	6	US-10-505-928-596	Sequence 596, App	224	11.8	62.1	1899	7	US-11-217-529-613	Sequence 613, App
C 152	12.2	64.2	135090	6	US-10-505-928-607	Sequence 607, App	225	11.8	62.1	1920	7	US-11-217-529-643	Sequence 643, App
C 153	12.2	64.2	138941	6	US-10-489-730-10	GENERAL INFORMATI	226	11.8	62.1	1931	1	US-09-949-925-78	Sequence 78, Appl
C 154	12.2	64.2	151830	6	US-10-519-335-37	Sequence 37, Appl	227	11.8	62.1	1932	1	US-09-949-925-12	Sequence 12, Appl
C 155	12.2	64.2	394191	6	US-10-506-549-3	Sequence 3, Appli	228	11.8	62.1	2049	7	US-11-217-529-2347	Sequence 2347, Ap
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C 168	11.8	62.1	25	7	US-11-217-529-55803	Sequence 55803, A	241	11.8	62.1	3117	7	US-11-217-529-774	Sequence 774, App
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C 170	11.8	62.1	25	7	US-11-217-529-146321	Sequence 146321, A	243	11.8	62.1	3273	7	US-11-217-529-4879	Sequence 4879, Ap
C 171	11.8	62.1	51	7	US-11-143-642-1319	Sequence 1319, Ap	244	11.8	62.1	3330	7	US-11-217-529-3415	Sequence 3415, Ap

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ALIGNMENTS

RESULT 1
US-11-217-529-6038
; Sequence 6038, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6038
; LENGTH: 2454
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (2284)..(2317)
; OTHER INFORMATION: a, c, g, t, unknown, or other
US-11-217-529-6038

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Best Local Similarity 93.8%; Pred. No. 20;
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US-11-217-529-77876
; Sequence 77876, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77876
; LENGTH: 1950
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77876

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Best Local Similarity 84.2%; Pred. No. 25;
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RESULT 3
US-11-217-529-5130/c
; Sequence 5130, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285

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; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5130
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5130

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Best Local Similarity 93.3%; Pred. No. 59;
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US-10-525-126-124/c
; Sequence 124, Application US/10525126
; Publication No. US20060093596A1
; GENERAL INFORMATION:
; APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
; TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
; FILE REFERENCE: 6899-6/PAR
; CURRENT APPLICATION NUMBER: US/10/525,126
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: PCT/CA03/01323
; PRIOR FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: 60/404,922
; PRIOR FILING DATE: 2002-08-22
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 124
; LENGTH: 814
; TYPE: DNA
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US-10-525-126-124

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Best Local Similarity 93.3%; Pred. No. 60;
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Db 254 AACGGAAGGCCTTT 240

RESULT 5
US-10-541-993-4
; Sequence 4, Application US/10541993
; Publication No. US20060099670A1
; GENERAL INFORMATION:
; APPLICANT: Matsushek, Markus
; APPLICANT: Heinekamp, Thorsten
; APPLICANT: Schmidt, Andre
; APPLICANT: Brakhaage, Axel
; TITLE OF INVENTION: Method for the genetic modification of organisms of the genus
; FILE REFERENCE: 13311-00010-US
; CURRENT APPLICATION NUMBER: US/10/541,993
; CURRENT FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: PCT/EP2004/000100
; PRIOR FILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: DE 103 00 549.4
; PRIOR FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: DE 103 41 272.7
; PRIOR FILING DATE: 2003-09-08

; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 11611
; TYPE: DNA
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Vector
; NAME/KEY: misc feature
; LOCATION: (227)..(227)
; OTHER INFORMATION: n is a, c, g, or t
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; OTHER INFORMATION: n is a, c, g, or t
US-10-541-993-4

Query Match          70.5%; Score 13.4; DB 6; Length 11611;
Best Local Similarity 93.3%; Pred. No. 83;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCTT 15
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RESULT 6
US-11-217-529-77805
; Sequence 77805, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77805
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77805

Query Match          69.5%; Score 13.2; DB 7; Length 471;
Best Local Similarity 83.3%; Pred. No. 72;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACGGAAGGCCTTT 19
Db 156 AACGGAAGGCCTTT 173

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RESULT 7
US-11-217-529-173378
; Sequence 173378, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 173378
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-173378

Query Match      69.5%; Score 13.2; DB 7; Length 492;
Best Local Similarity 83.3%; Pred. No. 72;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCTTTTCG 18
DB 439 GACGGAAGGCCTATTG 456

RESULT 8
US-11-217-529-76021/c
; Sequence 76021, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76021
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76021

Query Match      69.5%; Score 13.2; DB 7; Length 498;
Best Local Similarity 83.3%; Pred. No. 72;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACGGAAGGCCTTTTCG 19
DB 145 AACGGAAGGCCTTTTCG 128

RESULT 9
US-11-217-529-75/c
; Sequence 75, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
```

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; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75

Query Match      69.5%; Score 13.2; DB 7; Length 1269;
Best Local Similarity 83.3%; Pred. No. 81;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACGGAAGGCCTTTTCG 19
DB 507 AAGGGAAGGCCTGTAGG 490

RESULT 10
US-11-217-529-82302
; Sequence 82302, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82302
; LENGTH: 3102
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82302

Query Match      69.5%; Score 13.2; DB 7; Length 3102;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACGGAAGGCCTTTTCG 19
DB 1395 AATGGAATGCCATTTCG 1412

RESULT 11
US-11-217-529-91576
; Sequence 91576, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
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; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 91576
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-91576

Query Match      68.4%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGGAAAGGCCTTT 16
Db 9 CGGAAAGGCCTTT 21

RESULT 12
US-11-217-529-152160
; Sequence 152160, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 152160
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-152160

Query Match      68.4%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ACGGAAAGGCCTT 15
Db 10 ACGGAAAGGCCTT 22

RESULT 13
US-10-488-619-347/c
; Sequence 347, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 347
; LENGTH: 404
; TYPE: DNA
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(404)
; OTHER INFORMATION: n is g, c, a or t
US-10-488-619-347

Query Match      68.4%; Score 13; DB 6; Length 404;
Best Local Similarity 92.9%; Pred. No. 90;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGAAGGCCTTCG 18
Db 235 GGAAGGCCTTCG 222

RESULT 14
US-11-217-529-81537
; Sequence 81537, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81537
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-81537

Query Match      68.4%; Score 13; DB 7; Length 702;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ACGGAAAGGCCTT 15
Db 332 ACGGAAAGGCCTT 344

RESULT 15
US-11-217-529-76130
; Sequence 76130, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76130
; LENGTH: 2853
; TYPE: DNA
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; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76130

Query Match      68.4%; Score 13; DB 7; Length 2853;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CGGAAGGCTTTT 16
Db 2501 CGGAAGGCTTTT 2513

RESULT 16
US-11-217-529-115745/c
; Sequence 115745, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 115745
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-115745

Query Match      67.4%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ACGGAAGGCTTTCG 18
Db 16 ACGGAAGGCTTTCG 1

RESULT 17
US-11-217-529-152423/c
; Sequence 152423, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 152423
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-152423

Query Match      67.4%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTTT 16
Db 18 GAATGCAAGGCTTTT 3

RESULT 18
US-10-488-619-1860/c
; Sequence 1860, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1860
; LENGTH: 617
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1860

Query Match      67.4%; Score 12.8; DB 6; Length 617;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTTT 16
Db 582 GAAAAGAAAGGCTTTT 567

RESULT 19
US-10-488-619-1859
; Sequence 1859, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1859
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1859

Query Match      67.4%; Score 12.8; DB 6; Length 711;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTTT 16
Db 647 GAAAAGAAAGGCTTTT 662

RESULT 20
US-10-488-619-2939/c
; Sequence 2939, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619

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Query Match 67.4%; Score 12.8; DB 6; Length 1653;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CGGAAAGCGCTTTCGG 19
| | | | | | | | | |
Db 1582 CGGTAGACCTTTCGG 1567

RESULT 25
US-11-217-529-4098
; Sequence 4098, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4098
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; NAME/KEY: modified base
; LOCATION: (794)..(862)
; OTHER INFORMATION: a, c, g, t, unknown, or other
US-11-217-529-4098

Query Match 67.4%; Score 12.8; DB 7; Length 1695;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCGCTTT 16
| | | | | | | | | |
Db 939 GAACGGAAGCGCTTT 954

RESULT 26
US-11-217-529-81561/c
; Sequence 81561, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81561
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-81561

Query Match 67.4%; Score 12.8; DB 7; Length 1785;

Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCGCTTT 16
| | | | | | | | | |
Db 1369 GAATGCAAGCGCTTT 1354

RESULT 27
US-11-217-529-76599/c
; Sequence 76599, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76599
; LENGTH: 2178
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76599

Query Match 67.4%; Score 12.8; DB 7; Length 2178;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ACGGAAAGCGCTTTCG 18
| | | | | | | | | |
Db 249 ACTGAAAGCGCTGTCG 234

RESULT 28
US-11-217-529-78291/c
; Sequence 78291, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78291
; LENGTH: 2223
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78291

Query Match 67.4%; Score 12.8; DB 7; Length 2223;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ACGGAAAGCGCTTTCG 18
| | | | | | | | | |

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Db      1838 ACGAAAGCTTTTCG 1823

RESULT 29
US-11-226-605-50/c
; Sequence 50, Application US/11226605
; Publication No. US2006008859A1
; GENERAL INFORMATION:
; APPLICANT: Hosted, Thomas
; APPLICANT: Walker, Scott
; APPLICANT: Bayne, Marvin
; TITLE OF INVENTION: REPORTER ASSAY SCREENS FOR PROTEIN TARGETS IN SACCHAROMYCES CEREVISIAE
; FILE REFERENCE: IN06198US01
; CURRENT APPLICATION NUMBER: US/11/226,605
; CURRENT FILING DATE: 2005-09-14
; PRIOR APPLICATION NUMBER: 60/609940
; PRIOR FILING DATE: 2004-09-15
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 2387
; TYPE: DNA
; ORGANISM: Photinus pyralis
US-11-226-605-50

Query Match      67.4%; Score 12.8; DB 7; Length 2387;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 CGGAAGGCTTTTCG 19
      ||||| ||||| |||
Db      2180 CGGTAAGACCTTTTCG 2165

RESULT 30
US-11-217-529-6038/c
; Sequence 6038, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6038
; LENGTH: 2454
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (2284)..(2317)
; OTHER INFORMATION: a, c, g, t, unknown, or other
US-11-217-529-6038

Query Match      67.4%; Score 12.8; DB 7; Length 2454;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 AACGAAAGGCTTTTC 17
      ||||| ||||| |||
Db      1041 AAGAGAAAGGCTTTTC 1026

RESULT 31
```

```
US-11-217-529-79139/c
; Sequence 79139, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79139
; LENGTH: 2850
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79139

Query Match      67.4%; Score 12.8; DB 7; Length 2850;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GAACGAAAGGCTTTT 16
      ||||| ||||| |||
Db      375 GAACGTAAAGGCAATT 360

RESULT 32
US-11-217-529-80319/c
; Sequence 80319, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80319
; LENGTH: 2976
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-80319

Query Match      67.4%; Score 12.8; DB 7; Length 2976;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 ACGAAAGGCTTTTCG 18
      ||||| ||||| |||
Db      1487 ACAGAACGCGCTTTTCG 1472

RESULT 33
US-11-217-529-78066/c
; Sequence 78066, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
```

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; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78066
; LENGTH: 3267
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78066

Query Match      67.4%; Score 12.8; DB 7; Length 3267;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GAACGGAAGGCCTTT 16
Db      438 GTATGGAAGGCCTTT 423

RESULT 34
US-10-485-397-7/c
; Sequence 7, Application US/10485397
; Publication No. US20060099673A1
; GENERAL INFORMATION:
; APPLICANT: ALTANA Pharma AG
; TITLE OF INVENTION: Novel Recombinant Gene Expression Method
; FILE REFERENCE: B697USPC101
; CURRENT APPLICATION NUMBER: US/10/485,397
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 7873
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: pGFPstopneo is a circular Plasmid DNA
US-10-485-397-7

Query Match      67.4%; Score 12.8; DB 6; Length 7873;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 CGGAAAGGCCTTTCCG 19
Db      2575 CGGTAAGACCTTTCCG 2560

RESULT 35
US-10-485-397-8/c
; Sequence 8, Application US/10485397
; Publication No. US20060099673A1
; GENERAL INFORMATION:
; APPLICANT: ALTANA Pharma AG
; TITLE OF INVENTION: Novel Recombinant Gene Expression Method
; FILE REFERENCE: B697USPC101
; CURRENT APPLICATION NUMBER: US/10/485,397
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 7943
; TYPE: DNA
; ORGANISM: Artificial

```

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; FEATURE:
; OTHER INFORMATION: pGFPstopneoSECIS is a circular Plasmid DNA
US-10-485-397-8

Query Match      67.4%; Score 12.8; DB 6; Length 7943;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 CGGAAAGGCCTTTCCG 19
Db      2575 CGGTAAGACCTTTCCG 2560

RESULT 36
US-11-226-605-86/c
; Sequence 86, Application US/11226605
; Publication No. US20060088859A1
; GENERAL INFORMATION:
; APPLICANT: Hosted, Thomas
; APPLICANT: Walker, Scott
; APPLICANT: Bayne, Marvin
; TITLE OF INVENTION: REPORTER ASSAY SCREENS FOR PROTEIN TARGETS IN SACCHAROMYCES CEREVISIAE
; FILE REFERENCE: IN06198US01
; CURRENT APPLICATION NUMBER: US/11/226,605
; CURRENT FILING DATE: 2005-09-14
; PRIOR APPLICATION NUMBER: 60/609940
; PRIOR FILING DATE: 2004-09-15
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86
; LENGTH: 8090
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pSPRT50
US-11-226-605-86

Query Match      67.4%; Score 12.8; DB 7; Length 8090;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 CGGAAAGGCCTTTCCG 19
Db      1650 CGGTAAGACCTTTCCG 1635

RESULT 37
US-11-264-784-222/c
; Sequence 222, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Danude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quilin
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 222
; LENGTH: 95
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

```

OTHER INFORMATION: Primer D8-7A
US-11-264-784-222

Query Match 66.3%; Score 12.6; DB 7; Length 95;
Best Local Similarity 78.9%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCCTTTCGG 19
||||| ||||| ||||| |||||
Db 41 GAACGAAATGAGCTTTCGG 23

RESULT 38

US-11-264-784-223
; Sequence 223, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 223
; LENGTH: 95
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer D8-7B
US-11-264-784-223

Query Match 66.3%; Score 12.6; DB 7; Length 95;
Best Local Similarity 78.9%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCCTTTCGG 19
||||| ||||| ||||| |||||
Db 59 GAACGAAATGAGCTTTCGG 77

RESULT 39

US-11-264-784-246/c
; Sequence 246, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: Patentin version 3.3

SEQ ID NO 246
LENGTH: 264
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: 264 bp XhoI/SacI fragment of pT8 (7-9)
US-11-264-784-246

Query Match 66.3%; Score 12.6; DB 7; Length 264;
Best Local Similarity 78.9%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCCTTTCGG 19
||||| ||||| ||||| |||||
Db 37 GAACGAAATGAGCTTTCGG 19

RESULT 40

US-11-217-529-174297/c
; Sequence 174297, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIRO
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIRO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 174297
; LENGTH: 483
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (433)..(433)
; OTHER INFORMATION: a, c, g, t, unknown, or other
US-11-217-529-174297

Query Match 66.3%; Score 12.6; DB 7; Length 483;
Best Local Similarity 78.9%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCCTTTCGG 19
||||| ||||| ||||| |||||
Db 478 GAACGGAAAGCCTTTCGG 460

RESULT 41

US-10-488-619-2986
; Sequence 2986, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2986
; LENGTH: 587
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2986

Query Match 66.3%; Score 12.6; DB 6; Length 587;
 Best Local Similarity 78.9%; Pred. No. 1.6e+02;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGCCCTTCGG 19
 DB 433 GAACAGAAAGGTCTCTCAG 451

RESULT 42
 US-10-488-619-2985/c
 ; Sequence 2985, Application US/10488619
 ; Publication No. US20060099578A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Greenlee, Winner and Sullivan, P.C.
 ; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
 ; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
 ; FILE REFERENCE: 98-01 WO
 ; CURRENT APPLICATION NUMBER: US/10/488,619
 ; CURRENT FILING DATE: 2004-03-01
 ; NUMBER OF SEQ ID NOS: 3040
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2985
 ; LENGTH: 687
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(687)
 ; OTHER INFORMATION: n is g, c, a or t
 US-10-488-619-2985

Query Match 66.3%; Score 12.6; DB 6; Length 637;
 Best Local Similarity 78.9%; Pred. No. 1.6e+02;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGCCCTTCGG 19
 DB 505 GAACAGAAAGGTCTCTCAG 487

RESULT 43
 US-11-252-080-11/c
 ; Sequence 11, Application US/11252080
 ; Publication No. US20060090217A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Texas A&M University
 ; TITLE OF INVENTION: ISOLATION OF SUGARCANE PROTEINS INVOLVED IN POSTTRANSCRIPTIONAL G
 ; TITLE OF INVENTION: SILENCING AND METHODS OF USE
 ; FILE REFERENCE: 017575.0693 (TAMUS 1743)
 ; CURRENT APPLICATION NUMBER: US/11/252,080
 ; CURRENT FILING DATE: 2005-10-17
 ; PRIOR APPLICATION NUMBER: US/10/226,715
 ; PRIOR FILING DATE: 2002-08-23
 ; PRIOR APPLICATION NUMBER: 60/314863
 ; PRIOR FILING DATE: 2001-08-24
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 11
 ; LENGTH: 829
 ; TYPE: DNA
 ; ORGANISM: Saccharum hybrid cultivar Cp72-1210
 US-11-252-080-11

Query Match 66.3%; Score 12.6; DB 7; Length 829;
 Best Local Similarity 78.9%; Pred. No. 1.6e+02;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGCCCTTCGG 19
 DB 588 GAAGGGAACCCCTTTTGG 570

RESULT 44
 US-09-949-925-23/c
 ; Sequence 23, Application US/09949925
 ; Publication No. US20060099575A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 67 Human secreted proteins
 ; FILE REFERENCE: P2023P2
 ; CURRENT APPLICATION NUMBER: US/09/949,925
 ; CURRENT FILING DATE: 2001-09-12
 ; PRIOR APPLICATION NUMBER: US 60/232,150
 ; PRIOR FILING DATE: 2000-12-09
 ; PRIOR APPLICATION NUMBER: PCT/US99/01621
 ; PRIOR FILING DATE: 1999-01-27
 ; PRIOR APPLICATION NUMBER: US 60/073,160
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: US 60/073,159
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: US 60/073,165
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: US 60/073,164
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: US 60/073,167
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: US 60/073,162
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: US 60/073,161
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: US 60/073,170
 ; PRIOR FILING DATE: 1998-01-30
 ; NUMBER OF SEQ ID NOS: 298
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 23
 ; LENGTH: 1095
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (720)
 ; OTHER INFORMATION: n equals a,t,g, or c
 US-09-949-925-23

Query Match 66.3%; Score 12.6; DB 1; Length 1095;
 Best Local Similarity 78.9%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGCCCTTCGG 19
 DB 516 GAACAGAAAGGTTCGG 498

RESULT 45
 US-11-217-529-78935
 ; Sequence 78935, Application US/11217529
 ; Publication No. US20060099612A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUNTORY LIMITED
 ; APPLICANT: NAKAO, YOSHITIRO
 ; APPLICANT: NAKAMURA, NORIHISA
 ; APPLICANT: KODAMA, YUKIKO
 ; APPLICANT: FUJIMURA, TOMOKO
 ; APPLICANT: ASHIKARI, TOSHIHIKO
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 ; FILE REFERENCE: S-38-285
 ; CURRENT APPLICATION NUMBER: US/11/217,529
 ; CURRENT FILING DATE: 2005-09-02
 ; PRIOR APPLICATION NUMBER: US 10/932,182
 ; PRIOR FILING DATE: 2004-09-02
 ; NUMBER OF SEQ ID NOS: 197023
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 78935
 ; LENGTH: 1242


```
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78935

Query Match      66.3%; Score 12.6; DB 7; Length 1242;
Best Local Similarity 78.9%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTCGG 19
Db 65 GAACAGTAAGGCTTTTGG 83

RESULT 46
US-11-264-784-255/c
; Sequence 255, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 255
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D8S-3: synthetic delta 8-desaturase gene codon-optimized for
; OTHER INFORMATION: Yarrowia lipolytica in pDMW261
US-11-264-784-255

Query Match      66.3%; Score 12.6; DB 7; Length 1269;
Best Local Similarity 78.9%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTCGG 19
Db 675 GAACGGAAGGCGCTTTCGG 657

RESULT 47
US-11-264-784-209/c
; Sequence 209, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; ;

; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 209
; LENGTH: 1270
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D8S-1: Synthetic gene codon-optimized for expression in Yarrowia
; OTHER INFORMATION: lipolytica
US-11-264-784-209

Query Match      66.3%; Score 12.6; DB 7; Length 1270;
Best Local Similarity 78.9%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTCGG 19
Db 668 GAACGGAAGGCGCTTTCGG 650

RESULT 48
US-11-264-784-48/c
; Sequence 48, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 48
; LENGTH: 1272
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D8SF: synthetic delta-8 desaturase (codon-optimized for Yarrowia
; OTHER INFORMATION: lipolytica)
US-11-264-784-48

Query Match      66.3%; Score 12.6; DB 7; Length 1272;
Best Local Similarity 78.9%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTCGG 19
Db 676 GAACGGAAGGCGCTTTCGG 658

RESULT 49
US-11-264-784-263/c
; Sequence 263, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
```

; APPLICANT: Yadav, Narendra S.
 ; APPLICANT: Zhang, Hongxiang
 ; APPLICANT: Zhu, Quinn
 ; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
 ; FILE REFERENCE: CL3136 USNA
 ; CURRENT APPLICATION NUMBER: US/11/264,784
 ; CURRENT FILING DATE: 2005-11-01
 ; NUMBER OF SEQ ID NOS: 375
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 263
 ; LENGTH: 1272
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: chimeric gene
 US-11-264-784-263

Query Match 66.3%; Score 12.6; DB 7; Length 1272;
 Best Local Similarity 78.9%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTCGG 19
 ||||| ||||| ||||| ||||| |||||
 Db 676 GAACGGAAGGCTTCGG 658

RESULT 50
 US-11-217-529-1422/c
 ; Sequence 1422, Application US/11217529
 ; Publication No. US20060099612A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUNTORY LIMITED
 ; APPLICANT: NAKAO, YOSHIHIRO
 ; APPLICANT: NAKAMURA, NORIHISA
 ; APPLICANT: KODAMA, YUKIKO
 ; APPLICANT: FUJIMURA, TOMOKO
 ; APPLICANT: ASHIKARI, TOSHIHIKO
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 ; FILE REFERENCE: S-38-285
 ; CURRENT APPLICATION NUMBER: US/11/217,529
 ; CURRENT FILING DATE: 2005-09-02
 ; PRIOR FILING DATE: 2004-09-02
 ; NUMBER OF SEQ ID NOS: 197023
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 1422
 ; LENGTH: 1758
 ; TYPE: DNA
 ; ORGANISM: Saccharomyces pastorianus
 US-11-217-529-1422

Query Match 66.3%; Score 12.6; DB 7; Length 1758;
 Best Local Similarity 78.9%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTCGG 19
 ||||| ||||| ||||| ||||| |||||
 Db 285 GAACGGAAGGCTTCGG 267

RESULT 51
 US-11-217-529-182/c
 ; Sequence 182, Application US/11217529
 ; Publication No. US20060099612A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUNTORY LIMITED
 ; APPLICANT: NAKAO, YOSHIHIRO
 ; APPLICANT: NAKAMURA, NORIHISA
 ; APPLICANT: KODAMA, YUKIKO
 ; APPLICANT: FUJIMURA, TOMOKO
 ; APPLICANT: ASHIKARI, TOSHIHIKO
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 ; FILE REFERENCE: S-38-285

; CURRENT APPLICATION NUMBER: US/11/217,529
 ; CURRENT FILING DATE: 2005-09-02
 ; PRIOR FILING DATE: 2004-09-02
 ; NUMBER OF SEQ ID NOS: 197023
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 182
 ; LENGTH: 1788
 ; TYPE: DNA
 ; ORGANISM: Saccharomyces pastorianus
 US-11-217-529-182

Query Match 66.3%; Score 12.6; DB 7; Length 1788;
 Best Local Similarity 78.9%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTCGG 19
 ||||| ||||| ||||| ||||| |||||
 Db 1493 GAACGGAAGGCTTCGG 1475

RESULT 52
 US-11-217-529-79690/c
 ; Sequence 79690, Application US/11217529
 ; Publication No. US20060099612A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUNTORY LIMITED
 ; APPLICANT: NAKAO, YOSHIHIRO
 ; APPLICANT: NAKAMURA, NORIHISA
 ; APPLICANT: KODAMA, YUKIKO
 ; APPLICANT: FUJIMURA, TOMOKO
 ; APPLICANT: ASHIKARI, TOSHIHIKO
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 ; FILE REFERENCE: S-38-285
 ; CURRENT APPLICATION NUMBER: US/11/217,529
 ; CURRENT FILING DATE: 2005-09-02
 ; PRIOR FILING DATE: 2004-09-02
 ; NUMBER OF SEQ ID NOS: 197023
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 79690
 ; LENGTH: 1824
 ; TYPE: DNA
 ; ORGANISM: Saccharomyces pastorianus
 US-11-217-529-79690

Query Match 66.3%; Score 12.6; DB 7; Length 1824;
 Best Local Similarity 78.9%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTCGG 19
 ||||| ||||| ||||| ||||| |||||
 Db 746 GAACGGAAGGCTTCGG 728

RESULT 53
 US-11-264-784-250/c
 ; Sequence 250, Application US/11264784
 ; Publication No. US20060094092A1
 ; GENERAL INFORMATION:
 ; APPLICANT: E.I. duPont de Nemours & Co., Inc.
 ; APPLICANT: Damude, Howard Glenn
 ; APPLICANT: Gillies, Peter John
 ; APPLICANT: Macool, Daniel Joseph
 ; APPLICANT: Picataggio, Stephen K.
 ; APPLICANT: Pollak, Dana M. Walters
 ; APPLICANT: Ragghianti, James John
 ; APPLICANT: Xue, Zhixiong
 ; APPLICANT: Yadav, Narendra S.
 ; APPLICANT: Zhang, Hongxiang
 ; APPLICANT: Zhu, Quinn
 ; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
 ; FILE REFERENCE: CL3136 USNA

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; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 250
; LENGTH: 1852
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric DBS-1::XPR gene
US-11-264-784-250

Query Match          66.3%; Score 12.6; DB 7; Length 1852;
Best Local Similarity 78.9%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GAACGGAAAGCCTTCGG 19
      ||||| ||||| |||||
Db      1080 GAACGTAAGAGCTTCGG 1062

RESULT 54
US-11-264-784-251/c
; Sequence 251, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 251
; LENGTH: 1898
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric DBS-2::XPR gene
US-11-264-784-251

Query Match          66.3%; Score 12.6; DB 7; Length 1898;
Best Local Similarity 78.9%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GAACGGAAAGCCTTCGG 19
      ||||| ||||| |||||
Db      1080 GAACGTAAGAGCTTCGG 1062

RESULT 55
US-11-217-529-1481
; Sequence 1481, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285

US-11-217-529-1481
; Sequence 1481, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285

; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1481
; LENGTH: 1920
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1481

Query Match          66.3%; Score 12.6; DB 7; Length 1920;
Best Local Similarity 78.9%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GAACGGAAAGCCTTCGG 19
      ||||| ||||| |||||
Db      1210 GAACGAAAGACTCTCGG 1228

RESULT 56
US-10-505-928-487/c
; Sequence 487, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 487
; LENGTH: 2208
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-487

Query Match          66.3%; Score 12.6; DB 6; Length 2208;
Best Local Similarity 78.9%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GAACGGAAAGCCTTCGG 19
      ||||| ||||| |||||
Db      760 GAACGGAAAGGACATTGG 742

RESULT 57
US-11-217-529-728/c
; Sequence 728, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 728
; LENGTH: 2286
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
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; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: Patentin 3.2
; SEQ ID NO 346
; LENGTH: 3396
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-346

Query Match      66.3%; Score 12.6; DB 6; Length 3396;
Best Local Similarity 78.9%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCCTTTCCG 19
Db 182 GAAATGAAGGCATTACG 164

RESULT 62
US-10-511-937-2853
; Sequence 2853, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlseuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: US/10/511,937
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2853
; LENGTH: 3869
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-2853

Query Match      66.3%; Score 12.6; DB 6; Length 3869;
Best Local Similarity 78.9%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCCTTTCCG 19
Db 2166 GAAGGAAAGTCCATTACG 2184

RESULT 63
US-10-505-928-188
; Sequence 188, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US/10/505,928
; PRIOR FILING DATE: 2002-03-07
; SOFTWARE: Patentin 3.2
; SEQ ID NO 98
; LENGTH: 7008
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-188

Query Match      66.3%; Score 12.6; DB 6; Length 4204;
Best Local Similarity 78.9%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCCTTTCCG 19
Db 692 GAAGGAAAGCCTGTCTG 710

RESULT 64
US-11-217-529-3246
; Sequence 3246, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIRO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT FILING DATE: 2005-09-02
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 3246
; LENGTH: 5223
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3246

Query Match      66.3%; Score 12.6; DB 7; Length 5223;
Best Local Similarity 78.9%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCCTTTCCG 19
Db 324 GATCGGAAATGCGTTTGG 342

RESULT 65
US-11-263-326-98
; Sequence 98, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulley, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US/11/263,326
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 98
; LENGTH: 7008
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-263-326-98

```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-263-326-98

Query Match          66.3%; Score 12.6; DB 7; Length 7008;
Best Local Similarity 78.9%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCCTTTCGG 19
Db 1750 GAGAGGAGGCCTTTCGG 1768

RESULT 66
US-11-263-326-104
; Sequence 104, Application US/11263326
; Publication No. US2006009306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulley, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 104
; LENGTH: 7008
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-263-326-104

Query Match          66.3%; Score 12.6; DB 7; Length 7008;
Best Local Similarity 78.9%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCCTTTCGG 19
Db 1750 GAGAGGAGGCCTTTCGG 1768

RESULT 67
US-11-024-544A-129/c
; Sequence 129, Application US/11024544A
; Publication No. US20060094086A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Yadav, Narendra
; APPLICANT: Xue, Zhixiong
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: DIACYLGLYCEROL ACYLTRANSFERASES FOR ALTERATION OF POLYUNSATURATED
; FILE REFERENCE: CL2717
; CURRENT APPLICATION NUMBER: US/11/024,544A
; CURRENT FILING DATE: 2004-12-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 129
; LENGTH: 10448
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pK02UM26E
US-11-024-544A-129

Query Match          66.3%; Score 12.6; DB 7; Length 10448;
```

```
Best Local Similarity 78.9%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCCTTTCGG 19
Db 1648 GAACTGAATGAGCTTTCGG 1630

RESULT 68
US-11-190-750-112/c
; Sequence 112, Application US/11190750
; Publication No. US20060094088A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Yadav, Narendra
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: ACYLTRANSFERASE REGULATION TO INCREASE THE PERCENT OF
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN TOTAL LIPIDS AND OILS OF
; FILE REFERENCE: CL2718
; CURRENT APPLICATION NUMBER: US/11/190,750
; CURRENT FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 112
; LENGTH: 10448
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pK02UM26E
US-11-190-750-112

Query Match          66.3%; Score 12.6; DB 7; Length 10448;
Best Local Similarity 78.9%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCCTTTCGG 19
Db 1648 GAACTGAATGAGCTTTCGG 1630

RESULT 69
US-11-264-784-123/c
; Sequence 123, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 123
; LENGTH: 10448
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pDMW297
US-11-264-784-123

Query Match          66.3%; Score 12.6; DB 7; Length 10448;
```

```
Best Local Similarity 78.9%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTCGG 19
Db 1648 GAACTGAATGAGCTTTCGG 1630

RESULT 70
US-10-501-834-4/c
; Sequence 4, Application US/10501834
; Publication No. US2006008828A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Peter C., Ward, Christopher J., Rossetti, Sandro, and Torres,
; APPLICANT: Vicente E.
; TITLE OF INVENTION: Polycystic Kidney Disease Nucleic Acids
; FILE REFERENCE: 07039/386U81
; CURRENT APPLICATION NUMBER: US/10/501,834
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: PCT/US03/02038
; PRIOR FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: 60/351,110
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 12918
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-501-834-4

Query Match 66.3%; Score 12.6; DB 6; Length 12918;
Best Local Similarity 78.9%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTCGG 19
Db 3212 GAACGCAAGGCGCTGACGG 3194

RESULT 71
US-11-264-784-125
; Sequence 125, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 125
; LENGTH: 13295
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pDW314
; FEATURE:
; OTHER INFORMATION: Plasmid pDW314
; NAME/KEY: misc feature
; LOCATION: (10915)..(10918)
; OTHER INFORMATION: n is a, c, g, or t
```

```
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10923)..(10923)
; OTHER INFORMATION: n is a, c, g, or t
US-11-264-784-125

Query Match 66.3%; Score 12.6; DB 7; Length 13295;
Best Local Similarity 78.9%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTCGG 19
Db 3610 GAACTGAATGAGCTTTCGG 3628

RESULT 72
US-11-264-784-124
; Sequence 124, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 124
; LENGTH: 15543
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pZP2C16M899
US-11-264-784-124

Query Match 66.3%; Score 12.6; DB 7; Length 15543;
Best Local Similarity 78.9%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTCGG 19
Db 11264 GAACTGAATGAGCTTTCGG 11282

RESULT 73
US-11-264-784-127
; Sequence 127, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
```

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; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 127
; LENGTH: 16325
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pzKSL5598
US-11-264-784-127

Query Match          66.3%; Score 12.6; DB 7; Length 16325;
Best Local Similarity 78.9%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 GAACGGAAGGCCTTCGG 19
Db      14743 GAACGGAAGGCCTTCGG 14761

RESULT 74
US-11-284-877-17/c
; Sequence 17, Application US/11284877
; Publication No. US20060095984A1
; GENERAL INFORMATION:
; APPLICANT: Hadlaczky, Gyula
; Szalay, Aladar
; TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND METHODS
; FOR PREPARING ARTIFICIAL CHROMOSOMES
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 12390 El Camino Real
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92130
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/284,877
; FILING DATE: 21-Nov-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 10/808,689
; FILING DATE: 24-MAR-2004
; APPLICATION NUMBER: 10/219,694
; FILING DATE: 14-AUG-2002
; APPLICATION NUMBER: 10/151,081
; FILING DATE: 16-MAY-2002
; APPLICATION NUMBER: 10/151,078
; FILING DATE: 16-MAY-2002
; APPLICATION NUMBER: 10/125,767
; FILING DATE: 17-APR-2002
; APPLICATION NUMBER: 10/287,313
; FILING DATE: 01-NOV-2002
; APPLICATION NUMBER: 09/799,462
; FILING DATE: 05-MAR-2001
; APPLICATION NUMBER: 09/724,872
; FILING DATE: 28-NOV-2000
; APPLICATION NUMBER: 09/724,726
; FILING DATE: 28-NOV-2000
; APPLICATION NUMBER: 09/724,693
; FILING DATE: 28-NOV-2000
; APPLICATION NUMBER: 08/835,682
; FILING DATE: 10-APR-1997
; APPLICATION NUMBER: 08/695,191
; FILING DATE: 07-AUG-1996
; APPLICATION NUMBER: 08/682,080
; FILING DATE: 15-JUL-1996

; APPLICATION NUMBER: 08/629,822
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 17084-004018/402Q
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-678-4777
; TELEFAX: 202-626-7796
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42999 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-11-284-877-17

Query Match          66.3%; Score 12.6; DB 7; Length 42999;
Best Local Similarity 78.9%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 GAACGGAAGGCCTTCGG 19
Db      17125 GAACGGAAGGCCTTCGG 17107

RESULT 75
US-11-217-529-103956/c
; Sequence 103956, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHITIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 103956
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-103956

Query Match          65.3%; Score 12.4; DB 7; Length 25;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 ACGGAAGGCCTTT 16
Db      19 ACGGAAGGCATTT 6

RESULT 76
US-11-217-529-81840
; Sequence 81840, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
```



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; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 137023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81840
; LENGTH: 108
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-11-217-529-81840

Query Match      65.3%; Score 12.4; DB 7; Length 108;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 GAAAGGCGCTTTTCGG 19
      ||||| |||||
Db      72 GAAAGGCGCTTTTCGG 85

RESULT 77
US-10-488-619-319/c
; Sequence 319, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 319
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(462)
; OTHER INFORMATION: n is g, c, a or t
US-10-488-619-319

Query Match      65.3%; Score 12.4; DB 6; Length 462;
Best Local Similarity 92.9%; Pred. No. 1.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 GAAAGGCGCTTTTCGG 19
      ||||| |||||
Db      92 GAAAGGCGCTTTTCGG 79

RESULT 78
US-10-488-619-2561/c
; Sequence 2561, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
```

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; SEQ ID NO 2561
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2561

Query Match      65.3%; Score 12.4; DB 6; Length 526;
Best Local Similarity 92.9%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GAACGGAAGGCCT 14
      ||||| |||||
Db      216 GAACGGAAGGCCT 203

RESULT 79
US-10-488-619-1653/c
; Sequence 1653, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1653
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1653

Query Match      65.3%; Score 12.4; DB 6; Length 529;
Best Local Similarity 92.9%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 CGGAAAGGCCTTTC 17
      ||||| |||||
Db      356 CGGACAGGCCTTTC 343

RESULT 80
US-10-488-619-1654
; Sequence 1654, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1654
; LENGTH: 786
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(786)
; OTHER INFORMATION: n is a, c, g, or t
US-10-488-619-1654

Query Match      65.3%; Score 12.4; DB 6; Length 786;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 CGGAAAGGCCTTTC 17
      ||||| |||||
Db      407 CGGACAGGCCTTTC 420
```

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; CURRENT APPLICATION NUMBER: US/11/226,605
; CURRENT FILING DATE: 2005-09-14
; PRIOR APPLICATION NUMBER: 60/609940
; PRIOR FILING DATE: 2004-09-15
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1003
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-11-226-605-11

Query Match      65.3%; Score 12.4; DB 7; Length 1003;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3  ACGGAAGGCCTT 16
        |||||
Db      897  ACGGAAGGCCTT 884

RESULT 84
US-11-217-529-79938
; Sequence 79938, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79938
; LENGTH: 1158
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79938

Query Match      65.3%; Score 12.4; DB 7; Length 1158;
Best Local Similarity 92.9%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2  ACGGAAGGCCTT 15
        |||||
Db      775  ACGGAAGGCCTT 788

RESULT 85
US-11-217-529-76861/c
; Sequence 76861, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1003
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-11-226-605-7

Query Match      65.3%; Score 12.4; DB 7; Length 1003;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3  ACGGAAGGCCTT 16
        |||||
Db      897  ACGGAAGGCCTT 884

RESULT 83
US-11-226-605-11/c
; Sequence 11, Application US/11226605
; Publication No. US2006008859A1
; GENERAL INFORMATION:
; APPLICANT: Hosted, Thomas
; APPLICANT: Walker, Scott
; APPLICANT: Bayne, Marvin
; TITLE OF INVENTION: REPORTER ASSAY SCREENS FOR PROTEIN TARGETS IN SACCHAROMYCES CEREVISIAE
; FILE REFERENCE: IN06198U501
; CURRENT APPLICATION NUMBER: US/11/226,605
; CURRENT FILING DATE: 2005-09-14
; PRIOR APPLICATION NUMBER: 60/609940
; PRIOR FILING DATE: 2004-09-15
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1003
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-11-226-605-7

Query Match      65.3%; Score 12.4; DB 7; Length 1003;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3  ACGGAAGGCCTT 16
        |||||
Db      897  ACGGAAGGCCTT 884

RESULT 81
US-10-473-173-107/c
; Sequence 107, Application US/10473173
; Publication No. US2006008823A1
; GENERAL INFORMATION:
; APPLICANT: VAN ANDEL INSTITUTE
; TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
; TITLE OF INVENTION: Carcinoma: Prognosis and Drug Target Identification
; FILE REFERENCE: 38145-170094
; CURRENT APPLICATION NUMBER: US/10/473,173
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/279,411
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 498
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 107
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-473-173-107

Query Match      65.3%; Score 12.4; DB 6; Length 927;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  GAACGGAAGGCCT 14
        |||||
Db      558  GAACGGAAGGCCT 545

RESULT 82
US-11-226-605-7/c
; Sequence 7, Application US/11226605
; Publication No. US2006008859A1
; GENERAL INFORMATION:
; APPLICANT: Hosted, Thomas
; APPLICANT: Walker, Scott
; APPLICANT: Bayne, Marvin
; TITLE OF INVENTION: REPORTER ASSAY SCREENS FOR PROTEIN TARGETS IN SACCHAROMYCES CEREVISIAE
; FILE REFERENCE: IN06198U501
; CURRENT APPLICATION NUMBER: US/11/226,605
; CURRENT FILING DATE: 2005-09-14
; PRIOR APPLICATION NUMBER: 60/609940
; PRIOR FILING DATE: 2004-09-15
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1003
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-11-226-605-7
```

```
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76861
; LENGTH: 1275
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76861

Query Match          65.3%; Score 12.4; DB 7; Length 1275;
Best Local Similarity 92.9%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5  GGAAGGCGCTTTCG 18
Db      599  GGAAGGCGATTCG 586
          ||||| |||||
          ||||| |||||

RESULT 86
US-11-217-529-4877/c
; Sequence 4877, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4877
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4877

Query Match          65.3%; Score 12.4; DB 7; Length 1377;
Best Local Similarity 92.9%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2  AACGGAAGCGCTT 15
Db      81  AACGAAAGCGCTT 68
          ||||| |||||
          ||||| |||||

RESULT 87
US-11-217-529-79055
; Sequence 79055, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79055
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79055

Query Match          65.3%; Score 12.4; DB 7; Length 1695;
Best Local Similarity 92.9%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2  AACGGAAGCGCTT 15
Db      1468  AACGGAAGGCTCTT 1481
          ||||| |||||
          ||||| |||||

RESULT 88
US-11-217-529-78343
; Sequence 78343, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78343
; LENGTH: 1731
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78343

Query Match          65.3%; Score 12.4; DB 7; Length 1731;
Best Local Similarity 92.9%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5  GGAAGGCGCTTTCG 18
Db      901  GGAAGGCTCTTCG 914
          ||||| |||||
          ||||| |||||

RESULT 89
US-11-217-529-77238/c
; Sequence 77238, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77238
; LENGTH: 2646
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77238

Query Match          65.3%; Score 12.4; DB 7; Length 2646;
Best Local Similarity 92.9%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 3 ACGGAAAGGCCTT 16
Db 2161 ACGGAAAGGCATTT 2148

RESULT 90
US-11-217-529-76779/c
; Sequence 76779, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76779
; LENGTH: 2871
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76779

Query Match 65.3%; Score 12.4; DB 7; Length 2871;
Best Local Similarity 92.9%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCT 14
Db 1185 GAACGGAAGGCCT 1172

RESULT 91
US-11-181-115-36
; Sequence 36, Application US/11181115
; Publication No. US20060088511A1
; GENERAL INFORMATION:
; APPLICANT: Dana Farber Cancer Center
; TITLE OF INVENTION: Cancer Therapy Sensitizer
; FILE REFERENCE: 7032/2072
; CURRENT APPLICATION NUMBER: US/11/181,115
; CURRENT FILING DATE: 2005-07-14
; PRIOR APPLICATION NUMBER: PCT/US04/000901
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,009
; PRIOR FILING DATE: 2003-01-14
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 3669
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-181-115-36

Query Match 65.3%; Score 12.4; DB 7; Length 3669;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ACGGAAAGGCCTTT 16
Db 2485 ACGGAAAGGCCTTT 2498

RESULT 92
US-11-217-529-36553/c
; Sequence 36553, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36553
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-36553

Query Match 64.2%; Score 12.2; DB 7; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ACGGAAAGGCCTTCG 18
Db 19 AACTGAAAGGCCCTCCG 3

RESULT 93
US-11-217-529-48962/c
; Sequence 48962, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 48962
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-48962

Query Match 64.2%; Score 12.2; DB 7; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ACGGAAAGGCCTTCGG 19
Db 25 ACGGAAAGGCCTTCAGG 9

RESULT 94
US-11-217-529-61824/c
; Sequence 61824, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
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; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61824
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-61824

Query Match          64.2%; Score 12.2; DB 7; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ACGGAAAGCGCTTTTCG 19
Db 23 ACAGATAGCGCTTTTGG 7

RESULT 95
US-11-217-529-110320
; Sequence 110320, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 110320
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-110320

Query Match          64.2%; Score 12.2; DB 7; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACGGAAGCGCTTTTCG 18
Db 9 AACGGAAGCGCGTGC 25

RESULT 96
US-11-217-529-132068
; Sequence 132068, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

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; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 132068
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-132068

Query Match          64.2%; Score 12.2; DB 7; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ACGGAAAGCGCTTTTCG 19
Db 7 ACGGAGAGCGCTTGGCG 23

RESULT 97
US-11-301-554-1419
; Sequence 1419, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1419
; LENGTH: 390
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-301-554-1419

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Query Match 64.2%; Score 12.2; DB 7; Length 390;
Best Local Similarity 82.4%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCTTTC 17
|||||
DB 67 GAAAGGAAGTGCTTTC 83

RESULT 98

US-11-217-529-173452
; Sequence 173452, Application US/11217529
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 173452
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-173452

Query Match 64.2%; Score 12.2; DB 7; Length 402;
Best Local Similarity 82.4%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACGGAAGGCCTTCG 18
|||||
DB 45 AACGGAAGGATTTAG 61

RESULT 99

US-10-488-619-466/c
; Sequence 466, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 466
; LENGTH: 410
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(410)
; OTHER INFORMATION: n is g, c, a or t
US-10-488-619-466

Query Match 64.2%; Score 12.2; DB 6; Length 410;
Best Local Similarity 82.4%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCTTTC 17
|||||

Db 184 GAACGGAACGCCTGTC 168

RESULT 100

US-10-488-619-319
; Sequence 319, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 319
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(462)
; OTHER INFORMATION: n is g, c, a or t
US-10-488-619-319

Query Match 64.2%; Score 12.2; DB 6; Length 462;
Best Local Similarity 82.4%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCTTTC 17
|||||
DB 76 GACCCCAAGGCCTTTC 92

Search completed: May 19, 2006, 05:38:22
Job time : 13.7892 secs

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